CIRCULATING TUMOR DNA IN THE CANCER CARE CONTINUUM

by

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ABSTRACT

Circulating tumor DNA (ctDNA) analysis has become a valuable tool for the investigation of cancer biomarkers in both early- and late-stage scenarios. To evaluate the utility of ctDNA as a biomarker of response in patients with advanced lung cancer, we have developed an ultrasensitive measure of cell-free tumor load using targeted and whole genome sequencing approaches to assess responses to tyrosine kinase inhibitors. Analyses of patients treated with anti-EGFR or HER2 therapies revealed a bimodal distribution of ctDNA after therapy initiation, with molecular responders having nearly complete elimination of ctDNA (>98%). Molecular non-responders displayed limited changes in ctDNA levels post-treatment and experienced significantly shorter progression-free survival (median 1.6 vs. 13.7 months, $P < 0.0001$) which was detected on average four weeks earlier than CT imaging. To further explore the role of ctDNA as a biomarker for minimal residual disease, we have developed an approach to identify ctDNA alterations through ultrasensitive targeted sequencing analyses of matched cell-free DNA (cfDNA) and white blood cells from the same patient. Liquid biopsy analyses of 50 patients with resectable gastric cancer with available blood samples from multiple time points revealed that 52% of alterations in cfDNA were derived from the matched white blood cells. After filtering blood cell alterations from cfDNA, we found that the presence of ctDNA can predict recurrence when analyzed within nine weeks after preoperative treatment (median 18.4 months vs. median not reached, $P = 0.012$) and after surgery (median 18.7 months vs. median not reached, $P < 0.001$) in patients with gastric cancer eligible for multimodal treatment. We further developed a novel approach to evaluate genome-wide fragmentation patterns of cfDNA in patients with early-stage cancers. We applied this method to analyze fragmentation profiles of 236 patients with breast, colorectal, lung, ovarian, pancreatic, gastric, or bile duct cancers and 245 healthy individuals. A machine learning model incorporating genome-wide fragmentation features had sensitivities of detection ranging from 57% to >99% among the seven cancer types at 98% specificity. Fragmentation profiles could be used to identify

the tissue of origin of the cancers to a limited number of sites in 75% of cases. These observations highlight the utility of ctDNA as a broadly applicable approach for treatment monitoring, screening, and, early detection of human cancer.

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CHAPTER 1:

INTRODUCTION

Worldwide, over nine million cancer deaths were expected in 2018 alone (1). In the same global report, the International Agency for Research on Cancer from the World Health Organization states that the total number of individuals who were alive within five years of a cancer diagnosis was estimated to be 44 million. In parallel to these alarming cancer burden statistics, efforts on cancer genome characterization are transforming our understanding of tumor biology at an unprecedented level (2, 3), opening new venues for early detection and more efficient disease monitoring strategies. From that perspective, a variety of genomic approaches applied to tumor specimens have leveraged the development of biomarkers for cancer detection and prediction of treatment response (4). However, tumor tissue availability for molecular profiling usually requires invasive procedures that are prone to iatrogenic complications and inconvenient for serial assessment of tumor evolution. In the past few years, the development of noninvasive liquid biopsy approaches based on the ctDNA analysis has helped to circumvent some of the downsides associated with tissue processing and analysis (5), but there is still a long way to go in order to fully validate ctDNA assessment in the clinical setting.

The earliest evidence of increased cfDNA amounts in patients with cancer as well as the effect of therapy on its levels was demonstrated over 40 years ago (6). More recently, next-generation sequencing-based technologies, in combination with computational methods, has allowed the interrogation of cancer-specific genomic abnormalities at a broader set of applications than previously possible (7-15). Interestingly, these seminal ctDNA analyses have also enabled further assessment of intratumor heterogeneity along with the detection of subclonal alterations and the characterization of distinct genomic signatures (15-18). Either through direct detection of ctDNA or through analyses guided by tumor tissue sequencing, these approaches can be applied to response assessment in patients with late-stage cancers receiving systemic therapies, detection of minimal residual disease after curative surgery, and even noninvasive direct detection of solid tumors at very early stages.

We first assessed the utility of liquid biopsy approaches to evaluate early noninvasive detection of response to targeted therapy in patients with advanced non-small cell lung cancer (19). Overall, therapeutic efficacy of targeted therapies has been limited by incomplete pharmacological suppression of tumors or through the selection of resistance mutations in subclonal populations of tumor cells. Disease monitoring using computed tomography (CT) imaging is the current clinical practice for assessing response to targeted therapy, yet this approach does not fully represent the molecular and pathologic changes occurring in tumors during therapy. Repeat tissue biopsies of accessible cancer lesions have been used to provide insights into therapeutic decision-making but rarely capture the complexity of intra- and inter-tumoral heterogeneity and are invasive procedures with potential complications. Theoretically, the ability to noninvasively track specific clonal populations of tumor cells over time has the potential to rapidly and dynamically inform therapy sequence and combinatorial strategies. However, there are currently no approved or clinically recognized noninvasive molecularly defined strategies to assess early drug responsiveness or adaptive resistance in cancer patients before radiographic progression. A variety of studies have focused on changes in ctDNA during the course of therapy, but have largely focused on the analysis of specific or limited number of alterations that may only represent specific subclones of the tumor (9, 20-28). More recent studies have used panels of commonly mutated driver genes to allow detection of multiple driver clones, typically at the time of diagnosis (8, 14, 15, 18, 29). However, no study has yet assessed the clinical value of a comprehensive genome-wide analysis of ctDNA alterations to evaluate tumor burden at very early timepoints following commencement of targeted therapy.

We hypothesized that kinetic changes in the amount of DNA released from tumor cells may occur within hours to days of treatment administration. In this study, we used an ultrasensitive liquid biopsy approach to evaluate patients with advanced non-small cell lung cancer who had tumor responses or progression on tyrosine kinase inhibitors, including erlotinib, a first-generation

inhibitor of the epidermal growth factor receptor (EGFR), afatinib, a second-generation inhibitor of EGFR and erb-b2 receptor tyrosine kinase 2 (ERBB2) (30-32), as well as osimertinib and mavelertinib, third-generation tyrosine kinase inhibitors targeting EGFR with activating and resistance (T790M) mutations (33, 34). These analyses investigated whether rapid changes and the overall levels in the amounts of ctDNA can serve as real-time and predictive biomarkers of patient outcome to a targeted cancer therapy.

Through our analyses of liquid biopsies for treatment response assessment in patients with advanced lung cancer, we speculated that ctDNA dynamics could be a useful approach to predict treatment benefit in patients with resectable cancer receiving preoperative chemotherapy followed by surgery. However, blood-based deep sequencing approaches of multiples genes have raised concerns about detection and misclassification of white blood cell (WBC) derived variants in cfDNA associated with clonal hematopoiesis of indeterminate potential (CHIP) (15, 35-37). We then assessed the value of matched white blood cell and cell-free DNA analyses for detection response and minimal residual disease in patients with resectable gastric cancer (38). A major challenge after multimodal curative treatment for resectable gastric cancer is identifying patients with microscopic residual disease at high risk of recurrence after surgery (39-42). Currently available imaging techniques and traditional blood biomarkers to capture minimal residual disease (MRD) state after surgery have poor sensitivity and do not play a role in clinical practice (43). Histopathological assessment of the effects of neoadjuvant chemotherapy on resection specimens has become an important tool to provide prognostic information (44-46). However, microscopic residual tumor, lymph node infiltration, and poor histopathological response do not measure the real-time presence of residual disease. More recent approaches such as detection of ctDNA through liquid biopsies may provide new opportunities for identifying patients that would benefit from adjuvant treatment options and further follow-up (47).

Theoretically, the ability to non-invasively detect tumor-specific alterations in the circulation after neoadjuvant chemotherapy and surgery has the potential to rapidly and dynamically inform the presence of minimal residual disease. Cell-free ctDNA is released from tumor cells into the circulation and has been detected in patients with early and late stage cancers (13-15, 48-50). A key challenge of liquid biopsy approaches has been developing methods to detect and characterize small amounts of ctDNA in large populations of cfDNA. A variety of studies have focused on changes in ctDNA during the course of therapy, but mostly in the setting of metastatic disease and largely centered on the analysis of a limited number of genomic positions that may only represent a subset of clones of the tumor (9, 20-25, 51, 52). More recent studies have used panels of commonly mutated driver genes to allow detection of multiple driver clones, typically at the time of diagnosis, after surgery, or at disease progression (8, 12, 14, 15, 18, 19, 29, 51, 53). To date, no study has longitudinally assessed the value of deep sequencing matched white blood cells and cfDNA from the same patient to filter WBC alterations and identify high-probability tumor-specific cfDNA variants.

In this second study, we applied a matched cfDNA and WBC sequencing approach to accurately detect ctDNA alterations after preoperative chemotherapy and after surgery in patients with resectable gastric cancer. We hypothesized that ctDNA detection after completion of preoperative treatment as well as minimal residual disease detection after surgery can predict recurrence and survival in patients with resectable gastric cancer treated with multimodal therapeutic regimens. Overall, these analyses evaluated a new strategy to distinguish ctDNA alterations from cfDNA variants related to clonal hematopoiesis and investigated whether ctDNA elimination before or after surgery can serve as a predictive biomarker of patient outcome to perioperative treatment.

We finally extended our liquid biopsy analyses to explore patterns of genome-wide cfDNA fragmentation in healthy individuals and patients with early- and late-stage cancers. Analyses of alterations in cfDNA have largely focused on targeted sequencing of specific genes. Such studies

permit detection of a small number of tumor-specific alterations in patients with cancer but not all patients, especially those with early stage disease, have detectable changes (13, 15, 54). Whole genome sequencing of cfDNA can identify chromosomal abnormalities in cancer patients but detecting such alterations may be challenging due to the difficulty in distinguishing a small number of abnormal from normal chromosomal changes (9, 24, 55-57). Analyses of the size of cfDNA fragments have suggested that patients with cancer may have abnormal cfDNA, but these observations have been contradictory, indicating both increases (58-63) as well as decreases in the overall distribution of cfDNA (57, 64-66). Recent studies have suggested that size selection of small cfDNA can increase enrichment of mutations and somatic copy number alterations in late-stage cancer patients (64). Nucleosome positions (65, 67), cfDNA patterns near transcription start sites (67, 68), and the end positions of cfDNA molecules (69) may differ between cancer and normal tissues but the sequencing needed for nucleosome footprint evaluation of cfDNA is impractical for routine analyses. Conceptually, the sensitivity of any cfDNA approach depends on the number of alterations examined as well as the technical and biologic limitations of detecting such changes. As a typical blood sample contains ~2000 genome equivalents of cfDNA per milliliter of plasma (15), the theoretical limit of detection of a single alteration can be no better than one in a few thousand mutant to wild-type molecules.

In this third study, we hypothesized that an approach to detect a larger number of alterations in the same number of genome equivalents may be more sensitive for detecting cancer in the circulation. We developed an approach based on low coverage whole genome sequencing called DELFI (DNA Evaluation of Fragments for early Interception), that allows simultaneous evaluation of a large number of abnormalities in cfDNA through genome-wide analysis of fragmentation patterns. The results of DELFI analyses highlight important properties of cfDNA and provide a facile approach for screening, early detection, and monitoring of human cancer.

CHAPTER 2:

EARLY NONINVASIVE DETECTION OF RESPONSE TO TARGETED THERAPY IN NON-SMALL CELL LUNG CANCER

METHODS

Study Design

In this proof-of-principle retrospective study, we assessed serial blood draws from 28 advanced NSCLC patients undergoing treatment with targeted TKIs to directly detect somatic sequence and structural alterations in cfDNA, monitor ctDNA dynamics during therapy, determine cell-free tumor burden, and predict clinical outcome (Figure 2.1). Liquid biopsies were obtained immediately prior to treatment (baseline) and at serial timepoints until disease progression. This cohort included 12 patients with RECIST 1.1 partial response, 8 with stable disease, 5 with progressive disease, and 3 with unmeasurable disease but who derived clinical benefit. We used the ultrasensitive targeted error correction sequencing (TEC-Seq) approach (15) as well as whole genome sequencing to identify tumor-derived sequence alterations and chromosomal copy number changes in cfDNA. We evaluated the dynamics of alterations identified and developed a noninvasive measure of cfTL to evaluate real-time response to treatment. We analyzed changes in cfTL within hours to days after treatment compared to baseline and assessed whether cfTL could serve as a marker of patient outcome.

Patient and sample characteristics

Twenty-eight patients with metastatic non-small cell lung cancer undergoing treatment with TKIs at University of California San Diego or Johns Hopkins University were included in our study. Clinical and pathological characteristics for all patients are summarized in Tables 2.1 and 2.2, and tumor load dynamics are shown in Figure 2.2 and 2.3. Patient enrollment and genomic studies were conducted in accordance with the Declaration of Helsinki, were approved by the Institutional Review Board (IRB) and patients provided written informed consent for sample acquisition for research purposes.

The response evaluation criteria in solid tumors (RECIST) version 1.1 (70) were used for assessment of response. Of these 28 patients, twenty eventually experienced disease progression while eight continue to derive clinical benefit from targeted inhibition (Table 2.1).

For all patients, serial blood draws were collected over the course of treatment with targeted inhibition for isolation of plasma and extraction of cfDNA for genomic analyses. Timepoints were analyzed immediately prior to treatment for baseline assessment as well as at serial intervals until disease progression (Table 2.2).

Sample preparation and next-generation sequencing of cfDNA

Whole blood was collected in K2 EDTA tubes or Streck tubes and processed immediately or within 2 hours after storage at 4°C for EDTA tubes or room temperature for Streck tubes, respectively. Plasma and cellular components were separated by centrifugation at 800g for 10 minutes at 4°C. Plasma was centrifuged a second time at 18,000g at room temperature to remove any remaining cellular debris and stored at -80°C until the time of DNA extraction. DNA was isolated from plasma using the Qiagen Circulating Nucleic Acids Kit (Qiagen GmbH) and eluted in LoBind tubes (Eppendorf AG). Concentration and quality of cfDNA was assessed using the Bioanalyzer 2100 (Agilent Technologies).

TEC-Seq next-generation sequencing cell-free DNA libraries were prepared from 11 to 350 ng of cfDNA. Genomic libraries were prepared as previously described (15). Briefly, the NEBNext DNA Library Prep Kit for Illumina [New England Biolabs (NEB)] was used with four main modifications to the manufacturer's guidelines: i) The library purification steps utilized the on-bead Ampure XP approach, ii) reagent volumes were adjusted accordingly to accommodate the on-bead strategy, iii) a pool of 8 unique Illumina dual index adapters with 8 bp barcodes were used in the ligation reaction, and iv) cfDNA libraries were amplified with Hotstart Phusion Polymerase. Genomic library preparation was performed as previously described (15). Concentration and

quality of cfDNA genomic libraries were assessed using the Bioanalyzer 2100 (Agilent Technologies).

Targeted capture was performed using the Agilent SureSelect reagents and a custom set of hybridization probes targeting 58 genes (Table 2.3) per the manufacturer's guidelines. The captured library was amplified with HotStart Phusion Polymerase (NEB). The concentration and quality of captured cfDNA libraries was assessed on the Bioanalyzer (Agilent Technologies). TEC-seq libraries were sequenced using 100-bp paired end runs on the Illumina HiSeq 2500 (Illumina).

Primary processing of next-generation sequencing data and identification of putative somatic mutations

Primary processing of next-generation sequence data for analyses of sequence alterations in cfDNA samples was performed as previously described (15). Briefly, Illumina CASAVA (Consensus Assessment of Sequence and Variation) software (version 1.8) was used for demultiplexing and masking of dual index adapter sequences. Sequence reads were aligned against the human reference genome (hg19) using NovoAlign with additional realignment of select regions using the Needleman-Wunsch method (Table 2.4) (71).

Candidate somatic mutations, consisting of point mutations, small insertions, and deletions were identified using VariantDx (71) across the targeted regions of interest as previously described (Table 2.5) (15). Briefly, an alteration was considered a candidate somatic mutation only when: (i) Three distinct paired reads contained the mutation in the plasma and the number of distinct paired reads containing a particular mutation in the plasma was at least 0.1% of the total distinct read pairs; or (ii) Four distinct paired reads contained the mutation in the plasma and the number of distinct paired reads containing a particular mutation in the plasma was at least 0.05% and less than 0.1% of the total distinct read pairs; (iii) the mismatched base was not present in >1% of the reads in a panel of unmatched normal samples as well as not present in a custom database of common

germline variants derived from dbSNP; (iv) the altered base did not arise from misplaced genome alignments including paralogous sequences; and (v) the mutation fell within a protein coding region and was classified as a missense, nonsense, frameshift, or splice site alteration.

Candidate alterations were defined as somatic hotspots if the nucleotide change and amino acid change were identical to an alteration observed in ≥ 20 cancer cases reported in the COSMIC database. Alterations that were not hotspots were retained only if either (i) seven or more distinct paired reads contained the mutation in the plasma and the number of distinct paired reads containing a particular mutation in the plasma was at least 0.1% and less than 0.2%, of the total distinct read pairs, or (ii) six or more distinct paired reads contained the mutation in the plasma and the number of distinct paired reads containing a particular mutation in the plasma was at least 0.2% of the total distinct read pairs. In order to track clonal changes over time, any alteration identified in at least one blood draw was assessed in the remaining timepoints.

Common germline variants were identified and removed if present in ≥ 25% of reads or < 25% of reads if the variant was recurrent and the majority of alterations at that position had a mutant allele fraction ≥ 25%. Variants known to be at a somatic hotspot position or producing a truncating mutation in a tumor suppressor gene were not excluded as germline changes. Because of the high frequency of mutations in specific genes and the possible confounding between somatic and germline changes, we limited analyses in the APC gene to frameshift or nonsense mutations, and in KRAS, HRAS and NRAS to positions to 12, 13, 61, and 146. Finally, we excluded hematopoietic expansion related variants that have been previously described (35-37, 72, 73), including those in DNMT3A, IDH1, and IDH2 and specific alterations within ATM, GNAS, JAK2, or TP53 (Table 2.6).

Primary processing of next-generation sequence data for analyses of copy number alterations in cfDNA samples was performed as follows: Bam files were preprocessed by successively running

CleanSam and MarkDuplicates from Picard Tools version 2.9.0. (http://broadinstitute.github.io/picard). Sequence reads were aligned against the human reference genome (hg19) using NovoAlign.

Candidate somatic structural variants were identified through analyses of low-coverage whole-genome sequencing data obtained from off-target reads mapping outside of the targeted capture of 58 cancer driver genes (Table 2.3) in areas of the genome farther than 1000 base pairs from the start or end of a targeted region. Off-target reads were divided into 100kb bins with the exception of filtered bins i) with less than 10kb due to spacing of target regions, ii) having GC content less than 30% or greater than 70%, iii) where 25% fell within the ENCODE Duke Excluded Regions Track (http://genome.ucsc.edu/cgi-bin/hgFileUi?db=hg19&g=wgEncode Mapability). The total number of unique reads mapping to each bin were counted to exclude filtered regions:

$$s_b = log_2\left(\frac{100000}{x_b - f_b} \cdot r_b\right)$$

where r_b is the number of unique reads mapped to bin b, x_b is the length of bin b, and f_b is the number of filtered base pairs within bin b, and the normalized score, s_b, was assigned to each bin. To remove GC-bias and normalize for sequencing depth we used LOESS smoothing to predict a bin's normalized score from the bin-specific GC content. The GC-corrected score for each bin, $\widetilde{s_b}$, is defined for bin b by subtracting the predicted score from s_b and exponentiating this using base 2. We summed the GC-corrected scores for each chromosome arm. The summed score for a given chromosome arm was divided by the summed score using all bins to calculate the percentage of genomic representation.

Z scores were calculated as previously described (9) for each chromosome arm for each timepoint and patient assessed to determine areas of genome over or under representation. PA scores were calculated as previously described (9) for each timepoint for each patient assessed in order to

concisely represent the aneuploidy observed in each sample by using the five chromosomes arms with the largest absolute z scores (Table 2.7). PA scores higher than the threshold score of 2.4 provide a specificity greater than 90% (Student t distribution, three degrees of freedom) for the presence of aneuploid circulating tumor DNA.

Cell-free tumor load

We directly detected sequence and copy number alterations in cfDNA for each patient at each timepoint analyzed and used a tiered approach to evaluate tumor burden. For patients with detectable sequence alterations, the mutant allele fraction of the most abundant alteration in a clone targeted by the TKI was used as readout of cfTL. In patients without detectable sequence alterations, we evaluated the PA score as a binary readout of cfTL where a score above 2.4 indicated aneuploidy and evidence of tumor burden and a score below 2.4 indicated normal ploidy and the absence of detectable tumor burden in plasma.

Changes in cfTL were evaluated to compare tumor burden at baseline and at other timepoints during treatment using quantitative assessment of cfTL mutant allele fractions for patients with detectable sequence clones and qualitative assessment of change from aneuploidy to normal ploidy representing a complete response for patients without detectable sequence clones.

Statistical analysis

Significance was determined using a variety of methods. To assess the significance of reduction in cfTL, in the number of sequence mutations detected, and reduction in PA scores in patients with radiographic response or stable disease versus patients with no radiographic response post treatment we used the Wilcoxon signed rank test. The significance of newly emerging mutations in six of eight patients within the same day after initiation of therapy were evaluated by comparison to emerging alterations in two patients detected at earlier timepoints within 188 days prior to

therapy. The rates of emerging mutations in the presence (within 4-12 hours) and absence of selective pressure of therapy were compared using a Gamma-Poisson Bayesian model. A Gamma (1, 100) prior was used for both mutation rates. Reported rates were based on the posterior mean and 99% posterior credible intervals (CI). We compared progression-free survival in ctDNA responders versus ctDNA non-responders as well as in RECIST subgroups (partial response, stable disease, and progressive disease) using the Mantel-Cox log-rank test. Paired t test was used to assess the difference in the time to response assessment post therapy based on ctDNA analyses versus RECIST.

RESULTS

Overall approach

As a proof of concept, we evaluated cell-free DNA (cfDNA) from 28 patients with advanced non-small cell lung cancer. Of the twenty-eight patients, nine were initially diagnosed with stage IA, IIA, or IIIA disease, and the remaining presented with metastatic disease at initial diagnosis (Table 2.1). Prior to these analyses, patients received treatment with anti-EGFR agents (n=20), platinum-based chemotherapy (n=11), or immune checkpoint inhibitors (n=1) (Table 2.1). Nine patients initially treated with first- or second-generation EGFR TKIs developed the EGFR T790M resistance mutation and were subsequently treated with third generation EGFR TKIs (Table 2.1). We performed liquid biopsy analyses during treatment with targeted therapies, including osimertinib (n=15), afatinib (n=5), mavelertinib (n=5), or erlotinib (n=3) (Supplementary Table S1).

Tumor response for these patients was determined using response evaluation criteria in solid tumors (RECIST) version 1.1 (70). Of the 28 patients analyzed, 12 achieved a partial response based on their initial CT assessment after treatment initiation, while eight patients exhibited stable disease, and five developed progressive disease (Table 2.1). One patient with limited miliary metastases in the lungs and two with exclusive bone lesions were classified as having unmeasurable disease (Table 2.1).

For each patient, ~5 ml of plasma were collected immediately prior to therapy (baseline), at a median time of 19 days after therapy initiation, and at additional serial timepoints until disease progression was confirmed by radiographic assessment (Tables 2.1 and 2.2). To analyze changes in cfDNA in these patients and capture the clonal heterogeneity of metastatic disease, we developed a combined comprehensive approach for analysis of both sequence and chromosomal changes. For sequence analyses, we used our recently developed targeted error correction sequencing (TEC-Seq)

approach to evaluate 58 well-known cancer driver genes (Figure 2.1 and Tables 2.3, 2.4, and 2.5) (15). This method is based on targeted capture and deep sequencing (>30,000x) of DNA fragments to provide a high degree of specificity across 80,930 bp of coding gene regions and enables identification of tumor-specific alterations in ctDNA while distinguishing these from amplification and sequencing artifacts, germline changes, or alterations related to blood cell proliferation that may be present in cfDNA (15). To evaluate chromosomal changes that may be present in ctDNA, we used whole genome sequences obtained from off-target fragments that were not captured during analysis of targeted regions in manner similar to other genome wide copy number analyses, including Digital Karyotyping and related NGS approaches (9, 11, 74). The most aberrant alterations in the genome representation of individual chromosome arms were used to construct a plasma aneuploidy score (PA-Score) that was evaluated to detect changes in ctDNA during therapy (Table 2.7).

Dynamics of cell-free tumor load

We evaluated ctDNA in all patients at baseline (pre-treatment) and after the initiation of therapy. In the blood draws that were analyzed, we detected sequence alterations in 24 of 28 cases. At the baseline timepoint, patients had an average of 3.2 tumor-specific somatic mutations, affecting 16 driver genes, ranging from one to 14 alterations per case (Table 2.5). Of 24 patients with detectable sequence alterations, 23 had at least one targetable mutation in either *EGFR* or *ERBB2*, with ctDNA mutant allele fractions ranging from 0.10% to 53.71% (Table 2.5). Nine out of the 15 patients treated with osimertinib had *EGFR* T790M acquired resistance mutations in the circulation at baseline, with ctDNA mutant allele fractions ranging from 0.13% to 10.09% (Table 2.5), consistent with their previous treatment with EGFR TKIs (Table 2.1). Previously described alterations in genes involved in blood cell proliferation (35-37, 72, 73) were observed in 18 patients across all timepoints analyzed, and were removed from further analyses (Table 2.6). For a subset of patients, we analyzed chromosomal changes, and detected abnormalities in 13 of 15 cases analyzed. In most

patients, multiple chromosomal arms were aberrant (Figures 2.2 and 2.3 and Table 2.7), resulting in PA-Scores ranging from 1.3 to 14.9 at the baseline blood sample. Through our combined analyses we identified either a tumor-derived sequence or chromosomal change or both types of alterations in 25 of 28 cases.

Based on the alterations observed in cfDNA through analyses of multiple genes, we developed a new metric, termed cell-free tumor load (cfTL), which is defined as the contribution of the most abundant alterations in cfDNA at any particular timepoint during the course of tumor evolution (Figure 2.1 and Tables 2.5 and 2.7). In this study, the most abundant alterations were typically in driver genes targeted by the TKIs utilized (e.g., *EGFR* and *ERBB2*). We used a tiered approach to evaluate ctDNA levels, first using cfTL levels based on sequence changes, and then PA-Scores based on chromosomal changes if sequence alterations were not present. This approach has the benefit of providing a comprehensive assessment of tumor-derived alterations that would represent overall tumor burden during the course of disease and selective pressure of therapeutic interventions.

All patients with an initial objective radiographic response to targeted therapy displayed dramatic reduction of cfTL with mutant allele concentrations reduced from an average of 10.80% at baseline to 0.18% at a median time of 19 days after treatment initiation (>95% decrease, P<0.001, Wilcoxon signed rank test) (Figures 2.2, 2.3, and 2.4, and Table 2.1). Fig. 2 depicts a representative patient with metastatic disease (CGPLLU12) who had a rapid decline of cfTL from baseline to day 10 after initiation of osimertinib. This patient exhibited a progression-free survival of 7.0 months, then subsequently developed resistance in the primary lung lesion. In patients with radiographic stable disease, mutant allele concentrations were reduced from an average of 2.24% at baseline to 1.04% after treatment initiation (Figure 2.4 A, Table 2.5) ($P = 0.03$, Wilcoxon signed rank test). Likewise, PA-Scores decreased in responders (average decrease of 92%, $P = 0.002$, Wilcoxon signed rank test), including in patient CGPLLU97 who had no sequence alterations detected in the plasma

(Figure 2.5). In contrast, all five patients with radiographic progressive disease experienced limited variation in cfTL, as measured through both sequence and chromosomal alterations, ranging from an average mutant allele fraction of 14.23% at baseline to 11.84% after initiation of therapy (Figures 2.2, 2.3, 2.4 A, and 2.5) ($P = 0.6$, Wilcoxon signed rank test).

In addition to changes in cfTL, the average number of observed alterations also decreased in responders from 3.6 to 1.1 mutations per patient ($P < 0.01$, Wilcoxon signed rank test), while patients with stable or progressive disease had no significant change in the number of mutations observed during therapy (Figure 2.4 B). Clinical NGS testing performed to identify alterations in tumor tissue or plasma during the care of these patients independently confirmed 79.2% of the changes detected in our study (Figure 2.6). These observations suggest that both ctDNA levels and clonal heterogeneity are dramatically reduced at early timepoints in responding patients due to therapeutic selective pressure, and in non-responding patients the emergence and growth of tumor subclones can be detected earlier than radiographic progression.

Analysis of cfDNA within hours of therapy

For a subset of patients, we evaluated multiple follow-up blood draws at extremely early timepoints in therapy. An immediate timepoint within the same day at 4-12 hours after the initiation of the first dose of treatment was available for five patients who experienced a radiographic partial response on the first or second scan (CGPLLU12, CGPLLU14, CGPLLU86, CGPLLU99, and CGLU344), two clinical responders classified with non-measurable disease (CGLU315 and CGLU373), and one patient with progressive disease (CGLU294). In six of the eight patients for whom immediate timepoints were evaluated, increasing ctDNA levels allowed for the identification of eight tumor-derived alterations not previously detected at baseline including the targetable *EGFR* 746ELREATS>D clone in patient CGPLLU86 and an *EGFR*-resistance mutation T790M in patient CGLU344 (Figure 2.7 A). Mutant allele fractions of the newly detected clones ranged from

0.15% to 1.70% with an average of 0.57% and suggested that these alterations were likely below the limit of detection at baseline and were detected due to an increase in ctDNA levels. Evaluating the relative rate of emerging mutations in a Bayesian statistical model, we estimated a 110-fold increase in the rate of emerging mutations comparing post-treatment to pre-treatment levels (99% CI: 13 – 732). Overall cfDNA amounts remained relatively constant between baseline and timepoints 4-12 hours after treatment indicating that changes in ctDNA levels occurred due to changes in the relative abundance of mutated clones within cfDNA (Figure 2.7 B). These observations suggest that the emergence of novel ctDNA variants may be related to early effects of therapy and are consistent with studies showing BIM-mediated apoptosis in responsive tumors 6-48 hours after exposure to EGFR inhibitors (75, 76).

Cell-free tumor load and clinical outcome

We evaluated whether the dynamic cfTL changes observed at early timepoints after treatment initiation were associated with differences in clinical outcome. cfTL levels at these early time points were bimodal, with the lower group clustering at an average reduction in cfTL of 99.8% and the higher group having an average increase in cfTL of 0.06% (Figure 2.8 A). We defined ctDNA responders as those with reduction in cfTL levels within three standard deviations of average reduction of the lower group (greater than 98.4%) while non-responders were below this threshold. Eight of twelve patients who developed a complete ctDNA response (cfTL reduction of 100%) experienced progression-free survival longer than one year (Figures 2.8 B and 2.9). Of the six patients with radiographic stable disease, ctDNA analyses identified four patients with a molecular response (average PFS of 11.3 months) and two molecular non-responders (average PFS of 2.6 months). One patient who was a radiographic partial responder, but a molecular non-responder had a PFS of 3.9 months. Importantly, two patients with non-measurable disease by RECIST were clearly identified as molecular responders with an average PFS of 13.7 months. Overall, we observed a significantly shorter median progression-free survival for ctDNA non-responders

compared to ctDNA responders (1.6 months vs. 13.7 months, $P < 0.0001$, HR = 66.6, 95% CI: 13.0 to 341.7, Log-rank test) (Figure 2.8 C). Importantly, cfTL reduction at a median of 19 days appeared to be a more accurate predictor of clinical outcome compared to initial CT imaging performed an average of 47 days after initiation of therapy ($P < 0.0001$, Wilcoxon signed rank test) (Figures 2.8 C, D, E, and 2.9).

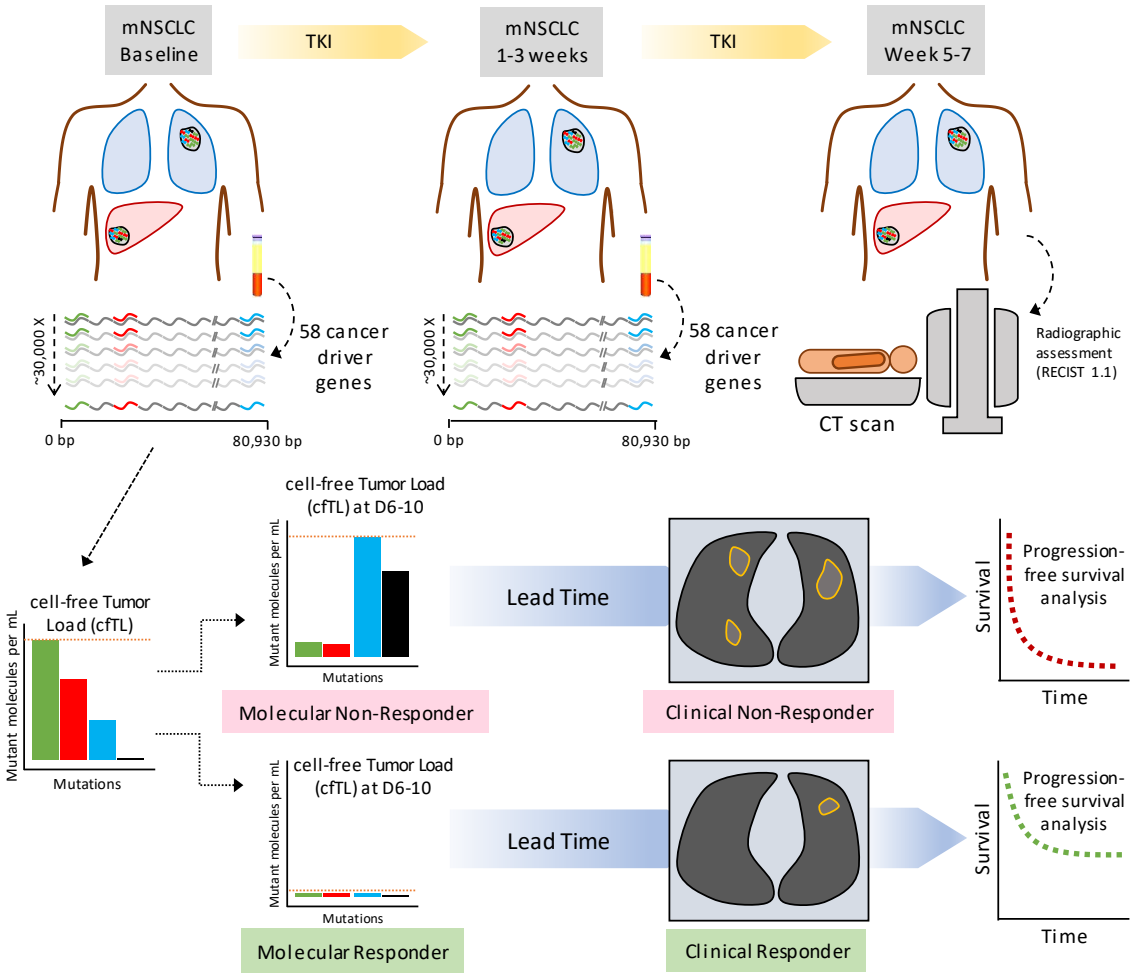


Figure 2.1. Schematic of cfTL determination and prediction of therapeutic response. Liquid biopsies from metastatic non-small-cell lung cancer (mNSCLC) patients undergoing treatment with tyrosine kinase inhibition (TKI) were analyzed at baseline and at serial time points after treatment. The TEC-Seq approach was used to directly identify sequence alterations across 58 genes encompassing 80,930 bases sequenced to >30,000X coverage, and whole-genome approaches were used to identify copy number changes in cfDNA. Cell-free tumor load (cfTL) was determined as the mutant allele fraction of the most abundant alteration in a clone targeted by TKI for patients with detected sequence alterations, or as the presence or absence of aneuploidy based on PA score in patients without detectable sequence alterations. Prediction of therapeutic response to targeted therapy based on ctDNA dynamics was assessed through changes in cfTL from baseline to subsequent time points treatment whereas response assessment through CT imaging was performed 5-7 weeks after treatment.

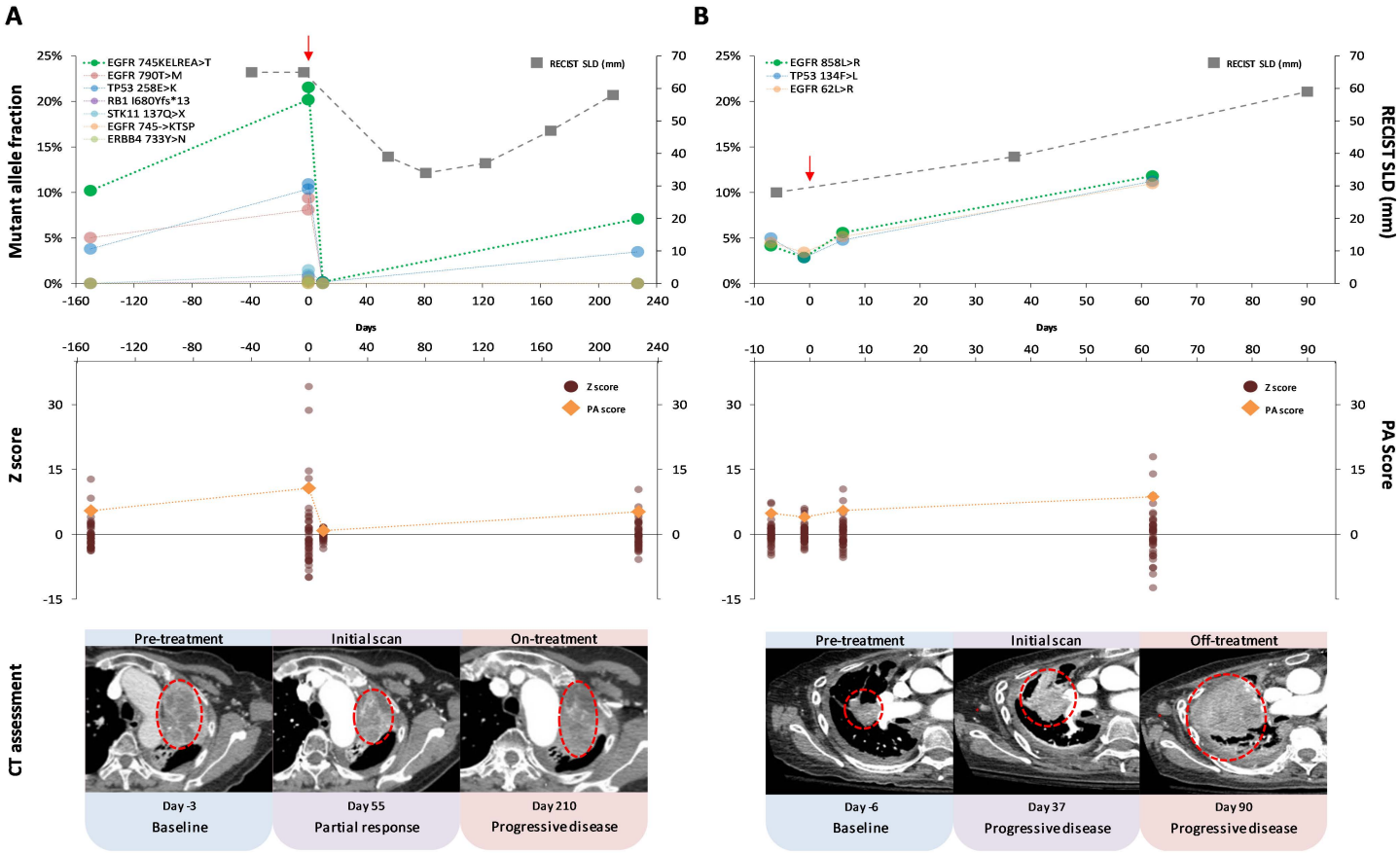
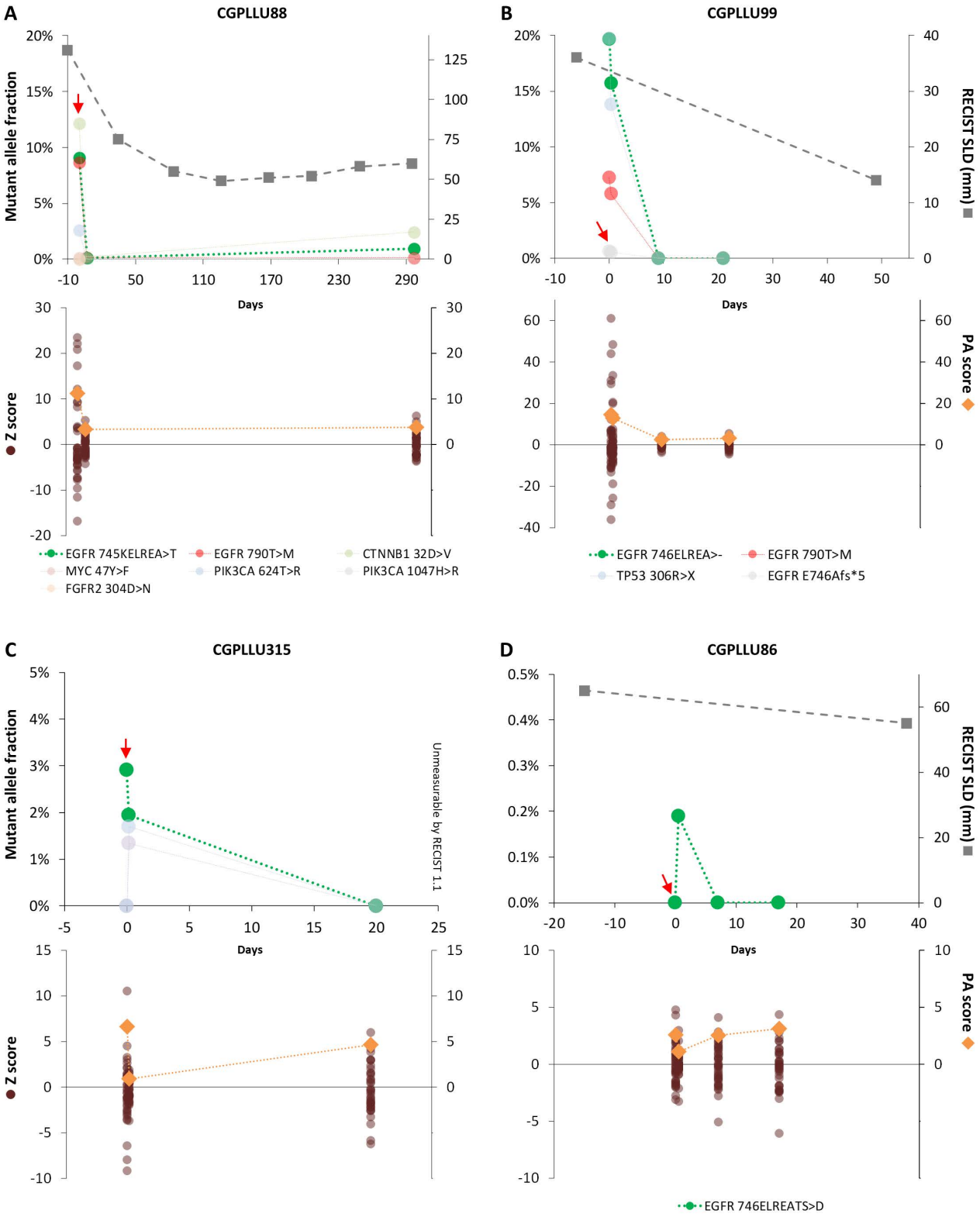
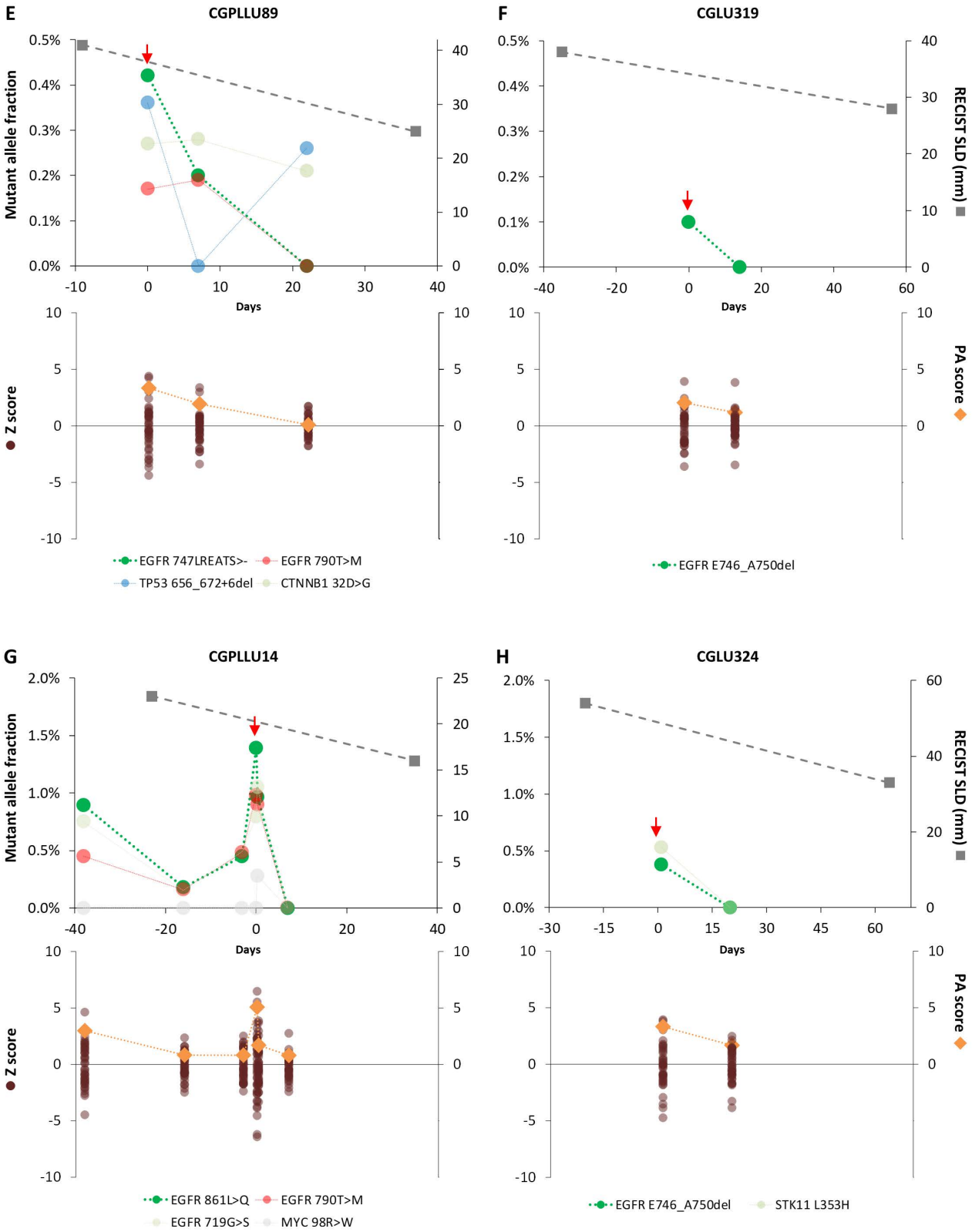
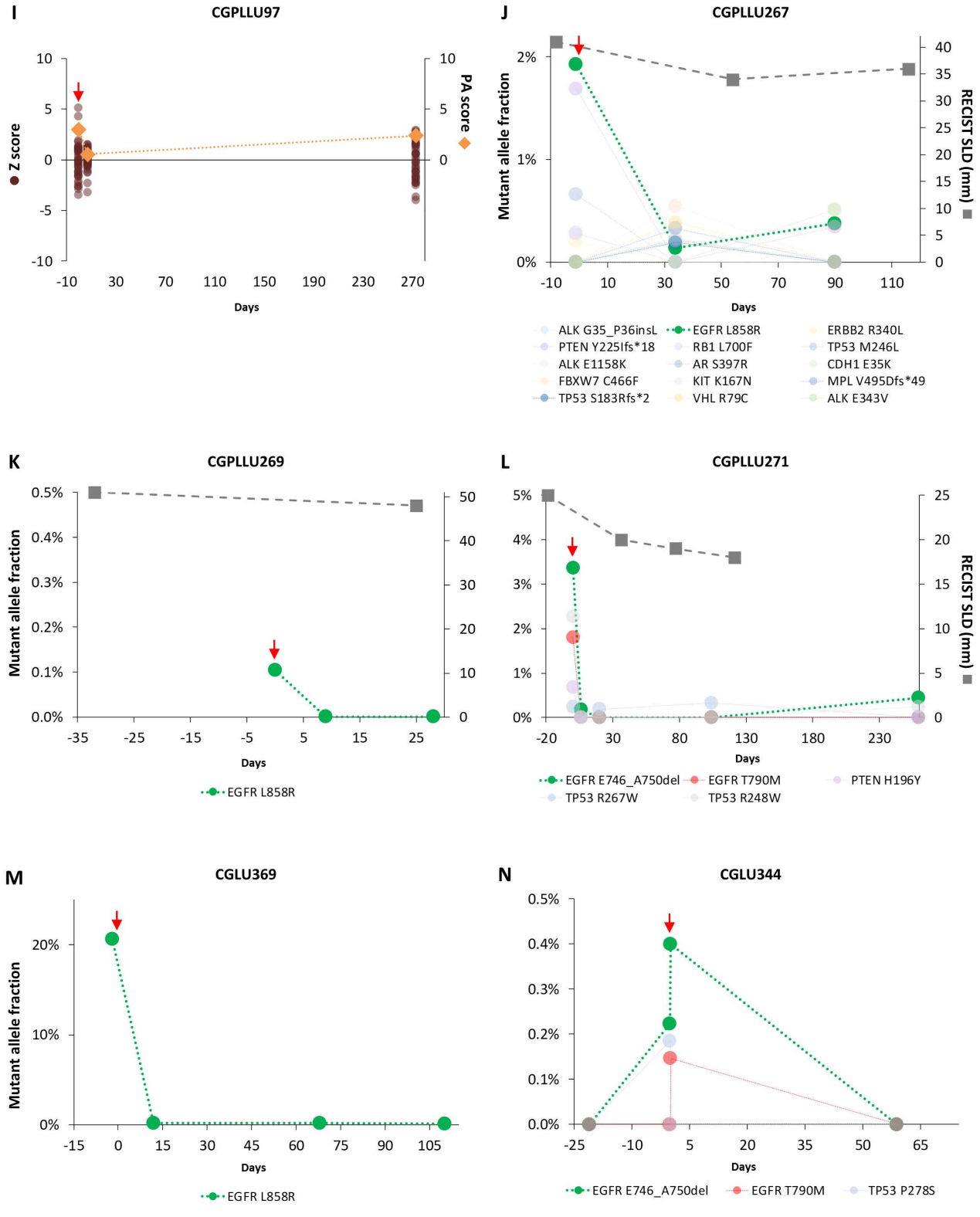
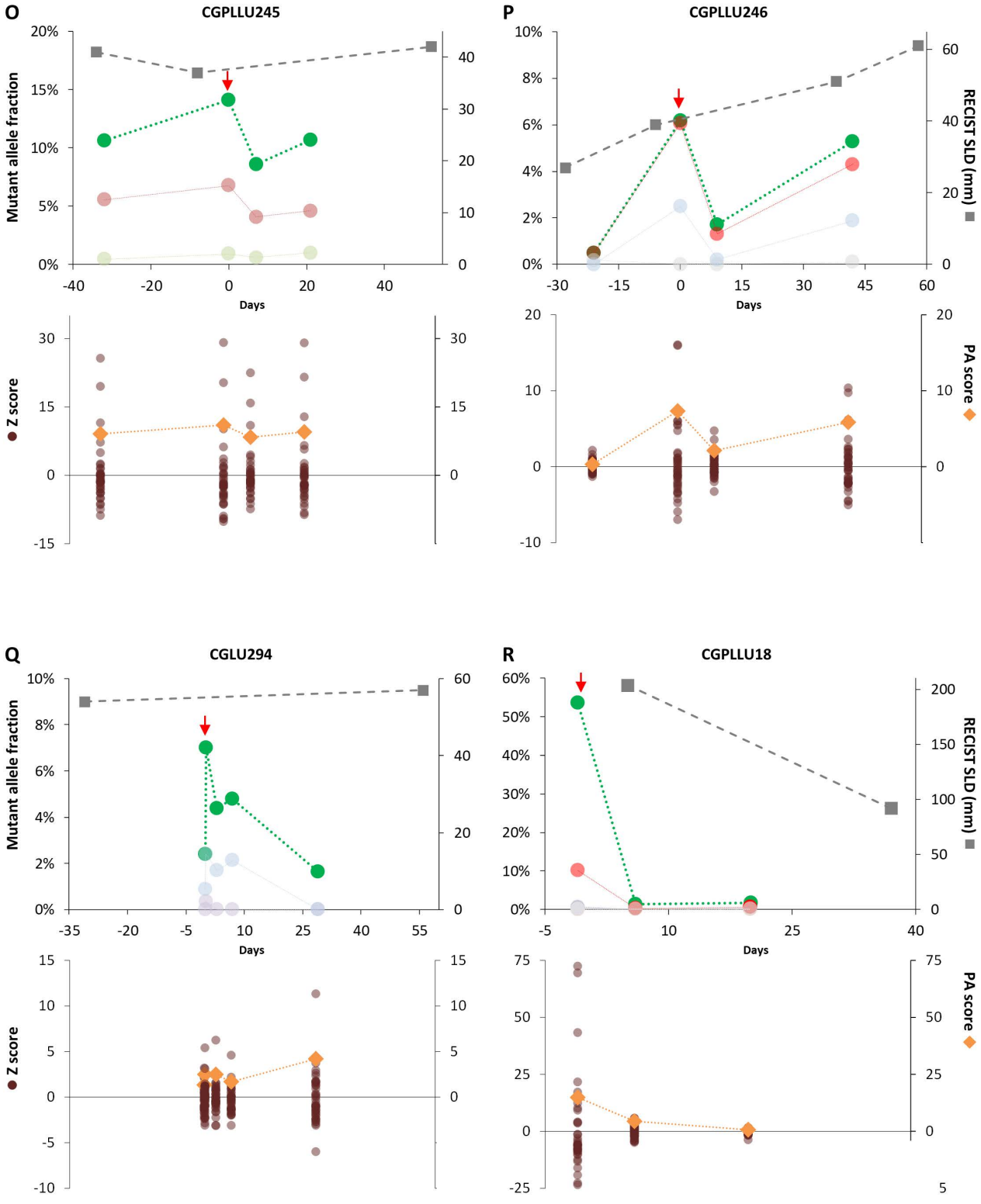


Figure 2.2. Dynamic changes of ctDNA during therapy. Characteristic patterns of ctDNA changes during therapy are shown for a responder (CGPLLU12) (A) and a non-responder (CGPLLU244) (B), both treated with osimertinib. Mutant allele fractions of clones identified in cfDNA through the TEC-Seq approach are shown for each timepoint analyzed with the ctDNA clone representing cfTL shown in bright green and treatment initiation highlighted with a red arrow (top). Copy number changes identified in cfDNA from analyses of whole-genome data are shown at each timepoint analyzed as Z scores (burgundy dots) for each chromosome arm and PA scores (orange diamonds) (middle). RECIST 1.1 sum of longest diameters (SLD, gray boxes) were measured from CT scans at intervals during therapy (top) and CT images show representative tumor lesions for each patient circled in red (bottom).


A
CGPLLU88
Mutant allele fraction
RECIST SLD (mm)
Days
Z score
PA score
EGFR 745KELREA>T
EGFR 790T>M
CTNNB1 32D>V
MYC 47Y>F
PIK3CA 624T>R
PIK3CA 1047H>R
FGFR2 304D>N
B
CGPLLU99
EGFR 746ELREA>-
EGFR 790T>M
TP53 306R>X
EGFR E746Afs*5
C
CGPLLU315
Unmeasurable by RECIST 1.1
D
CGPLLU86
EGFR 746ELREATS>D


E
CGPLLU89
Mutant allele fraction
RECIST SLD (mm)
Days
Z score
PA score
EGFR 747LREATS>-
EGFR 790T>M
TP53 656_672+6del
CTNNB1 32D>G
F
CGLU319
Days
PA score
EGFR E746_A750del
G
CGPLLU14
Mutant allele fraction
RECIST SLD (mm)
Days
Z score
PA score
EGFR 861L>Q
EGFR 790T>M
EGFR 719G>S
MYC 98R>W
H
CGLU324
Days
PA score
EGFR E746_A750del
STK11 L353H


I
CGPLLU97
Z score
PA score
Days
J
CGPLLU267
Mutant allele fraction
RECIST SLD (mm)
Days
ALK G35_P36insL
EGFR L858R
ERBB2 R340L
PTEN Y225Ifs*18
RB1 L700F
TP53 M246L
ALK E1158K
AR S397R
CDH1 E35K
FBXW7 C466F
KIT K167N
MPL V495Dfs*49
TP53 S183Rfs*2
VHL R79C
ALK E343V
K
CGPLLU269
Mutant allele fraction
Days
EGFR L858R
L
CGPLLU271
Mutant allele fraction
RECIST SLD (mm)
Days
EGFR E746_A750del
EGFR T790M
PTEN H196Y
TP53 R267W
TP53 R248W
M
CGLU369
Mutant allele fraction
Days
EGFR L858R
N
CGLU344
Days
EGFR E746_A750del
EGFR T790M
TP53 P278S


O
CGPLLU245
Mutant allele fraction
RECIST SLD (mm)
Days
Z score
PA score
P
CGPLLU246
Q
CGLU294
R
CGPLLU18

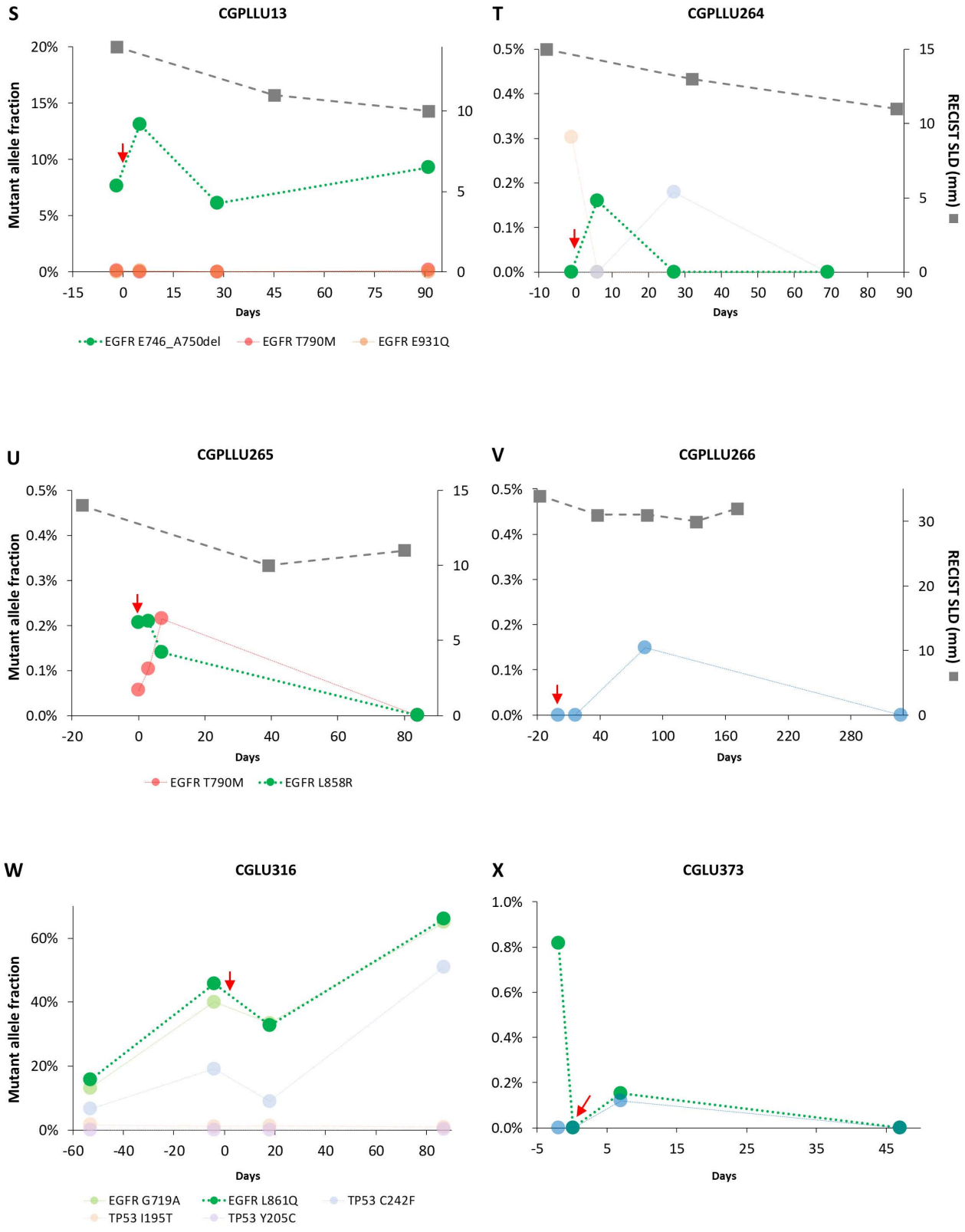

S
CGPLLU13
Mutant allele fraction
RECIST SLD (mm)
Days
EGFR E746_A750del
EGFR T790M
EGFR E931Q
T
CGPLLU264
U
CGPLLU265
EGFR T790M
EGFR L858R
V
CGPLLU266
W
CGLU316
EGFR G719A
EGFR L861Q
TP53 C242F
TP53 I195T
TP53 Y205C
X
CGLU373

Figure 2.3. Dynamic changes of ctDNA during therapy. Patterns of ctDNA changes during therapy are shown for patients with initial radiographic partial response (A, B, E-I, M, N, R), non-measureable disease (C, X), stable disease (D, J-L, S-V), or progressive disease (O-Q, W) after treatment with targeted therapy. Mutant allele fractions of clones identified in cfDNA through the TEC-Seq approach are shown for each timepoint analyzed with treatment initiation highlighted with a red arrow. Copy number changes identified in cfDNA from analyses of whole-genome data are shown at timepoints analyzed as Z scores (burgundy dots) for each chromosome arm and PA scores (orange diamonds). RECIST 1.1 sum of longest diameters (SLD, gray boxes) were measured from CT scans at intervals during therapy.

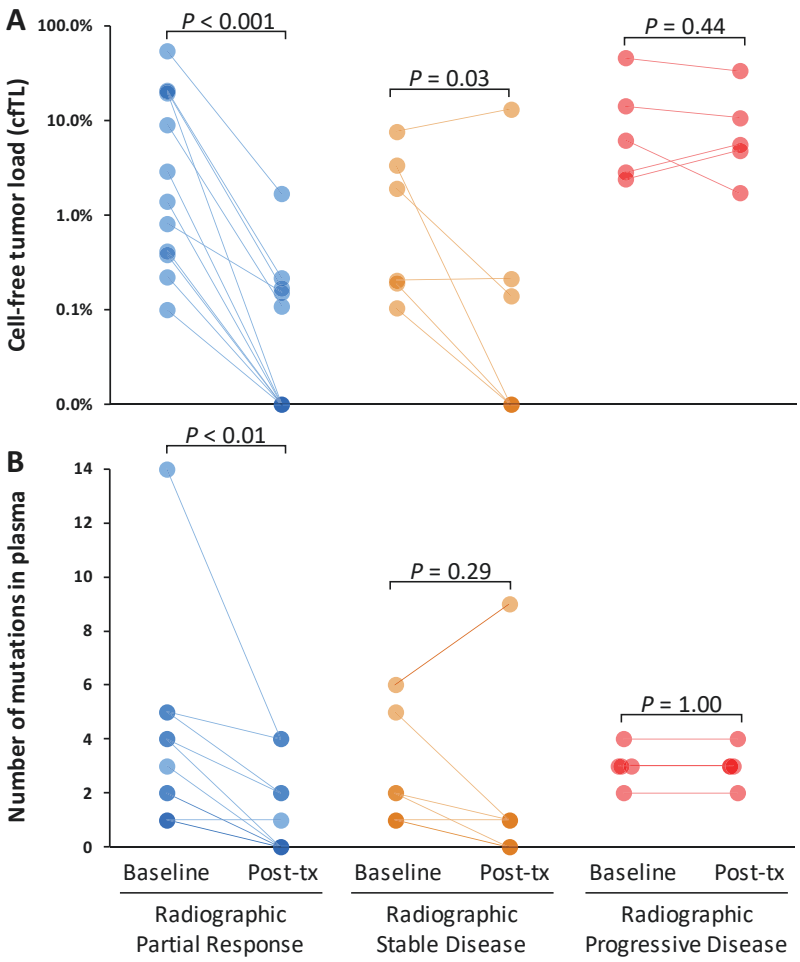


Figure 2.4. Characteristics of cell-free DNA in patients treated with tyrosine kinase inhibitors. Changes in cfTL (A) and the number of mutations in plasma (B) in patients with partial response (blue), stable disease (orange), and progressive disease (red) from baseline to the time of ctDNA assessment after initiation of therapy. The partial response subgroup also included two patients with non-measureable disease by RECIST who were classified as clinical responders.

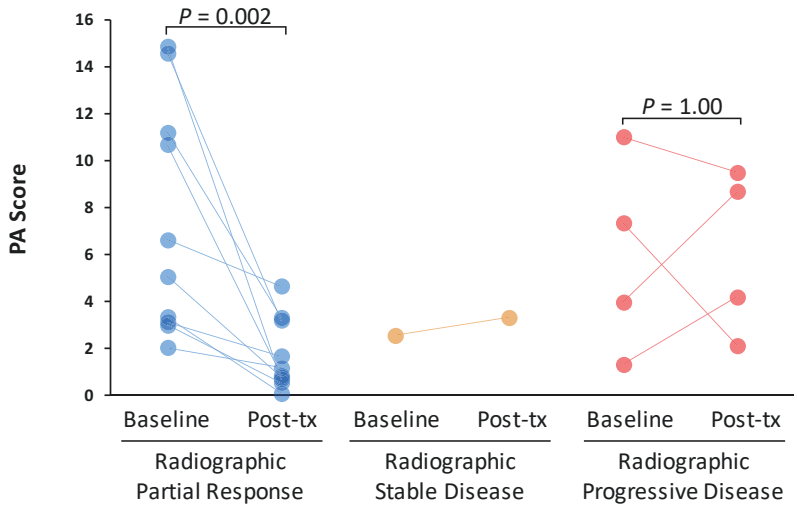


Figure 2.5. Copy number changes identified in cfDNA from analyses of whole-genome data. Changes in PA score based on initial radiographic assessment (P = 0.002: partial response, P = 1.00: progressive disease, Wilcoxon signed rank test). The radiographic partial response subgroup also included two patients with non-measureable disease by RECIST who were classified as clinical responders.

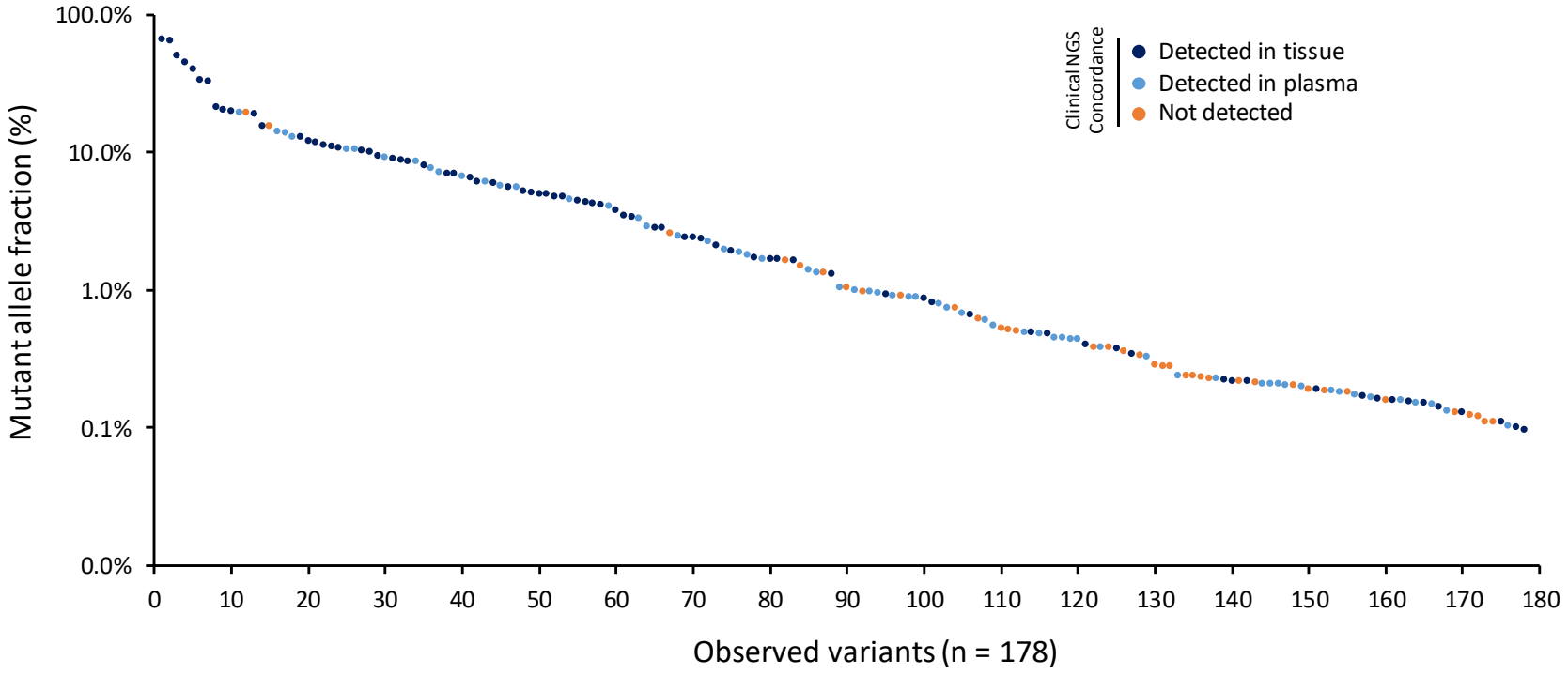


Figure 2.6. Concordance between alterations observed with TEC-Seq in the plasma and clinical NGS analyses in the tumor tissue or plasma. Mutant allele fractions of alterations directly detected in plasma through analyses with TEC-Seq are indicated. The presence of each alteration in matched tumor tissue or plasma specimen evaluated with clinical NGS tests are indicated with dark blue and light blue dots respectively whereas non-concordant mutations are indicated in orange. Overall, 141 alterations (79.2%) were concordant in either clinical tissue or plasma NGS analyses.

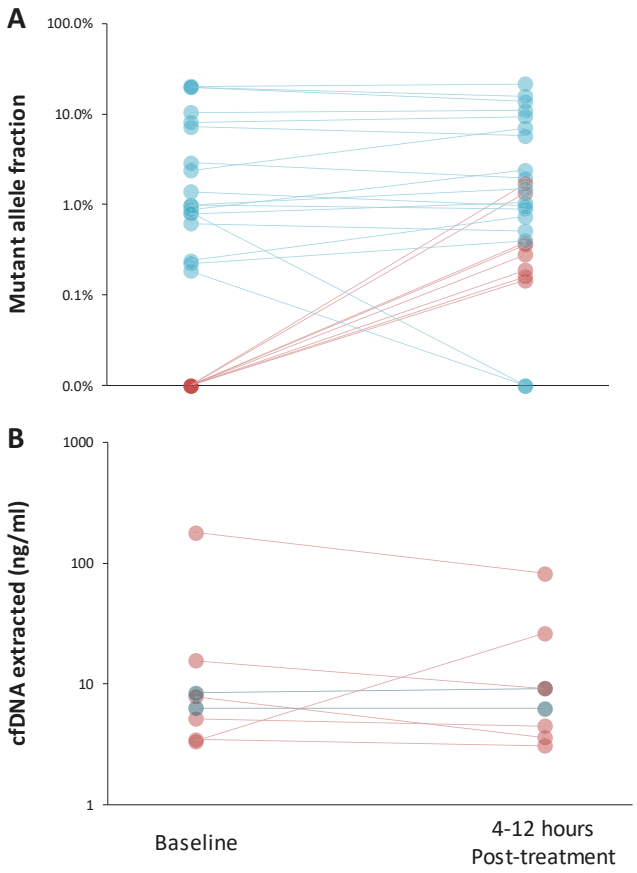


Figure 2.7. Detection of ctDNA variants within hours after tyrosine kinase inhibitor initiation. Changes in the levels of ctDNA (A) as well as of cfDNA extracted (B) are depicted for eight patients at baseline and at four to twelve hours after the initiation of targeted therapy. Emerging ctDNA alterations and the corresponding cfDNA amounts for patients with these alterations are depicted in red.

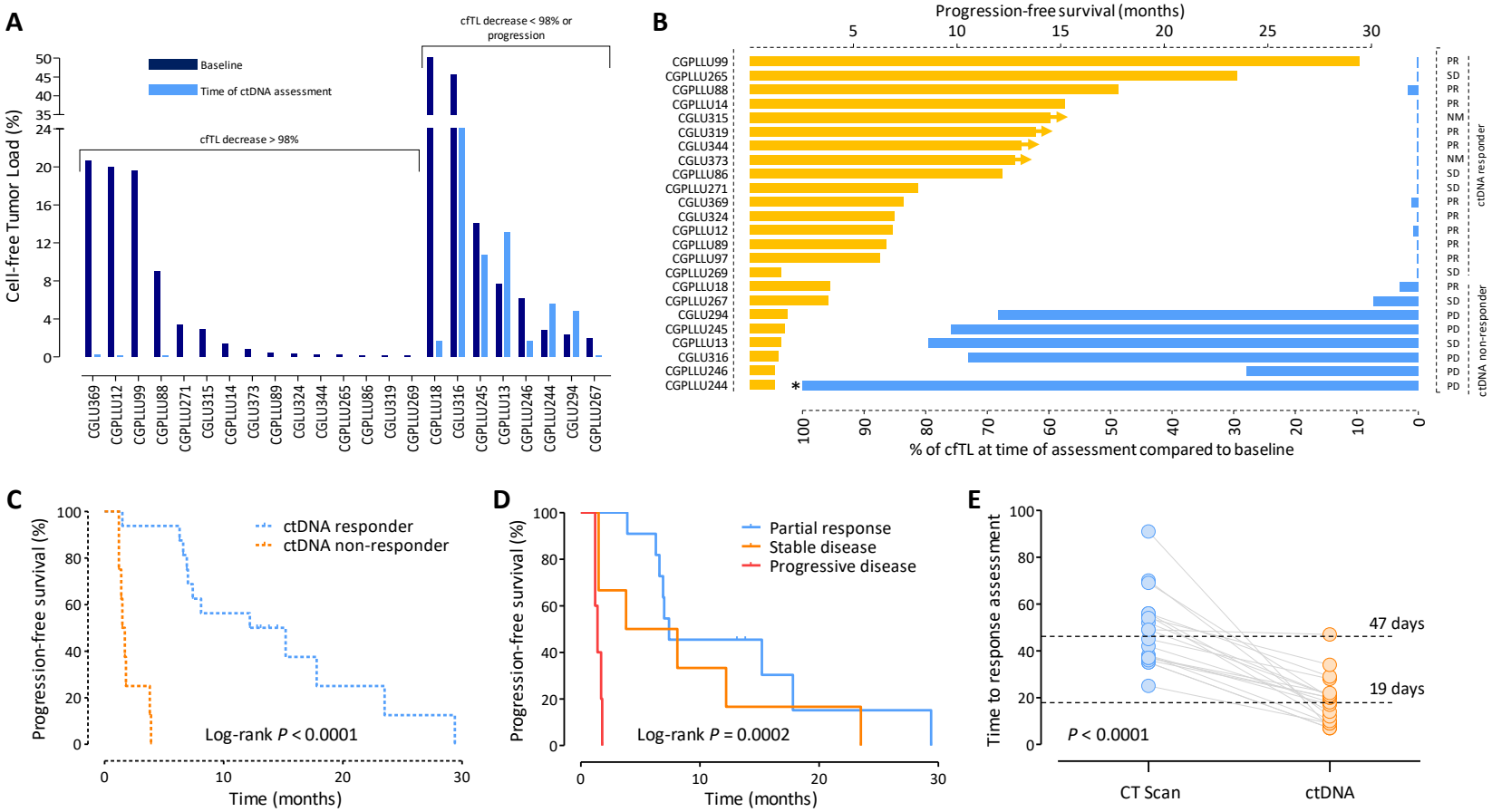


Figure 2.8. Changes in ctDNA and prediction of response to therapy. Changes in cfTL from baseline to the time of ctDNA assessment revealed a bimodal distribution (A). Patients with reduction of cfTL >98% and ≤98% were categorized as ctDNA responders and ctDNA non-responders, respectively. cfTL at the time of ctDNA assessment (blue) and PFS (orange) are depicted for patients analyzed (B). Radiographic assessment is indicated in the right column as partial response (PR), stable disease (SD), non-measurable disease (NM), or progressive disease (PD). Patient CGPLLU244 had cfTL levels >100% at the time of ctDNA assessment (*). Progression-free survival for ctDNA responders and non-responders ($P < 0.0001$, Mantel-Cox log rank test) (C). Progression-free survival based on initial radiographic assessment ($P = 0.0002$, Mantel-Cox log rank test) (D) Time to response assessment as determined by CT scans (blue) or analyses of ctDNA (orange) are indicated with median time to assessment shown in dotted lines ($P < 0.0001$, Wilcoxon signed rank test) (E).

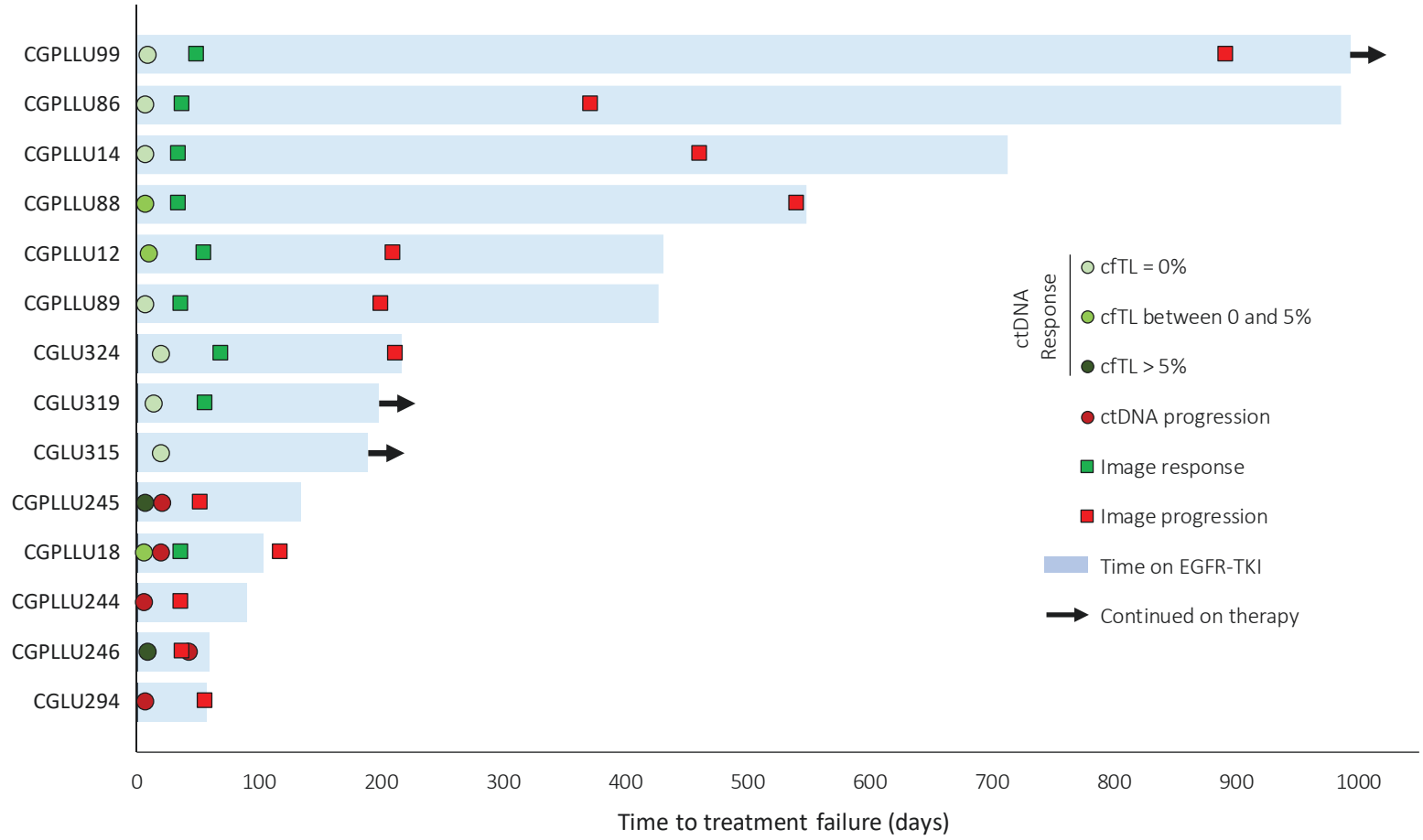


Figure 2.9. Timeline of ctDNA analyses, CT assessments, and treatment response. Interval between cfTL response assessment (colored circles) and CT scan response (colored squares) depicts the lead time between ctDNA and imaging analyses. Interval between treatment start and CT scan progression (red squares) depicts progression-free survival.

Table 2.1. Summary of clinical characteristics of patients analyzed.

Patient ID	Age	Gender	Smoking Status	Histopathological Diagnosis	Stage	TKI	Radiographic Response	Days on Treatment	Overall response at last follow-up	Status at last follow-up
CGPLLU99	53	Male	Never	Adenocarcinoma	IIIA	Osimertinib	Partial Response	893	Continued response	Alive
CGPLLU97	57	Female	Never	Adenocarcinoma	IV	Osimertinib	Partial Response	413	Progressive disease	Unknown
CGPLLU89	54	Female	Former	Adenocarcinoma	IV	Osimertinib	Partial Response	427	Progressive disease	Deceased
CGPLLU88	59	Male	Former	Adenocarcinoma	IIA	Osimertinib	Partial Response	548	Progressive disease	Deceased
CGPLLU86	55	Male	Never	Adenocarcinoma	IV	Osimertinib	Stable Disease	986	Progressive disease	Alive
CGPLLU43	57	Female	Never	Adenocarcinoma	IA	Erlotinib	Non-measurable*	831	Continued response	Alive
CGPLLU271	73	Male	Former	Adenocarcinoma	IV	Mavelertinib	Stable Disease	273	Progressive disease	Deceased
CGPLLU270	53	Female	Never	Adenocarcinoma	IV	Mavelertinib	Partial Response	216	Continued response	Alive
CGPLLU269	52	Female	Former	Adenocarcinoma	IV	Mavelertinib	Stable Disease	47	Progressive disease	Deceased
CGPLLU267	55	Female	Never	Squamous cell carcinoma	IV	Erlotinib	Stable Disease	238	Progressive disease	Alive
CGPLLU266	78	Male	Never	Adenocarcinoma	IIA	Mavelertinib	Stable Disease	336	Progressive disease	Alive
CGPLLU265	71	Female	Never	Adenocarcinoma	IA	Mavelertinib	Stable Disease	715	Progressive disease	Alive
CGPLLU264	84	Male	Never	Adenocarcinoma	IV	Osimertinib	Stable Disease	Ongoing	Continued response	Alive
CGPLLU246	65	Female	Never	Adenocarcinoma	IV	Osimertinib	Progressive Disease	59	Progressive disease	Deceased
CGPLLU245	49	Male	Never	Adenocarcinoma	IV	Osimertinib	Progressive Disease	134	Progressive disease	Alive
CGPLLU244	66	Female	Never	Adenocarcinoma	IV	Osimertinib	Progressive Disease	90	Progressive disease	Deceased
CGPLLU18	50	Female	Never	Adenocarcinoma	IIA	Osimertinib	Partial Response	104	Progressive disease	Deceased
CGPLLU14	55	Female	Never	Adenocarcinoma	IIA	Osimertinib	Partial Response	713	Progressive disease	Deceased
CGPLLU13	72	Female	Never	Adenocarcinoma	IV	Osimertinib	Stable Disease	136	Progressive disease	Deceased

CGPLLU12	67	Female	Never	Adenocarcinoma	IV	Osimertinib	Partial Response	431	Progressive disease	Deceased
CGLU373	56	Female	Never	Adenocarcinoma	IIIA	Afatinib	Non-measurable*	Ongoing	Continued response	Alive
CGLU369	48	Female	Never	Adenocarcinoma	IV	Erlotinib	Partial response	352	Progressive disease	Alive
CGLU344	65	Female	Never	Adenocarcinoma	IV	Osimertinib	Partial response	Ongoing	Continued response	Alive
CGLU324	60	Female	Former	Adenocarcinoma	IV	Afatinib	Partial response	212	Progressive disease	Alive
CGLU319	74	Female	Never	Adenocarcinoma	IV	Afatinib	Partial response	Ongoing	Continued response	Alive
CGLU316	50	Female	Former	Mixed carcinoma	IIIA	Osimertinib	Progressive Disease	73	Progressive disease	Alive
CGLU315	54	Male	Never	Adenocarcinoma	IV	Afatinib	Non-measurable*	Ongoing	Continued response	Alive
CGLU294	51	Male	Never	Adenocarcinoma	IV	Afatinib	Progressive Disease	57	Progressive disease	Alive

*Not measurable by RECIST; patient derives partial clinical benefit from treatment.

Table 2.2. Summary of serial timepoints analyzed.

Patient ID	Patient Timepoint	Significance of Timepoint	Days since Treatment	Volume of Plasma (ml)	cfDNA Extracted (ng)	cfDNA Input (ng)
CGPLLU12	CGPLLU12P_6	Pre Osimertinib	-150.0	5.00	350.30	350.30
CGPLLU12	CGPLLU12P_22	Pre Osimertinib	0.0	7.00	1254.20	250.00
CGPLLU12	CGPLLU12P_18	Post Osimertinib	0.2	6.80	559.60	250.00
CGPLLU12	CGPLLU12P_20	Post Osimertinib	10.0	6.00	324.30	250.00
CGPLLU12	CGPLLU12P_34	Post Osimertinib	227.0	5.00	191.00	191.00
CGPLLU14	CGPLLU14P_8	Pre Osimertinib	-38.0	4.20	59.50	59.50
CGPLLU14	CGPLLU14P_12	Pre Osimertinib	-16.0	4.20	47.00	47.00
CGPLLU14	CGPLLU14P_15	Pre Osimertinib	-3.0	5.00	72.00	72.00
CGPLLU14	CGPLLU14P_21	Pre Osimertinib	0.0	5.00	16.82	16.82
CGPLLU14	CGPLLU14P_19	Post Osimertinib	0.3	4.60	121.60	121.60
CGPLLU14	CGPLLU14P_23	Post Osimertinib	7.0	3.20	19.26	19.26
CGPLLU18	CGPLLU18P_4	Pre Osimertinib	-1.0	5.00	2196.70	250.00
CGPLLU18	CGPLLU18P_15	Post Osimertinib	6.0	6.00	446.30	250.00
CGPLLU18	CGPLLU18P_11	Post Osimertinib	20.0	3.00	24.00	24.00
CGPLLU244	CGPLLU244P_1	Pre Osimertinib	-7.0	4.50	80.26	80.26
CGPLLU244	CGPLLU244P_2	Pre Osimertinib	-1.0	4.10	132.44	125.00
CGPLLU244	CGPLLU244P_3	Post Osimertinib	6.0	4.70	255.79	125.00
CGPLLU244	CGPLLU244P_4	Post Osimertinib	62.0	2.90	74.95	74.95
CGPLLU245	CGPLLU245P_1	Pre Osimertinib	-32.0	4.70	91.28	91.28
CGPLLU245	CGPLLU245P_2	Pre Osimertinib	0.0	4.30	468.58	125.00
CGPLLU245	CGPLLU245P_3	Post Osimertinib	7.0	3.00	314.40	125.00
CGPLLU245	CGPLLU245P_4	Post Osimertinib	21.0	3.30	161.49	125.00
CGPLLU246	CGPLLU246P_1	Pre Osimertinib	-21.0	5.50	101.78	101.78
CGPLLU246	CGPLLU246P_2	Pre Osimertinib	0.0	5.00	118.00	118.00
CGPLLU246	CGPLLU246P_4	Post Osimertinib	9.0	3.30	43.48	43.48

CGPLLU246	CGPLLU246P_5	Post Osimertinib	42.0	3.40	46.51	46.51
CGPLLU86	CGPLLU86P_6	Pre Osimertinib	0.0	4.00	31.60	31.60
CGPLLU86	CGPLLU86P_1	Post Osimertinib	0.5	4.00	14.50	14.50
CGPLLU86	CGPLLU86P_8	Post Osimertinib	7.0	4.60	14.50	14.50
CGPLLU86	CGPLLU86P_9	Post Osimertinib	17.0	5.00	19.90	19.90
CGPLLU88	CGPLLU88P_2	Pre Osimertinib	0.0	5.00	138.31	138.31
CGPLLU88	CGPLLU88P	Post Osimertinib	7.0	5.00	32.43	32.43
CGPLLU88	CGPLLU88P_5	Post Osimertinib	297.0	4.00	12.16	12.16
CGPLLU89	CGPLLU89P	Pre Osimertinib	0.0	8.00	67.40	67.40
CGPLLU89	CGPLLU89P_2	Post Osimertinib	7.0	6.50	40.60	40.60
CGPLLU89	CGPLLU89P_5	Post Osimertinib	22.0	6.00	17.90	17.90
CGPLLU97	CGPLLU97P_11	Pre Osimertinib	0.0	6.50	26.10	26.10
CGPLLU97	CGPLLU97P_4	Post Osimertinib	7.0	6.40	22.23	22.23
CGPLLU97	CGPLLU97P_20	Post Osimertinib	273.0	6.00	27.54	27.54
CGPLLU99	CGPLLU99P_8	Pre Osimertinib	0.0	6.00	50.60	50.60
CGPLLU99	CGPLLU99P_10	Post Osimertinib	0.3	5.00	45.99	45.99
CGPLLU99	CGPLLU99P_12	Post Osimertinib	9.0	5.00	24.99	24.99
CGPLLU99	CGPLLU99P_11	Post Osimertinib	21.0	4.00	18.76	18.76
CGLU294	CGLU294P_1	Pre Afatinib	0.0	5.00	17.36	17.36
CGLU294	CGLU294P1_1	Post Afatinib	0.2	5.00	15.52	15.52
CGLU294	CGLU294P2_1	Post Afatinib	3.0	5.00	16.59	16.59
CGLU294	CGLU294P3_2	Post Afatinib	7.0	5.00	10.73	10.73
CGLU294	CGLU294P4_1	Post Afatinib	29.0	5.00	12.22	12.22
CGLU315	CGLU315P_1	Pre Afatinib	0.0	5.00	25.96	25.96
CGLU315	CGLU315P1_1	Post Afatinib	0.2	5.00	22.48	22.48
CGLU315	CGLU315P2_1	Post Afatinib	20.0	5.00	22.62	22.62
CGLU319	CGLU319P_1	Pre Afatinib	0.0	5.00	53.14	53.14
CGLU319	CGLU319P1_1	Post Afatinib	14.0	5.00	48.26	48.26

CGLU324	CGLU324P_1	Post Afatinib	1.0	5.00	32.96	32.96
CGLU324	CGLU324P1_1	Post Afatinib	20.0	5.00	26.71	26.71
CGLU373	CGLU373P_1	Pre Afatinib	-2.0	5.00	31.76	31.76
CGLU373	CGLU373P1_1	Post Afatinib	0.1	5.00	31.42	31.42
CGLU373	CGLU373P2_1	Post Afatinib	7.0	5.00	19.11	19.11
CGLU373	CGLU373P3_1	Post Afatinib	47.0	3.50	19.41	19.41
CGLU316	CGLU316P6_1	Pre Osimertinib	-53.0	5.00	11.90	11.90
CGLU316	CGLU316P7_1	Pre Osimertinib	-4.0	5.00	10.54	10.54
CGLU316	CGLU316P8_1	Post Osimertinib	18.0	5.00	4.36	5.37
CGLU316	CGLU316P9_1	Post Osimertinib	87.0	2.00	17.49	17.49
CGLU369	CGLU369P_1	Pre Erlotinib	-2.0	2.00	22.56	22.56
CGLU369	CGLU369P1_1	Post Erlotinib	12.0	5.00	50.43	50.43
CGLU369	CGLU369P2_1	Post Erlotinib	68.0	5.00	33.47	33.50
CGLU369	CGLU369P3_1	Post Erlotinib	110.0	5.00	42.06	42.10
CGLU344	CGLU344P1_1	Pre Osimertinib	-21.0	5.00	173.87	125.00
CGLU344	CGLU344P2_1	Pre Osimertinib	0.0	5.00	78.15	78.20
CGLU344	CGLU344P3_1	Post Osimertinib	0.2	5.00	46.11	46.10
CGLU344	CGLU344P5_1	Post Osimertinib	59.0	5.00	26.57	26.60
CGPLLU13	CGPLLU13P27	Pre Osimertinib	-2.0	5.00	38.37	38.37
CGPLLU13	CGPLLU13P28	Post Osimertinib	5.0	4.50	37.75	37.75
CGPLLU13	CGPLLU13P29	Post Osimertinib	28.0	3.20	27.71	27.71
CGPLLU13	CGPLLU13P30	Post Osimertinib	91.0	5.00	29.87	29.87
CGPLLU43	CGPLLU43P3	Pre Erlotinib	-1.0	4.90	10.65	10.65
CGPLLU43	CGPLLU43P4	Post Erlotinib	6.0	3.70	12.07	12.07
CGPLLU43	CGPLLU43P5	Post Erlotinib	27.0	4.00	16.46	16.46
CGPLLU43	CGPLLU43P6	Post Erlotinib	83.0	3.70	30.35	30.35
CGPLLU267	CGPLLU267P	Pre Erlotinib	-1.0	4.50	12.93	12.93
CGPLLU267	CGPLLU267P2	Post Erlotinib	34.0	4.50	15.04	15.04

CGPLLU267	CGPLLU267P3	Post Erlotinib	90.0	3.50	10.51	10.51
CGPLLU269	CGPLLU269P1	Pre PF7775	0.0	5.00	57.02	57.02
CGPLLU269	CGPLLU269P2	Post PF7775	9.0	5.00	41.77	41.77
CGPLLU269	CGPLLU269P3	Post PF7775	28.0	3.50	62.26	62.26
CGPLLU271	CGPLLU271P	Pre PF7775	0.0	5.00	94.30	94.30
CGPLLU271	CGPLLU271P1	Post PF7775	6.0	4.50	62.26	62.26
CGPLLU271	CGPLLU271P2	Post PF7775	20.0	3.50	47.12	47.12
CGPLLU271	CGPLLU271P3	Post PF7775	104.0	4.00	55.09	55.09
CGPLLU271	CGPLLU271P4	Post PF7775	259.0	4.00	18.80	18.80
CGPLLU264	CGPLLU264P	Pre Osimertinib	-1.0	4.00	91.89	91.89
CGPLLU264	CGPLLU264P1	Post Osimertinib	6.0	4.50	47.38	47.38
CGPLLU264	CGPLLU264P2	Post Osimertinib	27.0	3.00	21.44	21.44
CGPLLU264	CGPLLU264P3	Post Osimertinib	69.0	4.00	38.39	38.39
CGPLLU266	CGPLLU266P	Pre PF7775	0.0	5.00	26.61	26.61
CGPLLU266	CGPLLU266P2	Post PF7775	16.0	3.50	22.10	22.10
CGPLLU266	CGPLLU266P3	Post PF7775	83.0	5.00	38.22	38.22
CGPLLU266	CGPLLU266P4	Post PF7775	328.0	5.00	71.94	71.94
CGPLLU265	CGPLLU265P	Pre PF7775	0.0	4.20	30.09	30.09
CGPLLU265	CGPLLU265P1	Post PF7775	3.0	4.00	32.43	32.43
CGPLLU265	CGPLLU265P2	Post PF7775	7.0	4.20	31.62	31.62
CGPLLU265	CGPLLU265P3	Post PF7775	84.0	5.00	80.83	80.83
CGPLLU270	CGPLLU270P	Pre PF7775	0.0	5.00	25.64	25.64
CGPLLU270	CGPLLU270P2	Post PF7775	12.0	3.50	14.58	14.58
CGPLLU270	CGPLLU270P3	Post PF7775	83.0	5.00	16.26	16.26

Table 2.3. Summary of genes analyzed.

Gene	Region Analyzed	Gene Category
ABL1	Specific Exons	Cancer Driver Gene
AKT1	Specific Exons	Cancer Driver Gene
ALK	Full Coding Region	Cancer Driver Gene
APC	Specific Exons	Cancer Driver Gene
AR	Full Coding Region	Cancer Driver Gene
ATM	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
BRAF	Full Coding Region	Cancer Driver Gene
CDH1	Specific Exons	Cancer Driver Gene
CDK4	Full Coding Region	Cancer Driver Gene
CDK6	Full Coding Region	Cancer Driver Gene
CDKN2A	Specific Exons	Cancer Driver Gene
CSF1R	Specific Exons	Cancer Driver Gene
CTNNB1	Specific Exons	Cancer Driver Gene
DNMT3A	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
EGFR	Full Coding Region	Cancer Driver Gene
ERBB2	Specific Exons	Cancer Driver Gene
ERBB4	Full Coding Region	Cancer Driver Gene
ESR1	Full Coding Region	Cancer Driver Gene
EZH2	Specific Exons	Cancer Driver Gene
FBXW7	Specific Exons	Cancer Driver Gene
FGFR1	Specific Exons	Cancer Driver Gene
FGFR2	Specific Exons	Cancer Driver Gene
FGFR3	Specific Exons	Cancer Driver Gene
FLT3	Specific Exons	Cancer Driver Gene
GNA11	Specific Exons	Cancer Driver Gene
GNAQ	Specific Exons	Cancer Driver Gene
GNAS	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
HNF1A	Specific Exons	Cancer Driver Gene
HRAS	Full Coding Region	Cancer Driver Gene
IDH1	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
IDH2	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
JAK2	Full Coding Region	Cancer Driver and Clonal Hematopoiesis Gene
JAK3	Specific Exons	Cancer Driver Gene
KDR	Specific Exons	Cancer Driver Gene
KIT	Full Coding Region	Cancer Driver Gene
KRAS	Full Coding Region	Cancer Driver Gene
MAP2K1	Specific Exons	Cancer Driver Gene
MET	Specific Exons	Cancer Driver Gene

MLH1	Specific Exons	Cancer Driver Gene
MPL	Specific Exons	Cancer Driver Gene
MYC	Specific Exons	Cancer Driver Gene
NPM1	Specific Exons	Cancer Driver Gene
NRAS	Full Coding Region	Cancer Driver Gene
PDGFRA	Full Coding Region	Cancer Driver Gene
PIK3CA	Full Coding Region	Cancer Driver Gene
PIK3R1	Specific Exons	Cancer Driver Gene
PTEN	Full Coding Region	Cancer Driver Gene
PTPN11	Specific Exons	Cancer Driver Gene
RB1	Specific Exons	Cancer Driver Gene
RET	Specific Exons	Cancer Driver Gene
SMAD4	Specific Exons	Cancer Driver Gene
SMARCB1	Specific Exons	Cancer Driver Gene
SMO	Specific Exons	Cancer Driver Gene
SRC	Specific Exons	Cancer Driver Gene
STK11	Full Coding Region	Cancer Driver Gene
TERT	Specific Exons	Cancer Driver Gene
TP53	Full Coding Region	Cancer Driver Gene
VHL	Specific Exons	Cancer Driver Gene

Table 2.4. Summary of genomic analyses.

Patient ID	Patient Timepoint	Read Length	Bases Mapped to Genome	Bases in Target Region	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage of Target Regions	Distinct Coverage of Target Regions	Bases in Off-Target Region*	Bases Mapped to Off-Target Region	Percent Mapped to Off-Target Region	Total Coverage of Off-Target Region
CGPLLU12	CGPLLU12P_18	100	7,900,133,500	80,930	3,863,298,051	49%	45,929	8,508	2,846,140,175	1,855,865,100	23%	0.6521
CGPLLU12	CGPLLU12P_20	100	7,756,705,100	80,930	3,517,430,064	45%	40,943	5,816	2,846,140,175	2,302,262,600	30%	0.8089
CGPLLU12	CGPLLU12P_22	100	8,057,252,300	80,930	3,802,086,289	47%	45,136	7,805	2,846,140,175	2,071,248,200	26%	0.7277
CGPLLU12	CGPLLU12P_34	100	8,777,269,900	80,930	4,524,962,642	52%	52,841	5,766	2,846,140,175	1,905,315,600	22%	0.6694
CGPLLU12	CGPLLU12P_6	100	7,201,712,800	80,930	3,608,246,175	50%	44,081	2,867	2,846,140,175	1,580,319,900	22%	0.5553
CGPLLU14	CGPLLU14P_12	100	8,668,655,700	80,930	3,980,731,089	46%	48,628	3,148	2,846,140,175	2,405,208,900	28%	0.8451
CGPLLU14	CGPLLU14P_15	100	8,271,043,600	80,930	4,105,092,738	50%	50,152	4,497	2,846,140,175	1,962,306,900	24%	0.6895
CGPLLU14	CGPLLU14P_19	100	7,149,809,200	80,930	3,405,754,720	48%	40,382	6,170	2,846,140,175	1,796,929,400	25%	0.6314
CGPLLU14	CGPLLU14P_21	100	6,556,332,200	80,930	3,289,504,484	50%	39,004	4,081	2,846,140,175	1,354,209,200	21%	0.4758
CGPLLU14	CGPLLU14P_23	100	7,410,378,300	80,930	3,464,236,558	47%	41,108	4,259	2,846,140,175	1,982,005,900	27%	0.6964
CGPLLU14	CGPLLU14P_8	100	7,530,190,700	80,930	3,752,054,349	50%	45,839	2,469	2,846,140,175	1,630,985,900	22%	0.5731
CGPLLU18	CGPLLU18P_11	100	8,873,158,100	80,930	4,118,821,432	46%	48,136	5,160	2,846,140,175	2,493,973,600	28%	0.8763
CGPLLU18	CGPLLU18P_15	100	6,258,355,400	80,930	3,199,373,401	51%	37,270	7,926	2,846,140,175	1,319,217,600	21%	0.4635
CGPLLU18	CGPLLU18P_4	100	9,997,401,400	80,930	4,940,336,941	49%	57,994	6,805	2,846,140,175	2,212,495,700	22%	0.7774
CGPLLU244	CGPLLU244P_1	100	8,305,560,600	80,930	4,182,616,104	50%	50,851	7,569	2,846,140,175	1,933,915,900	23%	0.6795
CGPLLU244	CGPLLU244P_2	100	7,739,951,100	80,930	3,788,487,116	49%	45,925	8,552	2,846,140,175	1,972,044,700	25%	0.6929
CGPLLU244	CGPLLU244P_3	100	8,061,928,000	80,930	4,225,322,272	52%	51,279	8,646	2,846,140,175	1,700,788,200	21%	0.5976
CGPLLU244	CGPLLU244P_4	100	8,894,936,700	80,930	4,437,962,639	50%	53,862	7,361	2,846,140,175	2,219,056,500	25%	0.7797
CGPLLU245	CGPLLU245P_1	100	7,679,235,200	80,930	3,935,822,054	51%	47,768	7,266	2,846,140,175	1,633,713,800	21%	0.5740
CGPLLU245	CGPLLU245P_2	100	8,985,252,500	80,930	4,824,268,339	54%	58,338	10,394	2,846,140,175	1,897,728,900	21%	0.6668
CGPLLU245	CGPLLU245P_3	100	8,518,229,300	80,930	4,480,236,927	53%	54,083	10,125	2,846,140,175	1,958,617,000	23%	0.6882
CGPLLU245	CGPLLU245P_4	100	9,031,131,000	80,930	4,824,738,475	53%	58,313	10,598	2,846,140,175	1,871,678,500	21%	0.6576
CGPLLU246	CGPLLU246P_1	100	8,520,360,800	80,930	3,509,660,305	41%	42,349	8,086	2,846,140,175	3,090,140,500	36%	1.0857

CGPLLU246	CGPLLU246P_2	100	5,451,467,800	80,930	2,828,351,657	52%	34,243	8,256	2,846,140,175	1,183,329,500	22%	0.4158
CGPLLU246	CGPLLU246P_4	100	8,137,616,600	80,930	4,135,036,174	51%	50,121	6,466	2,846,140,175	1,889,464,200	23%	0.6639
CGPLLU246	CGPLLU246P_5	100	8,385,724,600	80,930	4,413,323,333	53%	53,495	7,303	2,846,140,175	1,673,217,100	20%	0.5879
CGPLLU86	CGPLLU86P_1	100	8,222,093,400	80,930	3,523,035,056	43%	41,165	3,614	2,846,140,175	2,702,667,600	33%	0.9496
CGPLLU86	CGPLLU86P_6	100	8,305,719,500	80,930	4,271,264,008	51%	49,508	6,681	2,846,140,175	1,787,964,500	22%	0.6282
CGPLLU86	CGPLLU86P_8	100	6,787,785,300	80,930	3,443,658,418	51%	40,192	3,643	2,846,140,175	1,430,288,100	21%	0.5025
CGPLLU86	CGPLLU86P_9	100	6,213,229,400	80,930	3,120,325,926	50%	36,413	3,560	2,846,140,175	1,301,442,800	21%	0.4573
CGPLLU88	CGPLLU88P	100	7,679,995,800	80,930	4,004,738,253	52%	46,951	6,387	2,846,140,175	1,458,370,000	19%	0.5124
CGPLLU88	CGPLLU88P_2	100	7,252,433,900	80,930	3,621,678,746	50%	42,719	8,599	2,846,140,175	1,578,804,800	22%	0.5547
CGPLLU88	CGPLLU88P_5	100	6,509,178,000	80,930	3,316,053,733	51%	39,274	2,661	2,846,140,175	1,275,075,600	20%	0.4480
CGPLLU89	CGPLLU89P	100	7,662,496,600	80,930	3,781,536,306	49%	44,097	7,909	2,846,140,175	1,795,332,800	23%	0.6308
CGPLLU89	CGPLLU89P_2	100	7,005,599,500	80,930	3,339,612,564	48%	38,977	5,034	2,846,140,175	1,753,053,800	25%	0.6159
CGPLLU89	CGPLLU89P_5	100	8,325,998,600	80,930	3,094,796,789	37%	36,061	2,822	2,846,140,175	3,367,580,600	40%	1.1832
CGPLLU97	CGPLLU97P_11	100	9,607,549,400	80,930	4,714,483,715	49%	55,065	3,275	2,846,140,175	2,049,397,700	21%	0.7201
CGPLLU97	CGPLLU97P_20	100	7,977,402,200	80,930	3,981,840,609	50%	46,594	4,592	2,846,140,175	1,733,523,000	22%	0.6091
CGPLLU97	CGPLLU97P_4	100	7,975,580,500	80,930	3,458,563,174	43%	40,224	4,228	2,846,140,175	2,490,544,100	31%	0.8751
CGPLLU99	CGPLLU99P_10	100	8,350,456,400	80,930	4,112,640,680	49%	48,035	7,434	2,846,140,175	1,849,135,400	22%	0.6497
CGPLLU99	CGPLLU99P_11	100	8,455,525,300	80,930	4,248,480,856	50%	49,401	3,388	2,846,140,175	1,723,529,200	20%	0.6056
CGPLLU99	CGPLLU99P_12	100	8,172,750,100	80,930	3,937,309,188	48%	46,100	3,983	2,846,140,175	1,970,825,300	24%	0.6925
CGPLLU99	CGPLLU99P_8	100	6,563,589,000	80,930	3,167,459,274	48%	36,917	7,020	2,846,140,175	1,606,184,600	24%	0.5643
CGLU294	CGLU294P_1	100	13,391,053,400	80,930	6,557,523,556	49%	78,449	4,975	2,846,140,175	3,021,967,400	23%	1.0618
CGLU294	CGLU294P1_1	100	6,123,688,700	80,930	2,559,160,575	42%	30,475	2,658	2,846,140,175	1,906,657,800	31%	0.6699
CGLU294	CGLU294P2_1	100	6,826,939,100	80,930	2,696,933,517	40%	32,177	2,227	2,846,140,175	2,343,809,200	34%	0.8235
CGLU294	CGLU294P3_2	100	6,537,975,900	80,930	2,964,372,304	45%	35,429	2,504	2,846,140,175	1,698,272,400	26%	0.5967
CGLU294	CGLU294P4_1	100	4,382,617,500	80,930	2,052,259,803	47%	24,503	764	2,846,140,175	1,002,848,200	23%	0.3524
CGLU315	CGLU315P_1	100	1,511,727,500	80,930	772,328,073	51%	9,226	498	2,846,140,175	295,051,200	20%	0.1037
CGLU315	CGLU315P1_1	100	3,516,057,800	80,930	1,651,476,480	47%	19,709	1,923	2,846,140,175	862,931,400	25%	0.3032
CGLU315	CGLU315P2_1	100	2,406,092,800	80,930	1,154,037,968	48%	13,766	956	2,846,140,175	521,497,300	22%	0.1832

CGLU319	CGLU319P_1	100	6,167,692,000	80,930	3,135,436,369	51%	37,285	3,583	2,846,140,175	1,336,584,600	22%	0.4696
CGLU319	CGLU319P1_1	100	5,458,775,500	80,930	2,458,429,678	45%	29,096	2,715	2,846,140,175	1,604,345,600	29%	0.5637
CGLU324	CGLU324P_1	100	6,404,352,500	80,930	3,124,992,053	49%	37,062	2,071	2,846,140,175	1,379,187,100	22%	0.4846
CGLU324	CGLU324P1_1	100	5,622,041,400	80,930	2,679,400,008	48%	31,829	2,574	2,846,140,175	1,354,233,400	24%	0.4758
CGLU373	CGLU373P_1	100	6,346,267,200	80,930	3,053,520,676	48%	36,137	6,251	2,846,140,175	ND	ND	ND
CGLU373	CGLU373P1_1	100	6,517,189,900	80,930	3,192,984,468	49%	38,066	8,040	2,846,140,175	ND	ND	ND
CGLU373	CGLU373P2_1	100	7,767,146,300	80,930	3,572,598,842	46%	42,378	5,306	2,846,140,175	ND	ND	ND
CGLU373	CGLU373P3_1	100	7,190,999,100	80,930	3,273,648,804	46%	38,784	4,454	2,846,140,175	ND	ND	ND
CGLU316	CGLU316P6_1	100	7,864,415,100	80,930	1,991,331,171	25%	23,601	3,565	2,846,140,175	ND	ND	ND
CGLU316	CGLU316P7_1	100	7,502,591,600	80,930	3,730,963,390	50%	44,262	3,966	2,846,140,175	ND	ND	ND
CGLU316	CGLU316P8_1	100	6,582,515,900	80,930	3,187,059,470	48%	37,813	3,539	2,846,140,175	ND	ND	ND
CGLU316	CGLU316P9_1	100	6,587,281,800	80,930	1,947,630,979	30%	23,094	4,439	2,846,140,175	ND	ND	ND
CGLU369	CGLU369P_1	100	7,080,245,300	80,930	1,271,457,982	18%	15,109	2,364	2,846,140,175	ND	ND	ND
CGLU369	CGLU369P1_1	100	7,078,131,900	80,930	1,482,448,715	21%	17,583	4,275	2,846,140,175	ND	ND	ND
CGLU369	CGLU369P2_1	100	6,904,701,700	80,930	2,124,660,124	31%	25,230	5,278	2,846,140,175	ND	ND	ND
CGLU369	CGLU369P3_1	100	7,003,452,200	80,930	3,162,195,578	45%	37,509	6,062	2,846,140,175	ND	ND	ND
CGLU344	CGLU344P1_1	100	6,151,628,500	80,930	2,748,983,603	45%	32,462	8,063	2,846,140,175	ND	ND	ND
CGLU344	CGLU344P2_1	100	7,842,910,900	80,930	1,147,703,178	15%	13,565	4,303	2,846,140,175	ND	ND	ND
CGLU344	CGLU344P3_1	100	5,838,083,100	80,930	2,291,108,925	39%	27,067	4,287	2,846,140,175	ND	ND	ND
CGLU344	CGLU344P5_1	100	7,685,989,200	80,930	3,722,274,529	48%	43,945	3,471	2,846,140,175	ND	ND	ND
CGPLLU13	CGPLLU13P27	100	5,659,546,100	80,930	1,721,618,955	30%	20,587	6,025	2,846,140,175	ND	ND	ND
CGPLLU13	CGPLLU13P28	100	6,199,049,700	80,930	2,563,659,840	41%	30,728	6,514	2,846,140,175	ND	ND	ND
CGPLLU13	CGPLLU13P29	100	5,864,396,500	80,930	1,194,237,002	20%	14,331	3,952	2,846,140,175	ND	ND	ND
CGPLLU13	CGPLLU13P30	100	5,080,197,700	80,930	1,373,550,586	27%	16,480	5,389	2,846,140,175	ND	ND	ND
CGPLLU264	CGPLLU264P	100	6,254,777,700	80,930	3,016,326,208	48%	36,164	12,138	2,846,140,175	ND	ND	ND
CGPLLU264	CGPLLU264P1	100	6,185,331,000	80,930	3,087,883,231	50%	37,003	8,388	2,846,140,175	ND	ND	ND
CGPLLU264	CGPLLU264P2	100	6,274,540,300	80,930	2,861,143,666	46%	34,308	6,817	2,846,140,175	ND	ND	ND
CGPLLU264	CGPLLU264P3	100	5,701,274,000	80,930	1,241,270,938	22%	14,886	4,273	2,846,140,175	ND	ND	ND

CGPLLU265	CGPLLU265P	100	6,091,276,800	80,930	2,922,585,558	48%	35,004	7,742	2,846,140,175	ND	ND	ND
CGPLLU265	CGPLLU265P1	100	6,430,107,900	80,930	2,945,953,499	46%	35,219	8,574	2,846,140,175	ND	ND	ND
CGPLLU265	CGPLLU265P2	100	5,869,510,300	80,930	2,792,208,995	48%	33,423	8,423	2,846,140,175	ND	ND	ND
CGPLLU265	CGPLLU265P3	100	5,884,330,900	80,930	2,588,386,038	44%	30,977	9,803	2,846,140,175	ND	ND	ND
CGPLLU266	CGPLLU266P	100	5,807,524,900	80,930	2,347,651,479	40%	28,146	5,793	2,846,140,175	ND	ND	ND
CGPLLU266	CGPLLU266P2	100	6,064,269,800	80,930	2,086,938,782	34%	24,994	6,221	2,846,140,175	ND	ND	ND
CGPLLU266	CGPLLU266P3	100	6,785,913,900	80,930	3,458,588,505	51%	41,432	7,765	2,846,140,175	ND	ND	ND
CGPLLU266	CGPLLU266P4	100	6,513,702,000	80,930	2,096,370,387	32%	25,142	6,598	2,846,140,175	ND	ND	ND
CGPLLU267	CGPLLU267P	100	6,610,761,200	80,930	2,576,886,619	39%	31,095	4,485	2,846,140,175	ND	ND	ND
CGPLLU267	CGPLLU267P2	100	6,156,102,000	80,930	2,586,081,726	42%	30,714	5,309	2,846,140,175	ND	ND	ND
CGPLLU267	CGPLLU267P3	100	6,180,799,700	80,930	2,013,434,756	33%	23,902	3,885	2,846,140,175	ND	ND	ND
CGPLLU269	CGPLLU269P1	100	6,221,168,600	80,930	1,499,602,843	24%	17,799	6,098	2,846,140,175	ND	ND	ND
CGPLLU269	CGPLLU269P2	100	5,353,961,600	80,930	1,698,331,125	32%	20,094	5,252	2,846,140,175	ND	ND	ND
CGPLLU269	CGPLLU269P3	100	5,831,612,800	80,930	1,521,114,956	26%	18,067	6,210	2,846,140,175	ND	ND	ND
CGPLLU270	CGPLLU270P	100	5,950,217,300	80,930	2,535,494,178	43%	30,291	5,666	2,846,140,175	ND	ND	ND
CGPLLU270	CGPLLU270P2	100	5,549,812,500	80,930	1,611,923,056	29%	19,275	4,080	2,846,140,175	ND	ND	ND
CGPLLU270	CGPLLU270P3	100	6,180,818,300	80,930	2,898,765,742	47%	34,697	5,488	2,846,140,175	ND	ND	ND
CGPLLU271	CGPLLU271P	100	6,134,366,400	80,930	1,351,029,627	22%	16,170	7,024	2,846,140,175	ND	ND	ND
CGPLLU271	CGPLLU271P1	100	6,491,884,900	80,930	1,622,578,435	25%	19,433	5,792	2,846,140,175	ND	ND	ND
CGPLLU271	CGPLLU271P2	100	5,742,881,200	80,930	2,349,421,128	41%	28,171	5,723	2,846,140,175	ND	ND	ND
CGPLLU271	CGPLLU271P3	100	5,503,999,300	80,930	1,695,782,705	31%	20,320	5,907	2,846,140,175	ND	ND	ND
CGPLLU271	CGPLLU271P4	100	6,229,704,000	80,930	1,481,468,974	24%	17,608	4,633	2,846,140,175	ND	ND	ND
CGPLLU43	CGPLLU43P3	100	6,575,907,000	80,930	3,002,048,491	46%	35,997	5,445	2,846,140,175	ND	ND	ND
CGPLLU43	CGPLLU43P4	100	6,204,350,900	80,930	3,016,077,187	49%	36,162	5,704	2,846,140,175	ND	ND	ND
CGPLLU43	CGPLLU43P5	100	5,997,724,300	80,930	2,989,608,757	50%	35,873	6,228	2,846,140,175	ND	ND	ND
CGPLLU43	CGPLLU43P6	100	6,026,261,500	80,930	2,881,177,658	48%	34,568	7,221	2,846,140,175	ND	ND	ND

* Bases mapped to off-target region include those not overlapping the targeted region or adjacent regions within 200 bases.

Table 2.5. Summary of somatic sequence alterations detected in cfDNA.

Patient ID	Patient Timepoint	Days since Treatment	Gene Symbol	Transcript Accession	Amino Acid (Protein)	Mutation Type	Consequence	Mutant Allele Fraction	Total Distinct Coverage	Distinct Mutant Coverage	Hot-spot Alteration
CGLU294	CGLU294P_1	0.0	ERBB2	CCDS32642.1	E770_A771insAYVM	Insertion	In-frame insertion	2.39%	4,098	98	No
CGLU294	CGLU294P_1	0.0	TP53	CCDS11118.1	S166*	Substitution	Nonsense	0.88%	3,864	34	No
CGLU294	CGLU294P1_1	0.2	ERBB2	CCDS32642.1	G776Yfs*17	Insertion	Frameshift	0.36%	2480	9	No
CGLU294	CGLU294P1_1	0.2	ERBB2	CCDS32642.1	E770_A771insAYVM	Insertion	In-frame insertion	7.01%	2410	169	No
CGLU294	CGLU294P1_1	0.2	TP53	CCDS11118.1	S166*	Substitution	Nonsense	2.41%	1909	46	No
CGLU294	CGLU294P2_1	3.0	ERBB2	CCDS32642.1	E770_A771insAYVM	Insertion	In-frame insertion	4.39%	1891	83	No
CGLU294	CGLU294P2_1	3.0	TP53	CCDS11118.1	S166*	Substitution	Nonsense	1.69%	1543	26	No
CGLU294	CGLU294P3_2	7.0	ERBB2	CCDS32642.1	E770_A771insAYVM	Insertion	In-frame insertion	4.80%	2227	107	No
CGLU294	CGLU294P3_2	7.0	TP53	CCDS11118.1	S166*	Substitution	Nonsense	2.13%	1782	38	No
CGLU294	CGLU294P4_1	29.0	ERBB2	CCDS32642.1	E770_A771insAYVM	Insertion	In-frame insertion	1.63%	490	8	No
CGLU315	CGLU315P_1	0.0	EGFR	CCDS5514.1	L861Q	Substitution	Nonsynonymous	2.91%	413	12	Yes
CGLU315	CGLU315P1_1	0.2	CTNNB1	CCDS2694.1	S45P	Substitution	Nonsynonymous	1.34%	1,417	19	Yes
CGLU315	CGLU315P1_1	0.2	EGFR	CCDS5514.1	L861Q	Substitution	Nonsynonymous	1.95%	1,592	31	Yes
CGLU315	CGLU315P1_1	0.2	TP53	CCDS11118.1	R273H	Substitution	Nonsynonymous	1.70%	1,232	21	Yes
CGLU316	CGLU316P6_1	-53.0	EGFR	CCDS5514.1	G719A	Substitution	Nonsynonymous	13.06%	2497	326	Yes
CGLU316	CGLU316P6_1	-53.0	EGFR	CCDS5514.1	L861Q	Substitution	Nonsynonymous	15.72%	2849	448	Yes
CGLU316	CGLU316P6_1	-53.0	TP53	CCDS11118.1	C242F	Substitution	Nonsynonymous	6.57%	1462	96	Yes
CGLU316	CGLU316P6_1	-53.0	TP53	CCDS11118.1	I195T	Substitution	Nonsynonymous	1.65%	2118	35	Yes
CGLU316	CGLU316P7_1	-4.0	EGFR	CCDS5514.1	G719A	Substitution	Nonsynonymous	40.03%	3837	1536	Yes
CGLU316	CGLU316P7_1	-4.0	EGFR	CCDS5514.1	L861Q	Substitution	Nonsynonymous	45.67%	4342	1983	Yes
CGLU316	CGLU316P7_1	-4.0	TP53	CCDS11118.1	C242F	Substitution	Nonsynonymous	19.06%	1836	350	Yes
CGLU316	CGLU316P7_1	-4.0	TP53	CCDS11118.1	I195T	Substitution	Nonsynonymous	1.04%	2206	23	Yes
CGLU316	CGLU316P8_1	18.0	EGFR	CCDS5514.1	G719A	Substitution	Nonsynonymous	33.38%	3247	1084	Yes

CGLU316	CGLU316P8_1	18.0	EGFR	CCDS5514.1	L861Q	Substitution	Nonsynonymous	32.63%	3543	1156	Yes
CGLU316	CGLU316P8_1	18.0	TP53	CCDS11118.1	C242F	Substitution	Nonsynonymous	8.91%	1661	148	Yes
CGLU316	CGLU316P8_1	18.0	TP53	CCDS11118.1	I195T	Substitution	Nonsynonymous	1.33%	2035	27	Yes
CGLU316	CGLU316P9_1	87.0	EGFR	CCDS5514.1	G719A	Substitution	Nonsynonymous	64.89%	5754	3734	Yes
CGLU316	CGLU316P9_1	87.0	EGFR	CCDS5514.1	L861Q	Substitution	Nonsynonymous	66.01%	7629	5036	Yes
CGLU316	CGLU316P9_1	87.0	TP53	CCDS11118.1	C242F	Substitution	Nonsynonymous	50.91%	1707	869	Yes
CGLU316	CGLU316P9_1	87.0	TP53	CCDS11118.1	Y205C	Substitution	Nonsynonymous	0.12%	2437	3	Yes
CGLU316	CGLU316P9_1	87.0	TP53	CCDS11118.1	I195T	Substitution	Nonsynonymous	0.90%	2105	19	Yes
CGLU319	CGLU319P_1	0.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.10%		3	Yes
CGLU324	CGLU324P_1	1.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.38%	1325	5	Yes
CGLU324	CGLU324P_1	1.0	STK11	CCDS45896.1	L353H	Substitution	Nonsynonymous	0.53%	1137	6	No
CGLU344	CGLU344P2_1	0.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.22%	2240	5	Yes
CGLU344	CGLU344P2_1	0.0	TP53	CCDS11118.1	P278S	Substitution	Nonsynonymous	0.19%	2156	4	Yes
CGLU344	CGLU344P3_1	0.2	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.40%	2999	12	Yes
CGLU344	CGLU344P3_1	0.2	EGFR	CCDS5514.1	T790M	Substitution	Nonsynonymous	0.15%	3412	5	Yes
CGLU369	CGLU369P_1	-2.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	20.61%	1946	401	Yes
CGLU369	CGLU369P1_1	12.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.22%	2307	5	Yes
CGLU369	CGLU369P2_1	68.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.16%	3071	5	Yes
CGLU369	CGLU369P3_1	110.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.10%	4190	4	Yes
CGLU373	CGLU373P_1	-2.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.82%	4155	34	Yes
CGLU373	CGLU373P2_1	7.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.15%	3255	5	Yes
CGLU373	CGLU373P2_1	7.0	TP53	CCDS11118.1	H214R	Substitution	Nonsynonymous	0.12%	3313	4	Yes
CGPLLU12	CGPLLU12P_6	-150.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	10.20%	2705	276	Yes
CGPLLU12	CGPLLU12P_6	-150.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	5.03%	3182	160	Yes
CGPLLU12	CGPLLU12P_6	-150.0	TP53	CCDS11118.1	258E>K	Substitution	Nonsynonymous	3.79%	1928	73	No
CGPLLU12	CGPLLU12P_22	0.0	RB1	CCDS31973.1	I680Yfs*13	Insertion	Frameshift	0.24%	4183	10	No
CGPLLU12	CGPLLU12P_22	0.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	20.19%	5141	1038	Yes
CGPLLU12	CGPLLU12P_22	0.0	STK11	CCDS45896.1	137Q>X	Substitution	Nonsense	0.98%	1326	13	No

CGPLLU12	CGPLLU12P_22	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	8.09%	7649	619	Yes
CGPLLU12	CGPLLU12P_22	0.0	TP53	CCDS11118.1	258E>K	Substitution	Nonsynonymous	10.37%	3356	348	No
CGPLLU12	CGPLLU12P_18	0.2	RB1	CCDS31973.1	I680Yfs*13	Insertion	Frameshift	0.74%	4480	33	No
CGPLLU12	CGPLLU12P_18	0.2	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	21.55%	5712	1231	Yes
CGPLLU12	CGPLLU12P_18	0.2	EGFR	CCDS5514.1	745->KTSP	Insertion	In-frame insertion	0.16%	5498	9	No
CGPLLU12	CGPLLU12P_18	0.2	STK11	CCDS45896.1	137Q>X	Substitution	Nonsense	1.49%	1410	21	No
CGPLLU12	CGPLLU12P_18	0.2	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	9.37%	8897	834	Yes
CGPLLU12	CGPLLU12P_18	0.2	ERBB4	CCDS2394.1	733Y>N	Substitution	Nonsynonymous	0.38%	3438	13	No
CGPLLU12	CGPLLU12P_18	0.2	TP53	CCDS11118.1	258E>K	Substitution	Nonsynonymous	10.93%	3768	412	No
CGPLLU12	CGPLLU12P_20	10.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	0.17%	4095	7	Yes
CGPLLU12	CGPLLU12P_20	10.0	TP53	CCDS11118.1	258E>K	Substitution	Nonsynonymous	0.16%	3688	6	No
CGPLLU12	CGPLLU12P_34	227.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	7.09%	4189	297	Yes
CGPLLU12	CGPLLU12P_34	227.0	TP53	CCDS11118.1	258E>K	Substitution	Nonsynonymous	3.47%	3802	132	No
CGPLLU13	CGPLLU13P27	-2.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	7.66%	2978	228	Yes
CGPLLU13	CGPLLU13P27	-2.0	EGFR	CCDS5514.1	T790M	Substitution	Nonsynonymous	0.13%	3763	5	Yes
CGPLLU13	CGPLLU13P28	5.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	13.10%	3504	459	Yes
CGPLLU13	CGPLLU13P28	5.0	EGFR	CCDS5514.1	E931Q	Substitution	Nonsynonymous	0.13%	6128	8	No
CGPLLU13	CGPLLU13P29	28.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	6.09%	1889	115	Yes
CGPLLU13	CGPLLU13P30	91.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	9.28%	2512	233	Yes
CGPLLU13	CGPLLU13P30	91.0	EGFR	CCDS5514.1	T790M	Substitution	Nonsynonymous	0.16%	3032	5	Yes
CGPLLU14	CGPLLU14P_8	-38.0	EGFR	CCDS5514.1	719G>S	Substitution	Nonsynonymous	0.75%	2141	16	Yes
CGPLLU14	CGPLLU14P_8	-38.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.45%	2456	11	Yes
CGPLLU14	CGPLLU14P_8	-38.0	EGFR	CCDS5514.1	861L>Q	Substitution	Nonsynonymous	0.89%	2357	21	Yes
CGPLLU14	CGPLLU14P_12	-16.0	EGFR	CCDS5514.1	719G>S	Substitution	Nonsynonymous	0.15%	2722	4	Yes
CGPLLU14	CGPLLU14P_12	-16.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.16%	3196	5	Yes
CGPLLU14	CGPLLU14P_12	-16.0	EGFR	CCDS5514.1	861L>Q	Substitution	Nonsynonymous	0.18%	2823	5	Yes
CGPLLU14	CGPLLU14P_15	-3.0	EGFR	CCDS5514.1	719G>S	Substitution	Nonsynonymous	0.49%	3888	19	Yes
CGPLLU14	CGPLLU14P_15	-3.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.48%	5004	24	Yes

CGPLLU14	CGPLLU14P_15	-3.0	EGFR	CCDS5514.1	861L>Q	Substitution	Nonsynonymous	0.45%	4233	19	Yes
CGPLLU14	CGPLLU14P_21	0.0	EGFR	CCDS5514.1	719G>S	Substitution	Nonsynonymous	0.79%	2801	22	Yes
CGPLLU14	CGPLLU14P_21	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.98%	3281	32	Yes
CGPLLU14	CGPLLU14P_21	0.0	EGFR	CCDS5514.1	861L>Q	Substitution	Nonsynonymous	1.39%	2876	40	Yes
CGPLLU14	CGPLLU14P_19	0.3	EGFR	CCDS5514.1	719G>S	Substitution	Nonsynonymous	1.05%	3697	39	Yes
CGPLLU14	CGPLLU14P_19	0.3	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.90%	4760	43	Yes
CGPLLU14	CGPLLU14P_19	0.3	EGFR	CCDS5514.1	861L>Q	Substitution	Nonsynonymous	0.96%	4383	42	Yes
CGPLLU14	CGPLLU14P_19	0.3	MYC	CCDS6359.2	98R>W	Substitution	Nonsynonymous	0.28%	3894	11	No
CGPLLU18	CGPLLU18P_4	-1.0	ABL1	CCDS35166.1	422V>I	Substitution	Nonsynonymous	0.17%	4028	7	No
CGPLLU18	CGPLLU18P_4	-1.0	BRAF	CCDS5863.1	145A>S	Substitution	Nonsynonymous	0.20%	3949	8	No
CGPLLU18	CGPLLU18P_4	-1.0	CDKN2A	CCDS56565.1	12S>L	Substitution	Nonsynonymous	0.52%	2478	13	No
CGPLLU18	CGPLLU18P_4	-1.0	CTNNB1	CCDS2694.1	60S>T	Substitution	Nonsynonymous	0.37%	3251	12	No
CGPLLU18	CGPLLU18P_4	-1.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	10.09%	17897	1806	Yes
CGPLLU18	CGPLLU18P_4	-1.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	53.71%	14755	7925	Yes
CGPLLU18	CGPLLU18P_4	-1.0	ERBB2	CCDS32642.1	827M>V	Substitution	Nonsynonymous	0.27%	5137	14	No
CGPLLU18	CGPLLU18P_4	-1.0	ERBB4	CCDS2394.1	566L>I	Substitution	Nonsynonymous	0.26%	3892	10	No
CGPLLU18	CGPLLU18P_4	-1.0	ESR1	CCDS5234.1	44L>M	Substitution	Nonsynonymous	0.75%	4528	34	No
CGPLLU18	CGPLLU18P_4	-1.0	ESR1	CCDS5234.1	61E>D	Substitution	Nonsynonymous	0.36%	3624	13	No
CGPLLU18	CGPLLU18P_4	-1.0	MYC	CCDS6359.2	174S>G	Substitution	Nonsynonymous	0.14%	4935	7	No
CGPLLU18	CGPLLU18P_4	-1.0	MYC	CCDS6359.2	48Q>H	Substitution	Nonsynonymous	0.36%	3939	14	No
CGPLLU18	CGPLLU18P_4	-1.0	MYC	CCDS6359.2	98R>W	Substitution	Nonsynonymous	0.15%	4728	7	No
CGPLLU18	CGPLLU18P_4	-1.0	PDGFRA	CCDS3495.1	37K>R	Substitution	Nonsynonymous	0.20%	4030	8	No
CGPLLU18	CGPLLU18P_15	6.0	AR	CCDS14387.1	31R>L	Substitution	Nonsynonymous	0.18%	3995	7	No
CGPLLU18	CGPLLU18P_15	6.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.26%	6660	17	Yes
CGPLLU18	CGPLLU18P_15	6.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	1.30%	5625	73	Yes
CGPLLU18	CGPLLU18P_11	20.0	AR	CCDS14387.1	31R>L	Substitution	Nonsynonymous	0.17%	3554	6	No
CGPLLU18	CGPLLU18P_11	20.0	CDKN2A	CCDS56565.1	12S>L	Substitution	Nonsynonymous	0.15%	2592	4	No
CGPLLU18	CGPLLU18P_11	20.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.63%	4423	28	Yes

CGPLLU18	CGPLLU18P_11	20.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	1.68%	4101	69	Yes
CGPLLU244	CGPLLU244P_1	-7.0	EGFR	CCDS5514.1	62L>R	Substitution	Nonsynonymous	4.48%	5898	264	No
CGPLLU244	CGPLLU244P_1	-7.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	4.13%	6681	276	Yes
CGPLLU244	CGPLLU244P_1	-7.0	TP53	CCDS11118.1	134F>L	Substitution	Nonsynonymous	4.98%	7524	375	No
CGPLLU244	CGPLLU244P_2	-1.0	EGFR	CCDS5514.1	62L>R	Substitution	Nonsynonymous	3.41%	5746	196	No
CGPLLU244	CGPLLU244P_2	-1.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	2.84%	7348	209	Yes
CGPLLU244	CGPLLU244P_2	-1.0	TP53	CCDS11118.1	134F>L	Substitution	Nonsynonymous	2.83%	8797	249	No
CGPLLU244	CGPLLU244P_3	6.0	EGFR	CCDS5514.1	62L>R	Substitution	Nonsynonymous	5.14%	6240	321	No
CGPLLU244	CGPLLU244P_3	6.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	5.57%	7526	419	Yes
CGPLLU244	CGPLLU244P_3	6.0	TP53	CCDS11118.1	134F>L	Substitution	Nonsynonymous	4.76%	8721	415	No
CGPLLU244	CGPLLU244P_4	62.0	EGFR	CCDS5514.1	62L>R	Substitution	Nonsynonymous	10.98%	6602	725	No
CGPLLU244	CGPLLU244P_4	62.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	11.80%	7043	831	Yes
CGPLLU244	CGPLLU244P_4	62.0	TP53	CCDS11118.1	134F>L	Substitution	Nonsynonymous	11.23%	8098	909	No
CGPLLU245	CGPLLU245P_1	-32.0	EGFR	CCDS5514.1	745KELREA>K	Deletion	In-frame deletion	10.60%	5869	622	Yes
CGPLLU245	CGPLLU245P_1	-32.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	5.56%	9722	541	Yes
CGPLLU245	CGPLLU245P_1	-32.0	PDGFRA	CCDS3495.1	293R>H	Substitution	Nonsynonymous	0.44%	6374	28	No
CGPLLU245	CGPLLU245P_2	0.0	EGFR	CCDS5514.1	745KELREA>K	Deletion	In-frame deletion	14.10%	8086	1140	Yes
CGPLLU245	CGPLLU245P_2	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	6.76%	14582	986	Yes
CGPLLU245	CGPLLU245P_2	0.0	PDGFRA	CCDS3495.1	293R>H	Substitution	Nonsynonymous	0.92%	8550	79	No
CGPLLU245	CGPLLU245P_3	7.0	EGFR	CCDS5514.1	745KELREA>K	Deletion	In-frame deletion	8.56%	6892	590	Yes
CGPLLU245	CGPLLU245P_3	7.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	4.07%	11765	479	Yes
CGPLLU245	CGPLLU245P_3	7.0	PDGFRA	CCDS3495.1	293R>H	Substitution	Nonsynonymous	0.60%	7673	46	No
CGPLLU245	CGPLLU245P_4	21.0	EGFR	CCDS5514.1	745KELREA>K	Deletion	In-frame deletion	10.69%	7287	779	Yes
CGPLLU245	CGPLLU245P_4	21.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	4.59%	13165	604	Yes
CGPLLU245	CGPLLU245P_4	21.0	PDGFRA	CCDS3495.1	293R>H	Substitution	Nonsynonymous	1.00%	8020	80	No
CGPLLU246	CGPLLU246P_1	-21.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.49%	7780	38	Yes
CGPLLU246	CGPLLU246P_1	-21.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	0.48%	5826	28	Yes
CGPLLU246	CGPLLU246P_1	-21.0	MAP2K1	CCDS10216.1	67D>N	Substitution	Nonsynonymous	0.18%	7080	13	No

CGPLLU246	CGPLLU246P_2	0.0	TP53	CCDS11118.1	P34Sfs*4	Deletion	Frameshift	2.48%	2181	54	No
CGPLLU246	CGPLLU246P_2	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	6.06%	8612	522	Yes
CGPLLU246	CGPLLU246P_2	0.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	6.17%	5933	366	Yes
CGPLLU246	CGPLLU246P_4	9.0	TP53	CCDS11118.1	P34Sfs*4	Deletion	Frameshift	0.20%	2461	5	No
CGPLLU246	CGPLLU246P_4	9.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	1.31%	6170	81	Yes
CGPLLU246	CGPLLU246P_4	9.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	1.72%	5051	87	Yes
CGPLLU246	CGPLLU246P_5	42.0	TP53	CCDS11118.1	P34Sfs*4	Deletion	Frameshift	1.87%	2669	50	No
CGPLLU246	CGPLLU246P_5	42.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	4.30%	7229	311	Yes
CGPLLU246	CGPLLU246P_5	42.0	EGFR	CCDS5514.1	858L>R	Substitution	Nonsynonymous	5.29%	5932	314	Yes
CGPLLU246	CGPLLU246P_5	42.0	MAP2K1	CCDS10216.1	67D>N	Substitution	Nonsynonymous	0.11%	6149	7	No
CGPLLU264	CGPLLU264P	-1.0	STK11	CCDS45896.1	V236M	Substitution	Nonsynonymous	0.30%	4293	13	No
CGPLLU264	CGPLLU264P1	6.0	EGFR	CCDS5514.1	D761N	Substitution	Nonsynonymous	0.16%	4358	7	No
CGPLLU264	CGPLLU264P2	27.0	FGFR3	CCDS3353.1	Y379S	Substitution	Nonsynonymous	0.18%	4455	8	No
CGPLLU265	CGPLLU265P	0.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.21%	4374	9	Yes
CGPLLU265	CGPLLU265P1	3.0	EGFR	CCDS5514.1	T790M	Substitution	Nonsynonymous	0.10%	5836	6	Yes
CGPLLU265	CGPLLU265P1	3.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.21%	4769	10	Yes
CGPLLU265	CGPLLU265P2	7.0	EGFR	CCDS5514.1	T790M	Substitution	Nonsynonymous	0.21%	5129	11	Yes
CGPLLU265	CGPLLU265P2	7.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.14%	4279	6	Yes
CGPLLU266	CGPLLU266P3	83.0	TP53	CCDS11118.1	R282G	Substitution	Nonsynonymous	0.15%	4691	7	Yes
CGPLLU267	CGPLLU267P	-1.0	PTEN	CCDS31238.1	Y225Ifs*18	Insertion	Frameshift	1.69%	2603	44	No
CGPLLU267	CGPLLU267P	-1.0	ALK	CCDS33172.1	G35_P36insL	Insertion	In-frame insertion	0.28%	2168	6	No
CGPLLU267	CGPLLU267P	-1.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	1.93%	2957	57	Yes
CGPLLU267	CGPLLU267P	-1.0	ERBB2	CCDS32642.1	R340L	Substitution	Nonsynonymous	0.20%	2953	6	No
CGPLLU267	CGPLLU267P	-1.0	RB1	CCDS31973.1	L700F	Substitution	Nonsynonymous	0.28%	2106	6	No
CGPLLU267	CGPLLU267P	-1.0	TP53	CCDS11118.1	M246L	Substitution	Nonsynonymous	0.66%	2276	15	No
CGPLLU267	CGPLLU267P2	34.0	MPL	CCDS483.1	V495Dfs*49	Deletion	Frameshift	0.33%	2105	7	No
CGPLLU267	CGPLLU267P2	34.0	TP53	CCDS11118.1	S183Rfs*2	Deletion	Frameshift	0.19%	3676	7	No
CGPLLU267	CGPLLU267P2	34.0	ALK	CCDS33172.1	E1158K	Substitution	Nonsynonymous	0.23%	3045	7	No

CGPLLU267	CGPLLU267P2	34.0	AR	CCDS14387.1	S397R	Substitution	Nonsynonymous	0.21%	2821	6	No
CGPLLU267	CGPLLU267P2	34.0	CDH1	CCDS10869.1	E35K	Substitution	Nonsynonymous	0.23%	3866	9	No
CGPLLU267	CGPLLU267P2	34.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.14%	3532	5	Yes
CGPLLU267	CGPLLU267P2	34.0	FBXW7	CCDS3777.1	C466F	Substitution	Nonsynonymous	0.55%	2379	13	No
CGPLLU267	CGPLLU267P2	34.0	KIT	CCDS3496.1	K167N	Substitution	Nonsynonymous	0.22%	3211	7	No
CGPLLU267	CGPLLU267P2	34.0	VHL	CCDS2597.1	R79C	Substitution	Nonsynonymous	0.39%	1808	7	No
CGPLLU267	CGPLLU267P3	90.0	PTEN	CCDS31238.1	Y225Ifs*18	Insertion	Frameshift	0.34%	2040	7	No
CGPLLU267	CGPLLU267P3	90.0	ALK	CCDS33172.1	E343V	Substitution	Nonsynonymous	0.51%	1370	7	No
CGPLLU267	CGPLLU267P3	90.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.38%	2394	9	Yes
CGPLLU269	CGPLLU269P1	0.0	EGFR	CCDS5514.1	L858R	Substitution	Nonsynonymous	0.10%	2894	3	Yes
CGPLLU271	CGPLLU271P	0.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	3.36%	2533	85	Yes
CGPLLU271	CGPLLU271P	0.0	EGFR	CCDS5514.1	T790M	Substitution	Nonsynonymous	1.80%	3440	62	Yes
CGPLLU271	CGPLLU271P	0.0	PTEN	CCDS31238.1	H196Y	Substitution	Nonsynonymous	0.68%	1476	10	No
CGPLLU271	CGPLLU271P	0.0	TP53	CCDS11118.1	R267W	Substitution	Nonsynonymous	0.23%	1749	4	Yes
CGPLLU271	CGPLLU271P	0.0	TP53	CCDS11118.1	R248W	Substitution	Nonsynonymous	2.28%	2197	50	Yes
CGPLLU271	CGPLLU271P1	6.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.17%	2859	5	Yes
CGPLLU271	CGPLLU271P2	20.0	TP53	CCDS11118.1	R267W	Substitution	Nonsynonymous	0.18%	2712	5	Yes
CGPLLU271	CGPLLU271P3	104.0	TP53	CCDS11118.1	R267W	Substitution	Nonsynonymous	0.33%	2458	8	Yes
CGPLLU271	CGPLLU271P4	259.0	EGFR	CCDS5514.1	E746_A750del	Deletion	In-frame deletion	0.44%	2251	10	Yes
CGPLLU271	CGPLLU271P4	259.0	TP53	CCDS11118.1	R248W	Substitution	Nonsynonymous	0.24%	2082	5	Yes
CGPLLU86	CGPLLU86P_1	0.5	EGFR	CCDS5514.1	746ELREATS>D	Deletion	In-frame deletion	0.19%	2626	5	Yes
CGPLLU88	CGPLLU88P_2	0.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	9.06%	6447	584	Yes
CGPLLU88	CGPLLU88P_2	0.0	CTNNB1	CCDS2694.1	32D>V	Substitution	Nonsynonymous	12.17%	5474	666	Yes
CGPLLU88	CGPLLU88P_2	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	8.65%	10829	937	Yes
CGPLLU88	CGPLLU88P_2	0.0	MYC	CCDS6359.2	47Y>F	Substitution	Nonsynonymous	0.11%	6119	7	No
CGPLLU88	CGPLLU88P_2	0.0	PIK3CA	CCDS43171.1	624T>R	Substitution	Nonsynonymous	2.57%	3188	82	No
CGPLLU88	CGPLLU88P	7.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	0.11%	3568	4	Yes
CGPLLU88	CGPLLU88P	7.0	CTNNB1	CCDS2694.1	32D>V	Substitution	Nonsynonymous	0.22%	3623	8	Yes

CGPLLU88	CGPLLU88P	7.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.15%	4095	6	Yes
CGPLLU88	CGPLLU88P	7.0	FGFR2	CCDS31298.1	304D>N	Substitution	Nonsynonymous	0.24%	3746	9	No
CGPLLU88	CGPLLU88P_5	297.0	EGFR	CCDS5514.1	745KELREA>T	Deletion	In-frame deletion	0.93%	2155	20	Yes
CGPLLU88	CGPLLU88P_5	297.0	CTNNB1	CCDS2694.1	32D>V	Substitution	Nonsynonymous	2.42%	2229	54	Yes
CGPLLU88	CGPLLU88P_5	297.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.13%	2394	3	Yes
CGPLLU89	CGPLLU89P	0.0	TP53	CCDS11118.1	656_672+6	Deletion	Frameshift	0.36%	5598	20	No
CGPLLU89	CGPLLU89P	0.0	EGFR	CCDS5514.1	747LREATS>-	Deletion	In-frame deletion	0.42%	5434	23	Yes
CGPLLU89	CGPLLU89P	0.0	CTNNB1	CCDS2694.1	32D>G	Substitution	Nonsynonymous	0.27%	5556	15	Yes
CGPLLU89	CGPLLU89P	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.17%	6320	11	Yes
CGPLLU89	CGPLLU89P_2	7.0	EGFR	CCDS5514.1	747LREATS>-	Deletion	In-frame deletion	0.20%	3540	7	Yes
CGPLLU89	CGPLLU89P_2	7.0	CTNNB1	CCDS2694.1	32D>G	Substitution	Nonsynonymous	0.28%	3595	10	Yes
CGPLLU89	CGPLLU89P_2	7.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	0.19%	3715	7	Yes
CGPLLU89	CGPLLU89P_5	22.0	TP53	CCDS11118.1	656_672+6	Deletion	Frameshift	0.26%	1929	5	No
CGPLLU89	CGPLLU89P_5	22.0	CTNNB1	CCDS2694.1	32D>G	Substitution	Nonsynonymous	0.21%	1870	4	Yes
CGPLLU99	CGPLLU99P_8	0.0	EGFR	CCDS5514.1	E746Afs*5	Insertion	Frameshift	0.62%	6095	38	No
CGPLLU99	CGPLLU99P_8	0.0	EGFR	CCDS5514.1	746ELREA>-	Deletion	In-frame deletion	19.65%	6533	1284	No
CGPLLU99	CGPLLU99P_8	0.0	TP53	CCDS11118.1	306R>X	Substitution	Nonsense	19.69%	5003	985	Yes
CGPLLU99	CGPLLU99P_8	0.0	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	7.24%	9626	697	Yes
CGPLLU99	CGPLLU99P_10	0.3	EGFR	CCDS5514.1	E746Afs*5	Insertion	Frameshift	0.51%	6246	32	No
CGPLLU99	CGPLLU99P_10	0.3	EGFR	CCDS5514.1	746ELREA>-	Deletion	In-frame deletion	15.67%	6626	1038	No
CGPLLU99	CGPLLU99P_10	0.3	TP53	CCDS11118.1	306R>X	Substitution	Nonsense	13.76%	5573	767	Yes
CGPLLU99	CGPLLU99P_10	0.3	EGFR	CCDS5514.1	790T>M	Substitution	Nonsynonymous	5.76%	8714	502	Yes

Table 2.6. Summary of blood cell proliferation alterations detected in cfDNA.

Patient ID	Patient Timepoint	Gene Symbol	Transcript Accession	Amino Acid (Protein)	Mutation Type	Consequence	Mutant Allele Fraction	Total Distinct Coverage	Distinct Mutant Coverage	Hot-spot Alteration
CGLU294	CGLU294P_1	DNMT3A	CCDS33157.1	G532S	Substitution	Nonsynonymous	0.63%	3026	19	No
CGLU344	CGLU344P3_1	DNMT3A	CCDS33157.1	N/A	Substitution	Splice site donor	0.22%	2709	6	No
CGLU344	CGLU344P5_1	DNMT3A	CCDS33157.1	R882H	Substitution	Nonsynonymous	0.22%	2779	6	Yes
CGLU369	CGLU369P_1	TP53	CCDS11118.1	R306*	Substitution	Nonsense	4.16%	1755	73	Yes
CGLU369	CGLU369P_1	JAK2	CCDS6457.1	V617F	Substitution	Nonsynonymous	4.05%	1407	57	Yes
CGLU369	CGLU369P1_1	TP53	CCDS11118.1	R306*	Substitution	Nonsense	0.13%	3107	4	Yes
CGLU369	CGLU369P1_1	JAK2	CCDS6457.1	V617F	Substitution	Nonsynonymous	5.26%	1824	96	Yes
CGLU369	CGLU369P2_1	TP53	CCDS11118.1	R306*	Substitution	Nonsense	0.13%	3825	5	Yes
CGLU369	CGLU369P2_1	JAK2	CCDS6457.1	V617F	Substitution	Nonsynonymous	3.93%	2316	91	Yes
CGLU369	CGLU369P3_1	JAK2	CCDS6457.1	V617F	Substitution	Nonsynonymous	2.37%	3251	77	Yes
CGPLLU12	CGPLLU12P_18	DNMT3A	CCDS33157.1	538T>A	Substitution	Nonsynonymous	0.17%	5740	10	No
CGPLLU12	CGPLLU12P_20	DNMT3A	CCDS33157.1	538T>A	Substitution	Nonsynonymous	0.25%	4323	11	No
CGPLLU12	CGPLLU12P_22	DNMT3A	CCDS33157.1	538T>A	Substitution	Nonsynonymous	0.28%	5282	15	No
CGPLLU12	CGPLLU12P_34	DNMT3A	CCDS33157.1	538T>A	Substitution	Nonsynonymous	0.25%	4828	12	No
CGPLLU12	CGPLLU12P_34	DNMT3A	CCDS33157.1	2173+1G>A	Substitution	Splice site donor	0.23%	4329	10	No
CGPLLU12	CGPLLU12P_6	DNMT3A	CCDS33157.1	538T>A	Substitution	Nonsynonymous	0.23%	2573	6	No
CGPLLU13	CGPLLU13P27	TP53	CCDS11118.1	R273H	Substitution	Nonsynonymous	0.27%	2640	7	Yes
CGPLLU13	CGPLLU13P30	TP53	CCDS11118.1	R273H	Substitution	Nonsynonymous	0.23%	2175	5	Yes
CGPLLU14	CGPLLU14P_12	DNMT3A	CCDS33157.1	905L>R	Substitution	Nonsynonymous	0.28%	2896	8	No
CGPLLU14	CGPLLU14P_12	TP53	CCDS11118.1	157V>F	Substitution	Nonsynonymous	0.26%	3106	8	Yes
CGPLLU14	CGPLLU14P_12	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	0.85%	2576	22	No
CGPLLU14	CGPLLU14P_15	DNMT3A	CCDS33157.1	905L>R	Substitution	Nonsynonymous	0.22%	4454	10	No
CGPLLU14	CGPLLU14P_15	TP53	CCDS11118.1	157V>F	Substitution	Nonsynonymous	0.46%	5178	24	Yes
CGPLLU14	CGPLLU14P_15	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	0.60%	3834	23	No

CGPLLU14	CGPLLU14P_19	DNMT3A	CCDS33157.1	905L>R	Substitution	Nonsynonymous	0.20%	4085	8	No
CGPLLU14	CGPLLU14P_19	TP53	CCDS11118.1	157V>F	Substitution	Nonsynonymous	0.86%	4877	42	Yes
CGPLLU14	CGPLLU14P_19	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	0.65%	3679	24	No
CGPLLU14	CGPLLU14P_21	TP53	CCDS11118.1	157V>F	Substitution	Nonsynonymous	0.77%	3254	25	Yes
CGPLLU14	CGPLLU14P_21	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	1.26%	2545	32	No
CGPLLU14	CGPLLU14P_23	TP53	CCDS11118.1	157V>F	Substitution	Nonsynonymous	0.77%	3254	25	Yes
CGPLLU14	CGPLLU14P_23	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	1.26%	2545	32	No
CGPLLU14	CGPLLU14P_23	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	0.68%	2349	16	No
CGPLLU14	CGPLLU14P_8	TP53	CCDS11118.1	157V>F	Substitution	Nonsynonymous	1.06%	2080	22	Yes
CGPLLU14	CGPLLU14P_8	TP53	CCDS11118.1	248R>G	Substitution	Nonsynonymous	1.64%	1890	31	No
CGPLLU18	CGPLLU18P_11	TP53	CCDS11118.1	Q104Rfs*19	Deletion	Frameshift	0.43%	3022	13	No
CGPLLU18	CGPLLU18P_11	DNMT3A	CCDS33157.1	2322+3A>G	Substitution	Splice site donor	1.70%	3295	56	No
CGPLLU18	CGPLLU18P_15	TP53	CCDS11118.1	Q104Rfs*19	Deletion	Frameshift	0.24%	3270	8	No
CGPLLU18	CGPLLU18P_15	DNMT3A	CCDS33157.1	2322+3A>G	Substitution	Splice site donor	0.97%	3913	38	No
CGPLLU18	CGPLLU18P_4	TP53	CCDS11118.1	Q104Rfs*19	Deletion	Frameshift	47.18%	2961	1397	No
CGPLLU18	CGPLLU18P_4	DNMT3A	CCDS33157.1	2322+3A>G	Substitution	Splice site donor	0.49%	3650	18	No
CGPLLU245	CGPLLU245P_2	TP53	CCDS11118.1	220Y>N	Substitution	Nonsynonymous	0.10%	7725	8	No
CGPLLU246	CGPLLU246P_1	DNMT3A	CCDS33157.1	536Y>X	Substitution	Nonsense	1.25%	6946	87	No
CGPLLU246	CGPLLU246P_1	DNMT3A	CCDS33157.1	882R>C	Substitution	Nonsynonymous	0.24%	6640	16	Yes
CGPLLU246	CGPLLU246P_1	DNMT3A	CCDS33157.1	735Y>S	Substitution	Nonsynonymous	0.34%	4939	17	No
CGPLLU246	CGPLLU246P_2	DNMT3A	CCDS33157.1	536Y>X	Substitution	Nonsense	1.37%	6783	93	No
CGPLLU246	CGPLLU246P_2	DNMT3A	CCDS33157.1	735Y>S	Substitution	Nonsynonymous	0.20%	3964	8	No
CGPLLU246	CGPLLU246P_2	DNMT3A	CCDS33157.1	882R>C	Substitution	Nonsynonymous	0.23%	5984	14	Yes
CGPLLU246	CGPLLU246P_4	DNMT3A	CCDS33157.1	536Y>X	Substitution	Nonsense	1.46%	5749	84	No
CGPLLU246	CGPLLU246P_4	DNMT3A	CCDS33157.1	882R>C	Substitution	Nonsynonymous	0.17%	5422	9	Yes
CGPLLU246	CGPLLU246P_4	DNMT3A	CCDS33157.1	735Y>S	Substitution	Nonsynonymous	0.28%	4264	12	No
CGPLLU246	CGPLLU246P_5	DNMT3A	CCDS33157.1	536Y>X	Substitution	Nonsense	1.65%	6068	100	No
CGPLLU246	CGPLLU246P_5	DNMT3A	CCDS33157.1	735Y>S	Substitution	Nonsynonymous	0.24%	4666	11	No

CGPLLU246	CGPLLU246P_5	DNMT3A	CCDS33157.1	882R>C	Substitution	Nonsynonymous	0.32%	6282	20	Yes
CGPLLU266	CGPLLU266P	DNMT3A	CCDS33157.1	E774K	Substitution	Nonsynonymous	0.63%	2388	15	No
CGPLLU266	CGPLLU266P2	DNMT3A	CCDS33157.1	E774K	Substitution	Nonsynonymous	0.24%	2947	7	No
CGPLLU266	CGPLLU266P3	DNMT3A	CCDS33157.1	E774K	Substitution	Nonsynonymous	0.32%	4064	13	No
CGPLLU266	CGPLLU266P4	DNMT3A	CCDS33157.1	E774K	Substitution	Nonsynonymous	0.62%	2742	17	No
CGPLLU267	CGPLLU267P2	DNMT3A	CCDS33157.1	A903S	Substitution	Nonsynonymous	0.22%	3193	7	No
CGPLLU269	CGPLLU269P1	TP53	CCDS11118.1	Y220C	Substitution	Nonsynonymous	0.15%	2662	4	Yes
CGPLLU269	CGPLLU269P2	DNMT3A	CCDS33157.1	D529Y	Substitution	Nonsynonymous	0.22%	2762	6	No
CGPLLU86	CGPLLU86P_1	DNMT3A	CCDS33157.1	720R>C	Substitution	Nonsynonymous	0.54%	2962	16	No
CGPLLU86	CGPLLU86P_6	DNMT3A	CCDS33157.1	720R>C	Substitution	Nonsynonymous	0.32%	5575	18	No
CGPLLU86	CGPLLU86P_8	DNMT3A	CCDS33157.1	720R>C	Substitution	Nonsynonymous	0.42%	2888	12	No
CGPLLU86	CGPLLU86P_9	DNMT3A	CCDS33157.1	720R>C	Substitution	Nonsynonymous	0.35%	2857	10	No
CGPLLU88	CGPLLU88P	DNMT3A	CCDS33157.1	1667+1G>A	Substitution	Splice site donor	1.98%	2678	53	No
CGPLLU88	CGPLLU88P_2	DNMT3A	CCDS33157.1	879N>D	Substitution	Nonsynonymous	0.19%	6691	13	No
CGPLLU88	CGPLLU88P_2	DNMT3A	CCDS33157.1	1667+1G>A	Substitution	Splice site donor	1.31%	4440	58	No
CGPLLU88	CGPLLU88P_5	DNMT3A	CCDS33157.1	1667+1G>A	Substitution	Splice site donor	2.23%	1886	42	No

Table 2.7. Summary of somatic structural alterations detected in cfDNA.

Patient ID	Z scores	chr1p	chr1q	chr2p	chr2q	chr3p	chr3q	chr4p	chr4q	chr5p	chr5q	chr6p	chr6q	chr7p	chr7q	chr8p	chr8q	chr9p	chr9q	chr10p	chr10q
CGPLLU244	Day -7	-1.98	2.30	0.56	-0.71	-4.89	-0.08	-0.95	-3.78	1.27	-0.27	0.31	-1.12	7.07	4.62	-2.33	0.12	-0.43	-0.34	-3.05	-2.80
CGPLLU244	Day -1	-1.76	1.42	-0.97	-1.07	-3.34	-1.03	0.15	-1.85	1.58	-1.75	-0.76	-1.29	5.95	4.85	-1.09	0.22	0.22	-0.62	-2.46	-2.94
CGPLLU244	Day 6	-2.56	3.19	-0.01	0.57	-5.40	-1.19	-1.37	-4.28	2.61	-1.00	0.84	0.41	10.44	4.83	-3.37	1.93	1.07	-0.33	-2.44	-4.83
CGPLLU244	Day 62	-1.92	7.13	2.18	-2.35	-9.22	1.89	-1.24	-7.79	2.09	-3.79	0.71	-5.05	17.92	8.98	-5.79	2.18	-1.48	-2.52	-4.98	-7.72
CGPLLU245	Day -32	-5.09	7.23	-1.34	0.17	-5.05	-3.07	-2.39	-1.49	11.49	4.94	0.07	-7.48	25.65	19.49	-1.25	2.48	0.27	1.41	-0.70	-0.96
CGPLLU245	Day 0	-6.36	10.12	-2.51	1.46	-6.07	-4.63	-2.68	-4.02	20.30	6.19	0.46	-10.17	41.91	29.09	-3.82	2.77	0.26	1.95	0.09	-2.36
CGPLLU245	Day 7	-3.94	4.45	-1.11	0.49	-5.23	-2.91	-1.14	-1.86	10.93	4.06	-0.21	-6.26	22.45	15.83	-1.46	-1.20	0.68	3.02	1.32	-1.76
CGPLLU245	Day 21	-4.69	6.53	-2.38	1.14	-5.22	-1.67	-2.17	-3.14	12.83	5.70	1.10	-6.19	29.01	21.51	-2.00	0.58	0.43	2.59	-0.01	-0.39
CGPLLU246	Day -21	-0.99	-1.31	-0.87	-0.38	-0.39	-0.84	0.89	0.86	1.18	0.89	-1.03	-0.16	0.82	1.61	0.76	-0.64	-0.07	0.10	0.93	0.82
CGPLLU246	Day 0	-1.18	-0.64	-4.76	-1.60	-5.93	-2.94	-0.76	-2.62	5.46	4.74	0.57	-2.21	16.05	15.95	-0.08	6.04	0.11	1.69	-3.54	-3.44
CGPLLU246	Day 9	-0.75	0.00	-0.28	0.74	-2.00	-3.28	-0.34	-0.71	1.89	-0.07	-0.60	-0.86	3.56	4.73	0.79	0.14	0.38	1.41	-0.71	-1.31
CGPLLU246	Day 42	-2.30	1.21	-2.10	0.71	-5.03	-3.29	-1.33	-1.68	2.59	3.62	0.45	1.08	9.75	10.37	0.34	6.18	1.83	1.89	-0.55	-4.57
CGLU294	Day 0	-1.32	2.07	1.02	2.39	-0.35	-2.08	-1.09	-0.93	-0.47	0.50	0.86	-1.33	1.46	3.19	0.80	0.48	0.57	0.87	-1.35	-1.64
CGLU294	Day 0.2	-1.49	0.08	0.28	1.45	0.02	-0.08	1.21	-0.86	0.90	-0.01	-1.83	-0.15	3.13	5.40	1.21	-0.54	-0.07	-0.36	0.33	-3.09
CGLU294	Day 3	-1.26	-0.03	-0.80	0.75	0.78	-0.70	1.19	0.60	0.30	1.57	-1.63	-0.44	2.42	6.24	0.34	-0.46	-0.07	-0.71	-0.65	-2.25
CGLU294	Day 7	-1.30	0.10	-0.04	2.19	-0.55	-2.00	-0.40	-0.78	0.12	1.51	-0.32	-1.94	1.85	4.59	0.86	-1.39	1.66	1.00	0.13	-3.11
CGLU294	Day 29	-0.01	2.93	-1.14	0.36	-1.48	-3.11	-0.99	-2.48	-0.31	11.33	0.92	-0.91	0.12	2.35	-1.35	-1.72	3.72	1.77	-0.71	1.50
CGLU315	Day 0	-0.21	3.25	-1.62	1.18	-1.27	-3.52	-2.11	-6.44	-0.34	10.53	1.42	-7.97	-1.43	1.49	-1.15	-3.16	6.54	4.51	2.15	2.64
CGLU315	Day 0.2	-1.69	0.51	-0.91	0.63	0.78	-0.81	-0.24	-0.17	1.07	1.88	-0.99	-1.54	0.87	0.97	0.41	-1.85	1.55	1.20	-0.87	0.49
CGLU315	Day 20	-0.17	1.54	-2.54	2.35	-2.54	-2.60	-1.86	-3.27	4.22	3.84	1.55	-5.86	-1.14	-1.21	0.78	-0.35	4.48	3.00	-0.33	2.96
CGLU319	Day 0	-1.21	2.43	0.22	1.28	-0.61	-1.48	-1.53	-0.09	0.03	3.91	0.65	-1.27	-1.51	1.98	0.88	0.38	0.91	0.55	-1.44	-2.42
CGLU319	Day 14	-0.74	0.51	0.75	-0.37	-0.90	0.05	0.07	-0.33	-1.20	3.83	-0.01	-0.82	-1.67	1.60	0.42	-1.59	0.36	0.95	-0.04	-0.21
CGLU324	Day 1	0.36	3.82	-1.84	1.31	-0.92	-0.80	-1.62	-0.96	3.93	3.03	-0.06	-2.94	0.12	-0.98	-0.25	-3.87	1.45	1.01	0.20	1.77
CGLU324	Day 20	-0.15	1.18	-1.04	1.43	-0.59	-1.71	-0.62	0.18	2.47	0.55	-0.10	-1.29	-0.85	-0.41	0.88	-3.28	1.35	1.35	-1.66	2.13
CGPLLU14	Day 0	3.19	1.71	0.89	2.31	-4.55	0.47	-2.38	-0.25	-0.65	-2.44	0.93	1.97	5.52	-0.47	-1.79	1.24	2.29	3.68	-3.87	-3.77
CGPLLU14	Day 0.33	1.12	-0.88	-0.55	1.50	-1.92	0.02	-1.65	-1.61	-1.43	-1.84	0.15	1.03	3.85	1.44	-0.79	-0.43	1.04	2.95	-2.48	-1.34

CGPLLU14	Day 7	0.31	-0.49	0.18	0.26	-0.56	0.65	-0.97	0.44	-1.10	-1.76	-0.76	0.79	1.04	0.49	-0.44	-0.94	1.32	2.74	-0.49	-0.48
CGPLLU14	Day -38	-0.49	1.88	0.13	1.48	-0.71	-0.90	-2.35	-1.50	-2.04	1.56	2.12	2.42	4.62	1.79	0.45	-1.53	1.73	1.98	-0.96	-0.91
CGPLLU14	Day -16	-0.16	0.64	0.30	1.06	-0.58	0.32	-1.81	-0.22	-2.49	1.30	1.59	0.46	0.49	1.59	-0.37	-0.84	0.60	2.35	-1.04	0.60
CGPLLU14	Day -3	-1.50	1.59	-0.97	1.30	-1.19	-1.74	-1.62	-2.39	-0.68	-0.51	1.91	-0.96	0.92	0.99	1.55	0.43	1.47	2.51	0.07	0.65
CGPLLU12	Day 0.17	-5.42	4.72	5.92	1.70	-8.47	3.30	-3.94	-6.89	14.83	-9.73	-2.62	-10.80	38.73	34.33	-6.15	-4.38	2.31	5.20	-6.84	-11.72
CGPLLU12	Day 10	0.03	-0.68	0.68	0.59	-0.55	0.74	-0.04	0.32	1.59	-0.91	-1.51	-0.65	1.28	1.67	0.85	-1.10	0.10	1.21	-1.84	-1.00
CGPLLU12	Day 227	-0.33	2.48	1.14	0.45	-5.84	-0.03	-2.82	-2.39	6.34	-4.08	-0.50	-3.04	10.36	4.65	1.15	-1.66	1.72	2.85	-3.59	-3.87
CGPLLU12	Day -150	-3.33	3.06	2.54	2.16	-3.14	0.00	-1.67	-3.19	3.98	-0.98	0.27	-1.66	12.73	8.33	-0.88	-1.73	2.44	2.67	-3.84	-3.09
CGPLLU12	Day 0	-4.87	3.94	6.01	0.96	-6.27	2.89	-3.31	-6.17	14.65	-8.36	-2.77	-9.99	34.17	28.68	-5.79	-2.12	1.55	4.27	-6.03	-9.94
CGPLLU18	Day 6	0.47	-0.34	0.29	1.84	-3.34	0.14	-1.99	-0.49	5.67	-4.50	1.92	2.63	4.10	-0.40	0.82	1.72	1.43	3.18	-4.46	-4.93
CGPLLU18	Day 20	-0.56	-0.92	0.01	-0.03	-1.43	0.39	-0.32	0.58	1.60	-1.11	-0.47	0.34	1.47	0.91	1.53	-0.29	0.33	1.05	-1.67	-1.43
CGPLLU18	Day -1	3.83	21.65	-5.72	-12.46	-22.73	9.29	-9.95	-16.07	43.29	15.48	15.51	4.07	72.46	-23.49	-8.98	-1.37	-1.45	-6.43	-8.21	-13.17
CGPLLU86	Day 0.5	-0.28	-0.88	0.53	-0.42	-0.38	-0.04	0.21	1.29	0.82	2.97	-0.48	-0.49	-0.40	0.46	0.61	-0.25	-0.18	0.06	0.66	1.19
CGPLLU86	Day 7	0.53	0.49	0.41	1.95	-2.24	-0.14	-2.14	-1.45	1.69	0.91	1.97	2.84	2.22	-0.98	-0.05	-0.66	1.32	1.53	-1.86	-0.44
CGPLLU86	Day 17	1.03	-0.08	0.89	3.14	-3.01	-0.40	-2.48	0.05	2.01	1.36	0.83	-0.54	2.78	-2.40	-0.11	2.28	1.33	2.97	-0.97	-1.94
CGPLLU86	Day 0	1.23	-0.26	-0.65	0.56	-1.71	-1.68	-1.52	-0.08	2.16	-2.76	0.41	0.17	0.63	0.78	1.89	0.91	0.88	1.53	-0.79	-1.97
CGPLLU89	Day 7	0.87	-0.33	0.83	0.13	-0.46	0.67	-0.88	-1.19	0.74	-3.39	-0.01	0.29	3.38	-1.27	0.51	-1.25	0.84	1.90	-2.03	-1.40
CGPLLU89	Day 22	0.00	-0.63	-0.65	-0.83	1.71	0.35	1.07	1.38	0.76	0.08	-1.26	0.06	-0.04	-0.10	0.42	-1.01	0.40	0.64	-0.22	-0.18
CGPLLU89	Day 0	0.85	-0.50	0.68	1.28	-3.68	-0.82	-2.15	-1.03	1.66	-2.61	1.20	0.77	4.38	-1.61	0.43	0.14	1.12	3.28	-4.39	-2.96
CGPLLU97	Day 7	1.18	-0.08	-0.24	-0.09	-0.02	-0.07	0.94	-0.28	0.80	-1.26	-0.13	-0.99	-1.21	0.92	0.26	-0.68	0.21	1.15	-0.51	-0.29
CGPLLU97	Day 273	0.63	-0.24	0.99	1.47	-1.95	0.53	-2.28	-0.90	2.25	-1.22	1.95	1.65	1.57	-0.31	0.60	0.51	2.13	2.80	-2.53	-3.66
CGPLLU97	Day 0	1.24	-0.17	1.23	0.87	-2.30	0.31	-1.64	0.10	0.56	-2.89	-0.02	0.81	4.26	0.95	-1.42	1.89	1.34	2.94	-0.57	-1.64
CGPLLU99	Day 0.33	6.40	3.42	-7.00	-4.80	-8.61	-0.72	-2.88	-2.51	19.91	20.52	-0.27	-18.85	48.38	1.65	-6.59	33.46	-1.50	-1.86	-4.56	-4.14
CGPLLU99	Day 9	1.39	0.09	2.21	1.61	-1.02	-0.98	-1.68	-0.84	-0.61	-0.15	-0.06	0.82	3.35	-1.05	-1.09	1.36	0.29	1.57	-1.18	-0.53
CGPLLU99	Day 21	2.11	1.05	1.97	0.77	-3.09	-0.70	-2.32	0.15	-0.14	0.34	-0.54	-0.05	2.92	-1.31	-0.44	0.64	1.10	2.08	-2.78	0.47
CGPLLU99	Day 0	6.82	5.32	-11.33	-8.79	-11.15	-1.03	-1.90	-2.41	29.40	31.04	-1.14	-29.03	61.00	6.24	-8.16	43.94	-3.25	-3.84	-3.60	-2.78
CGPLLU88	Day 0	-7.34	12.14	-4.36	-2.02	-11.59	3.61	-3.29	-9.61	17.24	-4.40	9.38	-16.83	22.10	23.46	-3.01	20.82	-2.04	-3.23	-3.57	-5.77
CGPLLU88	Day 297	-3.47	2.75	-0.51	2.30	-0.20	-0.63	-2.38	-2.43	1.66	1.42	3.82	1.56	6.25	2.18	1.31	5.00	0.60	-0.48	0.53	-2.38
CGPLLU88	Day 7	-2.43	1.39	-1.31	2.82	-0.78	-0.67	-1.60	-1.54	0.55	0.96	3.77	2.38	2.16	-1.40	2.61	5.26	0.73	0.79	-1.04	-2.53

Patient ID	Z scores	chr11p	chr11q	chr12p	chr12q	chr13q	chr14q	chr15q	chr16p	chr16q	chr17p	chr17q	chr18p	chr18q	chr19p	chr19q	chr20p	chr20q	chr21q	chr22q	PA score
CGPLLU244	Day -7	-0.97	-0.33	-1.41	-0.77	-4.35	7.34	1.53	1.80	-1.06	1.34	1.28	3.42	-1.56	0.76	2.14	0.60	-0.01	1.02	1.40	4.85
CGPLLU244	Day -1	-0.76	-0.45	-0.94	-0.86	-3.68	5.57	1.14	2.24	-0.41	0.70	1.13	2.64	-1.61	1.09	1.53	0.51	0.33	0.78	1.61	3.98
CGPLLU244	Day 6	-1.79	-1.38	-2.58	-1.80	-3.75	7.76	2.71	2.06	-1.48	1.66	1.63	3.42	-1.51	-0.42	1.48	0.90	-1.87	-1.47	1.08	5.52
CGPLLU244	Day 62	-1.18	0.95	-1.61	-0.64	-12.40	13.96	3.34	3.07	-1.10	0.34	1.46	4.98	-4.45	0.60	4.69	3.53	1.12	1.07	0.85	8.68
CGPLLU245	Day -32	-1.48	-3.99	-0.03	-1.64	-8.83	-3.77	-0.24	2.31	-1.64	-3.91	1.58	-6.46	-3.05	-1.42	-1.47	-2.42	-6.29	0.44	-0.04	9.08
CGPLLU245	Day 0	-1.92	-6.38	-1.01	-2.22	-9.48	-5.10	-1.58	3.60	-2.19	-4.31	1.76	-9.63	-4.46	-2.58	-1.85	-1.89	-8.97	-0.47	-2.23	11.00
CGPLLU245	Day 7	-1.69	-3.87	-0.75	-1.27	-7.40	-2.74	0.01	2.21	-1.30	-1.50	1.23	-2.51	-1.92	-1.03	-1.49	-1.30	-5.09	0.16	0.52	8.34
CGPLLU245	Day 21	-2.31	-4.55	-0.21	-2.93	-8.67	-3.89	0.25	1.65	-1.98	-2.09	1.81	-6.85	-3.30	-2.25	-2.15	-2.31	-8.27	-0.27	-0.62	9.50
CGPLLU246	Day -21	0.29	-0.48	0.13	0.12	0.19	0.57	-0.30	0.85	0.35	-0.77	-0.23	-0.45	-0.87	1.03	-0.33	-0.86	-0.16	2.15	0.11	0.31
CGPLLU246	Day 0	-0.34	-0.49	-2.04	-3.33	-6.98	5.99	0.91	1.84	-1.25	0.43	1.16	-2.43	-0.98	-1.48	-1.17	1.14	-4.23	5.59	0.80	7.33
CGPLLU246	Day 9	-1.48	-1.58	-1.15	-1.06	0.33	0.21	1.02	1.07	-0.78	0.64	1.04	1.55	-0.72	0.28	-0.44	0.14	-0.39	1.29	1.40	2.12
CGPLLU246	Day 42	-2.21	-2.25	-2.00	-2.74	-1.69	2.35	1.37	2.26	-2.17	-0.53	1.35	-0.15	0.29	-1.45	-2.09	-0.40	-4.45	0.55	-0.09	5.85
CGLU294	Day 0	-1.11	-0.96	-1.38	-1.74	-0.96	-1.05	0.99	0.44	-1.23	0.07	1.48	2.21	-0.23	-0.23	-1.11	0.00	0.24	-2.37	0.35	1.33
CGLU294	Day 0.2	1.21	0.36	-0.91	-0.99	-2.84	-2.28	0.11	0.73	-0.40	-2.36	1.01	0.63	-2.21	1.15	-0.13	-0.99	1.21	0.34	0.25	2.49
CGLU294	Day 3	1.54	0.28	-0.56	-0.87	-3.14	-0.56	-0.08	0.96	-0.46	-1.62	0.78	1.03	-3.10	1.28	-0.02	-1.13	-0.34	-0.45	-0.23	2.48
CGLU294	Day 7	-0.18	0.02	-1.66	-1.13	-1.75	-1.40	1.19	0.89	-1.31	-1.13	1.42	1.79	-1.43	0.42	-0.63	-1.30	-0.29	-1.92	0.57	1.68
CGLU294	Day 29	-1.76	-2.02	-1.99	-2.66	-5.99	-2.96	1.26	2.62	-1.48	-2.36	1.66	1.71	-2.72	0.27	-1.08	-2.41	-0.98	1.62	1.29	4.20
CGLU315	Day 0	-2.51	-2.75	-2.60	-2.95	-9.18	-1.95	2.99	1.05	-1.15	1.24	2.07	0.19	1.12	-0.62	-1.11	-0.63	0.30	-3.63	1.08	6.63
CGLU315	Day 0.2	-1.06	-0.87	-1.04	-1.03	-3.69	0.68	1.60	0.43	-0.24	0.13	1.12	-1.67	-1.98	0.86	-1.29	-0.80	0.44	-0.39	0.75	0.91
CGLU315	Day 20	-1.69	-1.86	-1.44	-2.17	-6.23	-2.25	2.93	0.87	-2.18	1.34	2.03	5.99	0.45	0.55	-1.74	-1.56	-0.56	-4.06	-0.77	4.65
CGLU319	Day 0	-1.78	-0.39	-1.54	-1.79	-3.60	0.73	0.95	0.64	-1.39	1.69	1.65	0.81	0.61	0.60	-1.31	-0.94	-0.74	-2.47	0.17	2.04
CGLU319	Day 14	-0.15	-0.90	-0.47	-0.28	-3.46	0.61	-0.25	-0.21	-0.52	0.75	0.88	0.78	-0.94	1.50	0.07	-0.78	0.47	-0.40	0.22	1.18
CGLU324	Day 1	-1.51	-0.92	-1.02	-1.79	-4.74	0.59	1.15	-0.35	-1.45	1.65	1.61	-0.02	-0.10	0.44	-1.27	-1.16	-0.10	-3.54	2.09	3.32
CGLU324	Day 20	-1.33	-0.12	-0.69	-0.88	-3.86	-0.56	0.49	0.27	-0.94	1.48	1.14	1.00	-0.98	0.72	-0.39	-1.84	0.94	-1.75	1.43	1.67
CGPLLU14	Day 0	-3.31	-0.13	-1.17	-0.81	-6.22	0.06	2.32	-2.60	-2.65	1.35	2.18	6.46	-1.23	-1.87	-3.23	-1.73	-6.43	2.68	1.37	5.07
CGPLLU14	Day 0.33	-0.33	0.67	-0.14	-0.21	-3.34	0.19	0.90	-0.64	-1.20	1.15	1.11	3.68	-1.69	-0.55	-1.58	-0.59	-2.52	2.55	1.56	2.47
CGPLLU14	Day 7	-0.16	0.09	0.42	0.44	-2.09	-1.41	0.31	-0.47	-0.68	-0.10	0.59	0.25	-1.51	0.10	-1.10	-1.23	-2.42	0.67	0.60	0.79
CGPLLU14	Day -38	0.08	-2.60	-1.77	-1.78	0.59	0.99	1.12	-1.21	-1.61	-1.35	1.28	-1.25	1.36	-2.12	-2.78	0.65	-4.48	-0.43	1.00	2.52

CGPLLU14	Day -16	-0.05	-0.61	-0.04	-0.78	-0.74	-0.74	0.23	-1.11	-0.84	-1.43	0.78	-1.79	-0.39	-0.82	-2.14	-0.69	-0.77	1.19	1.23	0.82
CGPLLU14	Day -3	-0.81	-1.68	-1.31	-1.74	-0.04	1.99	0.60	0.03	-1.02	0.26	1.71	-0.30	-0.54	-0.39	-1.78	-0.35	-1.70	0.78	1.41	0.81
CGPLLU12	Day 0.17	-2.51	-5.06	-2.71	-3.84	2.01	14.32	-5.86	-1.95	-5.24	-6.73	2.41	-1.88	0.77	0.75	5.62	0.44	-3.19	3.37	-1.26	11.26
CGPLLU12	Day 10	-0.30	-0.22	-0.49	0.08	-3.35	0.72	0.01	-0.14	-0.18	1.46	0.65	0.68	-2.39	0.56	-0.20	-0.87	-1.36	1.16	1.33	0.85
CGPLLU12	Day 227	-1.83	-0.21	-1.78	-0.64	-1.99	4.01	-0.54	-1.19	-2.34	2.68	2.77	3.19	-1.22	-0.16	-0.06	-2.71	-3.38	0.76	1.26	5.20
CGPLLU12	Day -150	-0.41	-3.10	-2.12	-2.17	1.84	5.63	-0.97	-0.39	-3.10	-3.46	1.24	-2.12	1.71	-1.04	0.30	-0.23	-3.83	-2.79	0.07	5.45
CGPLLU12	Day 0	-1.52	-3.87	-2.34	-3.22	0.66	12.90	-5.14	-1.40	-4.34	-7.19	1.57	-1.19	-0.13	1.37	5.00	0.83	-1.97	3.07	-1.21	10.67
CGPLLU18	Day 6	-2.34	-0.90	-1.80	-1.33	-3.44	2.84	1.27	-0.61	-2.31	3.53	2.35	5.75	-1.72	-1.08	-2.24	-1.04	-4.04	0.66	1.04	4.41
CGPLLU18	Day 20	0.19	-0.58	-0.09	-0.16	-3.76	0.98	0.00	0.50	-0.55	1.19	0.68	1.61	-1.32	1.32	-0.33	-1.36	-1.81	0.95	1.43	0.69
CGPLLU18	Day -1	-6.01	-3.20	-5.96	-10.27	-6.77	69.49	-7.35	17.13	-5.90	-8.85	3.57	-19.21	-7.74	-4.23	-5.16	-7.91	10.18	12.39	-8.20	14.86
CGPLLU86	Day 0.5	0.17	0.00	0.43	-0.02	-3.27	-0.31	-0.38	-0.07	0.07	-0.25	-0.06	2.05	-2.12	0.85	0.01	-0.62	-0.92	1.04	0.01	1.11
CGPLLU86	Day 7	-1.84	-0.24	-1.30	-0.83	-2.79	-1.04	1.60	0.06	-1.98	1.19	1.39	4.09	-1.29	-1.19	-1.73	-0.19	-5.08	0.89	0.62	2.54
CGPLLU86	Day 17	-2.36	-0.66	-1.23	-0.25	-2.33	-1.88	2.03	-0.44	-2.24	0.19	1.06	4.35	0.00	-1.88	-2.34	0.29	-6.07	-0.25	0.26	3.12
CGPLLU86	Day 0	-2.03	-0.23	-0.90	-0.59	-3.11	-0.54	1.28	0.10	-1.42	4.77	1.84	4.30	-1.89	-0.43	-0.74	-1.51	-1.79	0.36	2.02	2.57
CGPLLU89	Day 7	-0.70	0.77	-0.15	0.15	-2.31	1.01	0.34	-0.36	-0.66	1.87	0.63	2.99	-2.31	0.34	-0.32	-0.84	-2.05	0.38	1.83	1.94
CGPLLU89	Day 22	0.56	-0.15	0.42	1.03	-0.87	-0.25	-1.32	-0.37	0.32	-0.92	-0.32	-0.25	-1.76	1.73	0.16	-0.65	-1.79	1.10	-1.13	0.09
CGPLLU89	Day 0	-2.02	-0.32	-0.57	-0.14	-3.30	1.13	1.01	-0.47	-1.42	3.04	1.52	4.24	-1.15	-0.44	-0.77	0.21	-3.04	0.84	2.41	3.34
CGPLLU97	Day 7	-0.10	0.03	0.12	-0.38	-3.24	-0.62	-0.29	0.76	-0.18	1.51	0.53	1.52	-2.35	0.74	0.09	-0.40	-0.57	0.58	1.30	0.55
CGPLLU97	Day 273	-2.33	-1.13	-1.54	-1.66	-1.92	-0.15	1.34	-0.81	-2.28	2.89	1.70	2.73	0.11	-1.23	-1.73	-0.56	-4.02	2.23	1.32	2.39
CGPLLU97	Day 0	-2.11	-0.71	-1.20	-0.15	-3.50	-2.63	1.72	-0.37	-1.70	1.19	0.85	5.10	-0.79	-0.29	-1.20	-1.08	-2.65	1.05	1.10	2.99
CGPLLU99	Day 0.33	-1.48	-1.34	-1.26	-0.89	-25.72	-1.51	-1.65	7.60	3.97	-8.33	1.08	4.89	-7.45	-4.56	-3.67	-9.22	1.85	1.92	-4.28	12.91
CGPLLU99	Day 9	-0.23	-0.37	-0.44	-0.36	-3.00	-0.59	1.57	-0.61	-1.39	-0.66	0.42	4.02	-0.79	-1.24	-1.78	0.61	-3.76	2.02	2.56	2.54
CGPLLU99	Day 21	-0.84	0.00	-0.98	0.29	-4.49	-1.70	1.82	-1.08	-1.74	-0.73	1.24	5.44	-1.92	-0.98	-2.06	-0.67	-3.71	0.88	2.38	3.20
CGPLLU99	Day 0	-1.53	-1.36	-0.85	-0.98	-36.10	-2.02	-4.66	12.25	7.23	-10.65	0.72	2.01	-10.19	-4.73	-3.78	-13.23	6.75	4.62	-6.64	14.58
CGPLLU88	Day 0	-2.54	-2.85	-1.15	2.94	-7.41	8.22	-3.45	-0.75	-1.69	-4.63	3.64	-5.62	-7.75	-0.75	-0.89	-3.30	9.19	-2.83	3.91	11.20
CGPLLU88	Day 297	-1.51	-2.21	-2.40	-1.39	3.52	0.22	1.38	-0.22	-2.19	-2.96	0.97	1.20	2.40	-2.23	-2.19	-0.06	-2.91	-3.71	-0.24	3.76
CGPLLU88	Day 7	-1.73	-2.40	-2.22	-1.90	0.29	0.42	1.81	-0.93	-2.13	0.84	1.72	0.49	3.77	-3.00	-2.77	0.16	-4.24	-1.93	0.56	3.32

CHAPTER 3:

MATCHED WHITE BLOOD CELL AND CELL-FREE DNA ANALYSES FOR DETECTION OF CIRCULATING TUMOR DNA AND MINIMAL RESIDUAL DISEASE IN PATIENTS WITH GASTRIC CANCER

METHODS

Experimental study design

The current study is a planned exploratory analysis of the predictive value of cfDNA assessment in 50 randomly selected patients from the CRITICS study (NCT00407186) who had plasma samples available and suitable for genomic analyses from at least two timepoints (Figures 3.1 A, 3.2, and Table 3.1). The CRITICS study is an investigator-initiated, open-label, multi-center, phase III randomized controlled trial of perioperative chemotherapy (chemotherapy group) versus preoperative chemotherapy with postoperative chemoradiotherapy (chemoradiotherapy group) in patients with resectable gastric cancer (77). A total of 788 patients from 56 hospitals in the Netherlands, Sweden, and Denmark were randomized upfront to receive three preoperative 21-day cycles of intravenous epirubicin, cisplatin or oxaliplatin, and oral capecitabine followed by three postoperative cycles of intravenous epirubicin, cisplatin or oxaliplatin, and oral capecitabine (chemotherapy group) or to receive the same preoperative regimen followed by postoperative radiotherapy combined with daily capecitabine and weekly cisplatin (chemoradiotherapy group) (Figures 3.1 A, 3.2, and Table 3.1). Baseline blood samples at the time of trial enrollment were used for both cfDNA and white blood cell targeted deep sequencing (30,000X), followed by independent variant calling and further tumor-specific mutation detection using the white blood cell filtering approach (Figure 3.1 A). Tumor-specific mutations from the consecutive timepoints were identified using the white blood cell sequencing data from the same patient at baseline.

Patients and characteristics

Patients were eligible for the study if they had histologically proven gastric adenocarcinoma (as defined by the American Joint Committee on Cancer, 6th edition), stage IB-IVA (78), as assessed by esophagogastroduodenoscopy and CT of the chest, abdomen, and pelvis. Patients with tumors of the gastroesophageal junction were permitted to enroll when the bulk of the tumor was

predominantly located in the stomach and could therefore consist of Siewert types II (true gastroesophageal junction) and III (subcardial stomach) tumors. Patients with Siewert type I (distal esophagus) tumors were not eligible. An exploratory laparoscopy was indicated when the preoperative CT scan suggested peritoneal carcinomatosis. Patient enrollment and genomic studies were conducted in accordance with the Declaration of Helsinki, were approved by the Institutional Review Board (IRB) and all patients provided written informed consent for sample acquisition for research purposes.

Pathological assessment of response, mismatch repair status and EBV status determination

Pathology slides from the resection specimen from each patient were collected and centrally reviewed by NCTvG to confirm histologic subtypes according to the Lauren's classification criteria (79). Histopathological regression was determined by NCTvG according to Mandard's tumor regression grade (TRG) system: i) TRG1, no residual tumor left (pathological complete response); ii) TRG2, scattered tumor cells left; iii) TRG3, fibrosis outgrows tumor; iv) TRG4, tumor outgrows fibrosis; and v) TRG5, no histological signs of regression (Table 3.1). For detection of Epstein-Barr virus (EBV), the tumor areas were demarcated on H&E slides of the resection specimens. In case of sufficient amount of tumor tissue, 3 cores per tumor were taken for construction of a tissue microarray (TMA). TMA sections were cut and used for Epstein-Barr virus encoded RNA in-situ hybridization (EBER-ISH). In case little or no tumor was left in the resection specimen due to chemotherapy-induced pathological (near) complete response EBER-ISH was performed on the diagnostic biopsy specimen. EBER-ISH was performed using the U INFORM iViEW Blue ISH (v1.02.0023) and the INFORM EBER probe on the Benchmark Ultra IHC/ISH staining module (Roche Diagnostics, the Netherlands) according to the manufacturer's protocol (Table 3.1).

Formalin-fixed paraffin-embedded (FFPE) tissue blocks from the diagnostic biopsy specimen were used for MSI analysis. The tumor area was demarcated on an H&E slide. DNA was isolated from

the demarcated tumor area. MSI analysis was performed using the MSI Analysis System (MSI Multiplex System Version 1.2, Promega) consisting of five nearly monomorphic mononucleotide markers *(BAT-25, BAT-26, NR-21, NR-24, MONO-27)* according to the manufacturer's instructions. PCR products were separated by capillary electrophoresis using an ABI 3500 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA), and analyzed using GeneMapper Software (Applied Biosystems, Foster City, CA, USA). An internal lane size standard was added to the PCR samples for accurate sizing of alleles and to adjust for run-to run variations. When all markers were stable, the tumor was interpreted as microsatellite stable (MSS). The tumor was interpreted as MSI-low (MSI-L) if one marker was unstable and MSI-high (MSI-H) if two or more markers showed instability. MSI-L tumors were included in the MSS category (Table 3.1).

Sample preparation and next-generation sequencing of cfDNA and genomic DNA from white blood cells

Whole blood was collected in K_2EDTA tubes, sent to the central pathology lab at VUmc, Amsterdam, and processed within 1 day after collection. Plasma and cellular components were separated by centrifugation at 1,300 rpm for 5 minutes in 1.5 ml microcentrifuge tubes at 4°C and therefore stored at -20°C until the time of DNA extraction. cfDNA was isolated from plasma using the Qiagen Circulating Nucleic Acids Kit (Qiagen GmbH) and eluted in LoBind tubes (Eppendorf AG). High-molecular weight DNA from white blood cells was extracted using the Qiagen DNA Blood Mini Kit (Qiagen GmbH) followed by shearing using a focused-ultrasonicator (Covaris). Concentration and quality of cfDNA was assessed using the Bioanalyzer 2100 (Agilent Technologies). cfDNA samples with saturated concentrations of high-molecular weight DNA based on fluorescence intensity were excluded from the study.

Next-generation sequencing libraries from cfDNA and sheared high-molecular weight DNA from white blood cells were prepared from 8.4 to 250 ng (Table 3.2). Genomic libraries were prepared

as previously described (15). Briefly, the NEBNext DNA Library Prep Kit for Illumina [New England Biolabs (NEB)] was used with four main modifications to the manufacturer's guidelines: i) the library purification steps utilized the on-bead Ampure XP approach, ii) reagent volumes were adjusted accordingly to accommodate the on-bead strategy, iii) a pool of 8 unique Illumina dual index adapters with 8 bp barcodes were used in the ligation reaction, and iv) cfDNA libraries were amplified with HotStart Phusion Polymerase. Genomic library preparation was performed as previously described (15). Concentration and quality of cfDNA genomic libraries were assessed using the Bioanalyzer 2100 (Agilent Technologies). Targeted capture was performed using the Agilent SureSelect reagents and a custom set of hybridization probes targeting 58 genes (Table 3.3) per the manufacturer's guidelines. The captured library was amplified with HotStart Phusion Polymerase (NEB). The concentration and quality of captured cfDNA libraries was assessed on the Bioanalyzer (Agilent Technologies). Libraries were sequenced using 100-bp paired end runs on the Illumina HiSeq 2500 (Illumina).

Primary processing of next-generation sequencing data and identification of putative somatic mutations using the white blood cell filtering approach

Primary processing of next-generation sequence data for analyses of sequence alterations in cfDNA and white blood cell samples were performed as previously described (15). Briefly, Illumina CASAVA (Consensus Assessment of Sequence and Variation) software (version 1.8) was used for demultiplexing and masking of dual index adapter sequences. Sequence reads were aligned against the human reference genome (hg19) using NovoAlign with additional realignment of select regions using the Needleman-Wunsch methods (71).

Candidate tumor-specific mutations in cfDNA, consisting of point mutations, small insertions, and deletions were identified using VariantDx (71) (Personal Genome Diagnostics) across the targeted regions of interest as previously described (15). Briefly, an alteration was considered a candidate

somatic mutation only when: (i) Three distinct paired reads contained the mutation in the cfDNA and the number of distinct paired reads containing a particular mutation in the plasma was at least 0.05% of the total distinct read pairs; or (ii) one distinct paired read contained the mutation in the cfDNA and the mutation had also been detected in at least one additional timepoint at the level specified in (i); (iii) the mismatched base or small indel was not identified in matched white blood cell sequencing data of samples collected at baseline at the level of one distinct read; (iv) the mismatched base or small indel was not present in a custom database of common germline variants derived from dbSNP; (v) the altered base did not arise from misplaced genome alignments including paralogous sequences; and (vi) the mutation fell within a protein coding region and was classified as a missense, nonsense, frameshift, or splice site alteration. Candidate alterations were defined as somatic hotspots if the nucleotide change and amino acid change were identical to an alteration observed in ≥ 20 cancer cases reported in the COSMIC database.

Statistical analyses

Significance was determined using a variety of methods. Wilcoxon rank sum test or Kruskal-Wallis test were performed for continuous variables and Fisher's exact test for categorical variables. Analyses of groups of mutations were carried out in R using the package *maftools* (80). Correlation coefficients were determined for the association between WBC variants and their correspondent alterations identified in cfDNA, as well as for the association between the number of WBC variants and age. Univariate survival analyses and a multivariate Cox proportional-hazards model were carried out in R using packages *survival* and *coxphf* (https://cran.r-project.org).

For mutations identified by cfDNA sequencing but not identified by WBC sequencing, we computed the probability for the model that the mutation was tumor derived relative to the probability for the model that the mutation was hematopoietic. The sampling distribution of the observed number of reads with an altered mutation in cfDNA and WBC sequencing is a binomial

parameterized by the total coverage at that mutation and unknown probability theta. Under the tumor derived model, theta_WBC is zero and only theta_plasma is unknown. For the hematopoietic model, we assume that theta_WBC and theta_plasma are the same. As a prior for theta_plasma, we used a beta distribution with shape parameters 2.4 and 340 that loosely centers most of the mass on the observed mutation allele frequencies in samples for which mutations were identified in both cfDNA and WBC sequencing. This prior is equivalent to a sample with 2.4 altered reads per 340 distinct molecules. Simulating a large number of theta's from the prior, we computed the probability of the observed data for each simulated theta. The ergodic average of these probabilities approximates the likelihood of the observed data conditional on the model but unconditional on theta. Assuming a prior odds of 1, the posterior odds (PO) was the same as the Bayes factor and we obtained the probability that the mutation was tumor derived by PO/(1+PO). We performed this analysis for each mutation that was identified only by cfDNA sequencing.

RESULTS

Overall approach

The current study was an exploratory analysis of the predictive value of ctDNA assessment in a subset of patients from CRITICS study (NCT00407186), an investigator-initiated, open-label, multi-center, phase III randomized controlled trial of perioperative chemotherapy (chemotherapy group) versus preoperative chemotherapy with postoperative chemoradiotherapy (chemoradiotherapy group) for patients with resectable gastric cancer (77). Between Jan 11, 2007, and April 17, 2015, a total of 788 patients from 56 hospitals in the Netherlands, Sweden, and Denmark were randomized upfront to receive three preoperative 21-day cycles of intravenous epirubicin, cisplatin or oxaliplatin, and oral capecitabine followed by three postoperative cycles of intravenous epirubicin, cisplatin or oxaliplatin, and oral capecitabine (chemotherapy group) or to receive the same preoperative regimen followed by radiation combined with daily capecitabine and weekly cisplatin (chemoradiotherapy group) (Figures 3.1 A, 3.2, and Table 3.1).

As a proof-of-principle study, we sequenced and analyzed matched cfDNA and WBC samples from 50 treatment-naïve patients from the Netherlands who had plasma samples available for genomic analyses at two or more timepoints to detect tumor-specific mutations in ctDNA (Figures 3.1 A, 3.2, and Table 3.1). Our goal was to predict survival outcomes based on ctDNA assessment after preoperative therapy and minimal residual disease analyses after surgery with curative intent. Of the patients analyzed, 24 had diffuse subtype, 24 had intestinal subtype according to Lauren's classification, and one was diagnosed with adenosquamous gastric carcinoma (Figure 3.1 B and Table 3.1). Twenty-one patients were surgically treated with distal gastrectomy, 17 with total gastrectomy, four with esophagocardiac resection, and one with proximal gastrectomy (Figure 3.1 B and Table 3.1). Despite initial eligibility at the time of treatment enrollment, six patients showed evidence of advanced disease during the exploratory laparotomy and were not submitted to surgical

resection. One additional patient did not undergo surgical treatment for unknown reasons. Histopathological regression after preoperative therapy was determined according to Mandard's tumor regression grade (TRG). Three patients achieved complete regression after three cycles of preoperative chemotherapy at the time of surgery (TRG 1) while 10, 15, 13, and 2 patients presented with pathological stage I, II, III, and IV, respectively (Figure 3.1 B and Table 3.1). Centrally reviewed pathological assessment of resection specimens after three cycles of preoperative chemotherapy showed that 20 patients did not have evidence of lymph node involvement (ypN0), while 23 patients had lymph node infiltration, including 10 patients with ypN1 (including 3 ypN1mi), 7 patients with ypN2, and 6 patients with ypN3 disease (Table 3.1). Twenty-six patients received postoperative treatment with radiation combined with cisplatin and capecitabine, and 24 patients were postoperatively treated with three cycles of epirubicin, cisplatin, and capecitabine without radiation after surgery (Figure 3.1 B and Table 3.1).

For each patient, plasma and buffy coat were collected at the time of trial enrollment (baseline timepoint), after patients received three cycles of preoperative chemotherapy (preoperative timepoint), and after surgery but before the initiation of the adjuvant treatment (postoperative timepoint) (Figure 3.1 A, Tables 3.1 and 3.2). We developed an approach to identify tumor-specific alterations in the circulation independent of tissue analyses by parallel deep sequencing of cfDNA and WBCs, followed by identification of cfDNA alterations and removal of hematopoietic-related changes detected in WBCs (Figure 3.1 A). For sequencing analyses of cfDNA and WBCs, we used a next generation deep sequencing approach to evaluate 58 cancer driver genes (Figure 3.1 A and Tables 3.3, 3.4, and 3.5). This method is based on targeted capture and deep sequencing (>30,000x) of DNA fragments to identify single base substitutions and small insertions or deletions in cfDNA across 80,930 bp of coding gene regions while distinguishing these from PCR amplification and sequencing artifacts (15). For alterations detected in cfDNA that were not identified by matched white blood cell sequencing, we determined the posterior probability that such an alteration was

tumor derived from a Bayesian statistical model using the frequency of altered alleles and total coverage of cfDNA and WBCs sequences.

To estimate the theoretical sensitivity of detection of the sequencing approach in gastric cancer, we determined the proportion of gastric adenocarcinomas in the TCGA Pan-Cancer Atlas (81) with alterations in one or more of the 58 analyzed genes. These analyses showed that our targeted panel would have a sensitivity of ~88% as 384 of 436 gastric cancer cases had at least one alteration in these genes (Figure 3.3). Overall, we observed that median levels of mutant allele fractions at baseline were significantly higher in patients with intestinal subtype when compared to diffuse subtype (0.295% vs 0%, p = 0.015, Wilcoxon rank sum test) (Figure 3.4 A). There was no statistically significant difference among levels of mutant allele fractions among well, moderately, or poorly differentiated tumors (p = 0.07, Kruskal-Wallis test) (Figure 3.4 B). In our study, patients with intestinal and diffuse gastric adenocarcinoma experienced similar event-free (Figure 3.4 C and Table 3.1) and overall survival (Figure 3.4 D and Table 3.1). Consistent with the findings of the original trial (77), we did not observe significant differences in survival outcomes related to the postoperative treatment arm in which patients had been randomized (Figures 3.4 E, 3.4 F and Table 3.1).

Detection of clonal hematopoiesis and identification of tumor-specific alterations

We evaluated cfDNA in all 50 patients at baseline and after 3 cycles of preoperative chemotherapy. At baseline, we detected sequence alterations in cfDNA from 40 patients (80%) (Figure 3.5 A and Table 3.6) and in WBCs from 31 patients (62%) (Figure 3.5 B and Table 3.7). After removing WBC-derived alterations from cfDNA data, we detected 54 alterations that were likely tumor-specific in 27 patients (54%) (Figure 3.5 C and Table 3.8). The most frequently altered genes detected in WBCs were *DNMT3A* (45%), *TP53* (29%), *EGFR* (10%), *APC* (6%), *AR* (6%), *ATM* (6%), and *MLH1* (6%), while the most frequently altered genes detected in ctDNA were *TP53*

(22%), *MYC* (15%), *PIK3CA* (15%), *KRAS* (11%), *HRAS* (11%), *BRAF* (11%), *ALK* (11%), *ATM* (11%), *KIT* (11%), and *CDH1* (7%) (Figures 3.5 B, 3.5 C and Table 3.8). In accord with the molecular classification of gastric adenocarcinomas proposed by the TCGA (82), we found a higher frequency (60%) of *PIK3CA* mutations in the blood of patients with EBV positive (n = 3) or MSI-high tumors (n = 2) compared to the frequency (3%) in EBV negative (n = 36) and MSS tumors (n = 37). The median mutant allele fraction among 43 WBC-derived variants was 0.31% (IQR 0.18% – 0.63%), which was similar to the median mutant allele fraction among 53 tumor-specific variants identified in cfDNA (0.31%, IQR 0.20% – 0.55%, $p = 0.96$, Wilcoxon rank sum test) (Figure 3.5 D). We observed a high correlation between levels of mutant allele fractions in WBCs and levels of corresponding alterations in cfDNA (Pearson correlation coefficient = 0.91) (Figure 3.5 E). As expected, the number of alterations detected in WBCs increased with age ($r^2 = 0.36$, exponential correlation) (Figure 3.5 F).

We detected 21 sequence alterations in *TP53* in cfDNA, including 17 missense mutations, two nonsense mutations, one in-frame deletion, and one splice site mutation (Figure 3.5 G and Table 3.6). Of the cfDNA sequence changes observed in *TP53,* we identified 15 in WBC sequences as well as three alterations in WBC's that were not present in matched cfDNA (Figure 3.5 G and Table 3.7). From the 21 *TP53* alterations initially detected in cfDNA at baseline, only 6 were identified as tumor-specific mutations, including two with stop alterations (Q192* and S166*) as well as four missense mutations (R175H, V216M, N239S, R248W). We further evaluated fragment length distributions of the 21 *TP53* alterations detected in cfDNA. We observed that fragments harboring tumor-specific *TP53* mutations in the circulation were significantly shorter than fragments harboring *TP53* variants associated with clonal hematopoiesis ($p < 0.001$, Kolmogorov–Smirnov test), as well as fragments harboring wild-type *TP53* coding regions ($p < 0.001$, Kolmogorov–Smirnov test) (Figure 3.5 H and Tables 3.7, 3.8, and 3.9). Interestingly, we detected WBC variants in *DNMT3A*, *TP53*, *ERBB4*, *MLH1*, *PDGFRA*, *FGFR3*, *ESR1*, *IDH2*, and *ATM* among multiple

time points analyzed in 11 patients that did not harbor any tumor-specific alterations in cfDNA (Figures 3.6 A-K). Overall, detection of WBC variants or tumor-derived ctDNA variants at baseline did not reveal statistically significant differences in event-free or overall survival (Figures 3.7 A-D).

Preoperative ctDNA is a surrogate biomarker for pathological response in gastric cancer

After identification of ctDNA alterations using the parallel sequencing of cfDNA and WBCs indicated above, we evaluated ctDNA levels before and after preoperative chemotherapy. Of the 30 patients with measurable ctDNA at baseline or at the preoperative time point after filtering WBC sequence alterations (Figure 3.5 C), 11 experienced a complete elimination of ctDNA levels after nine weeks of systemic treatment (Figures 3.8, 3.9, and Table 3.5). As an example, patient CGST33, who presented with intestinal subtype gastric adenocarcinoma at diagnosis had mutant allele fraction concentrations of 2.32% and 0.64% for *TP53* Q192* and *ERBB2* R756Cfs*2, respectively that were completely eliminated at the preoperative timepoint. This drop in ctDNA occurred in conjunction with a major pathological response (TRG 2) in the specimen obtained at the time of surgery (Figure 3.10 A). In contrast, 19 patients had detectable ctDNA at the preoperative timepoint (Figures 3.8, 3.9, and Table 3.5), including as an example in patient CGST110 who had mutant allele fractions of 0.15% for *ERBB4* T639M at baseline and 0.12% at the preoperative timepoint (Figure 3.10 B). This patient did not experience tumor regression after nine weeks of systemic treatment (TRG 5) and eventually died from recurrent disease 35 months after the initial diagnosis (Supplementary Table S1).

After preoperative chemotherapy, we identified seven responders of whom three achieved complete pathological response (TRG 1) and four achieved a major pathological response, exhibiting fibrotic surgical specimens with scattered tumor cells (TRG 2). All seven responders had no ctDNA detected at the preoperative timepoint (Figure 3.10 C). We observed that patients with lower degrees of tumor regression (TRG 3-5) and at least one involved lymph node (ypN1, ypN2, and

ypN3) presented more frequently with detectable ctDNA at the preoperative timepoint (Figures 3.10 C and 3.11 A). In contrast, the absence of ctDNA at the preoperative timepoint was significantly associated with major pathological regression (TRG 1-2) at the time of surgery (p = 0.03, Fisher's exact test) (Figure 3.10 D). As expected, recurrence was also associated with lower degrees of pathological response (p = 0.03, Fisher's exact test) (Figure 3.10 E), at least one involved lymph node (p = 0.002, Fisher's exact test) (Figure 3.10 F), and detectable ctDNA at the preoperative timepoint (p = 0.02, Fisher's exact test) (Figure 3.10 G). TRG score (TRG 1-2 versus TRG 3-5) and pathological lymph node status (ypN0 versus ypN+) were strongly associated with survival outcomes (Figures 3.11 B and 3.11 C). It is noteworthy that detection of mutations in cfDNA without a WBC sequence filter at the preoperative timepoint did not predict risk of recurrence (Figure 3.10 H) or death (Figure 3.12 A). However, when we applied the WBC-guided hematopoietic filter, we observed that ctDNA detected at the preoperative timepoint was associated with a significantly higher risk of recurrence and shorter median event-free survival (18.4 months versus median not reached) (Log-rank p = 0.012; HR = 3.0; 95% CI = 1.3-6.9) (Figure 3.10 I) as well as higher risk of death and shorter median overall survival (28.7 months versus median not reached) (Log-rank p = 0.03; HR = 2.7; 95% CI = 1.1-6.7) (Figure 3.12 B).

Minimal residual disease predicts survival outcome after surgery in gastric cancer

We used the WBC-filtering approach to evaluate minimal residual disease after surgery from all 20 patients with blood samples available from a postoperative timepoint. Blood samples were collected at a median time of 6.5 weeks after surgery (Table 3.1). We observed complete elimination of tumor-specific mutations in cfDNA at the postoperative time point for four patients with major tumor responses (TRG 1 and TRG 2), including in patient CGST32, who exhibited baseline mutant allele fraction concentrations of 0.65% and 0.24% for *BRAF* G469A and *KRAS* G13R, respectively (Figure 3.13 A). The two hotspot ctDNA mutations in this patient were not detected at either the pre- or postoperative timepoint, in agreement with the surgical specimen

assessment that showed major tumor regression (TRG 2) (Figure 3.13 A, Tables 3.1 and 3.8). In contrast, we detected postoperative tumor specific mutations in nine out of 16 patients with minor or no pathologic tumor responses (TRG 3-5), including in patient CGST68, who presented with mutant allele fraction of 0.03% for *HRAS* D54Efs*53 frameshift mutation at the baseline timepoint. This patient exhibited progressive increases in mutant allele fractions of *HRAS* at preoperative and postoperative timepoints, followed by the emergence of *ERBB4* D1184*, detected at 0.16% mutant allele fraction after surgery (Figure 3.13 B, Tables 3.1 and 3.8). After a median follow-up of 42 months, we observed that all eleven patients without detectable tumor-specific mutations at the postoperative timepoint were alive and free of recurrence (Figure 3.13 C and Table 3.1). On the other hand, six out of nine patients with detectable tumor-specific mutations at the postoperative timepoint developed disease recurrence and died from metastatic disease (Figure 3.13 C and Table 3.1). Again, detection of mutations in cfDNA without a WBC filter after surgery did not predict recurrence (Figure 3.14 A) or death (Figure 3.13 D). In contrast, with the WBC-guided hematopoietic filter, we observed a significant shorter median event-free survival and a higher risk of disease recurrence for patients with detectable tumor-specific mutations after surgery (18.7 months versus median not reached; Log-rank $p < 0.001$; HR = 21.8; 95% CI = 3.9-123.1) (Figure 3.14 B) as well as a significantly shorter median overall survival (28.7 versus median not reached; Log-rank $p < 0.001$; HR = 21.8; 95% CI = 3.9-123.1) (Figure 3.13 E).

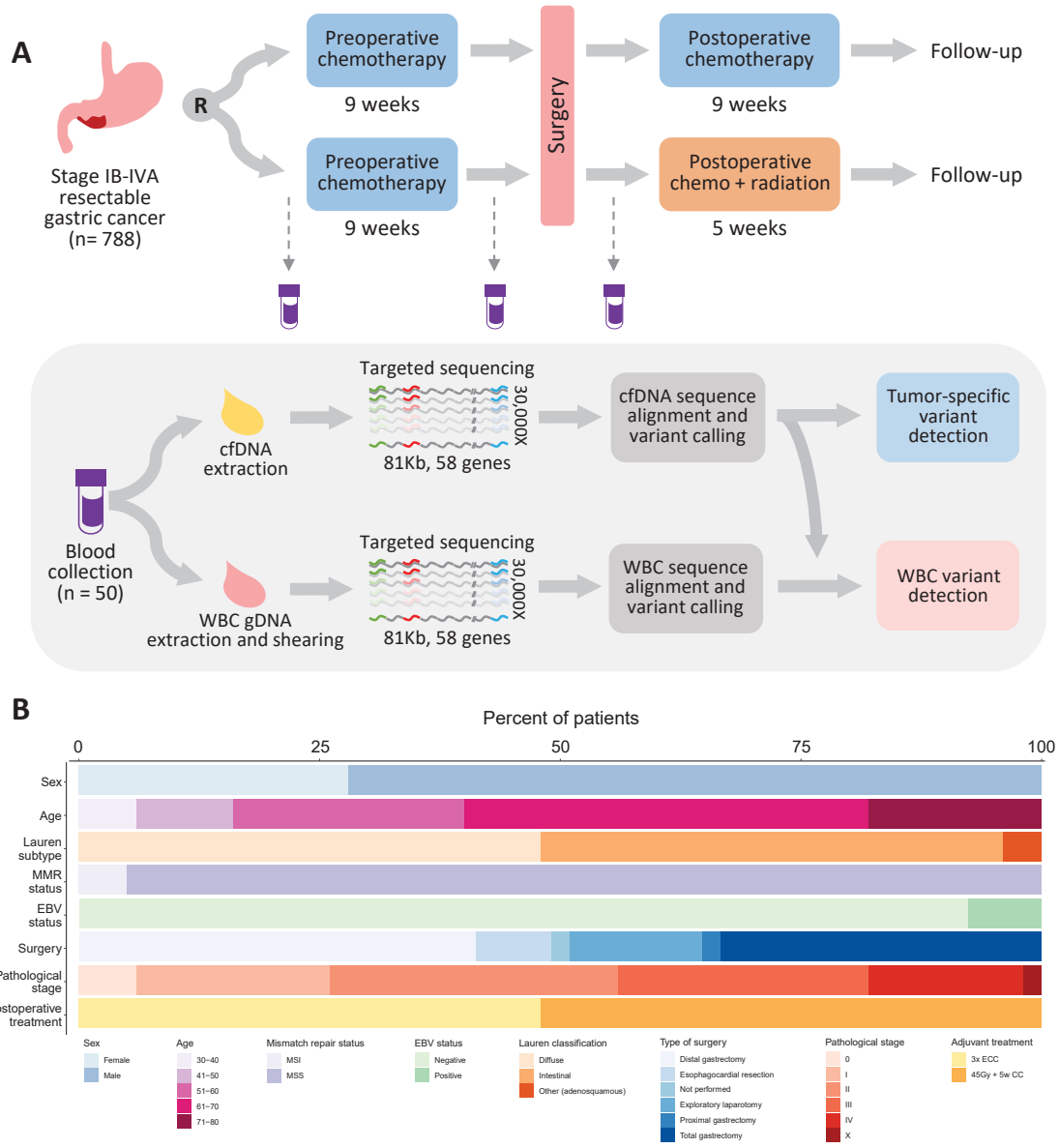


Figure 3.1. Analysis of cfDNA in patients with resectable gastric cancer. A, Study schematic. Patients with confirmed stage IB-IVA gastric adenocarcinoma eligible for perioperative treatment with systemic chemotherapy were randomized upfront to receive three cycles of preoperative chemotherapy followed by three cycles of postoperative chemotherapy or to receive the same preoperative regimen followed by postoperative radiotherapy combined with chemotherapy. A blood draw was collected for each patient at the time of study enrollment (baseline), after three cycles of preoperative chemotherapy (preoperative timepoint), and after surgery (postoperative timepoint). Blood samples were initially processed to allow proper extraction of cfDNA from plasma and genomic DNA (gDNA) from white blood cells (WBC). Both cfDNA and WBC gDNA libraries were hybrid captured with custom RNA oligo pools encompassing 80,930 bases across 58 cancer driver genes. Capture libraries were sequenced at high coverage (>30,000X), followed by sequence alignment, error correction, and variant calling. Mutations detected in WBCs were identified in cfDNA and removed, allowing the identification of tumor-specific mutations in cfDNA. B, Clinicopathological characteristics, type of surgical treatment, pathological stage, and type of postoperative treatment for the subset of patients analyzed in this translational study (n = 50). MSI, microsatellite instability; MSS, microsatellite stability; EBV, Epstein-Barr virus; ECC, epirubicin, cisplatin, capecitabine; CC, cisplatin, capecitabine.

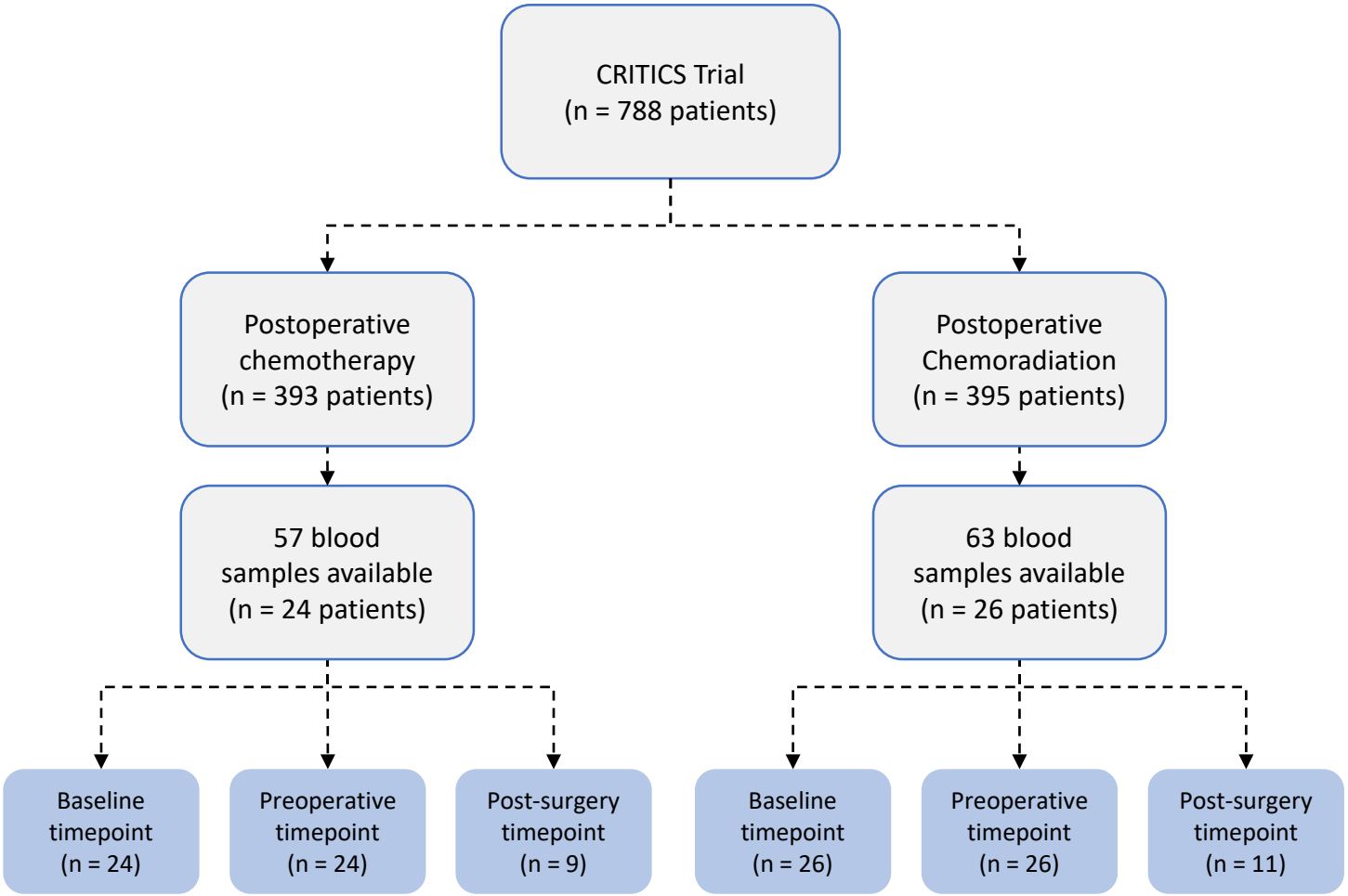


Figure 3.2. Consort diagram of patients enrolled in the CRITICS trial cohort. Patients with operable stage IB-IVA gastric cancer (n=788) were initially treated with three cycles of preoperative chemotherapy with epirubicin, cisplatin or oxaliplatin, and oral capecitabine followed by surgery. They were randomly assigned to receive postoperative treatment with the same chemotherapy regimen (n=393) or postoperative radiation with cisplatin and oral capecitabine (n=395). Plasma samples used for ctDNA analyses were provided by study centers in The Netherlands.

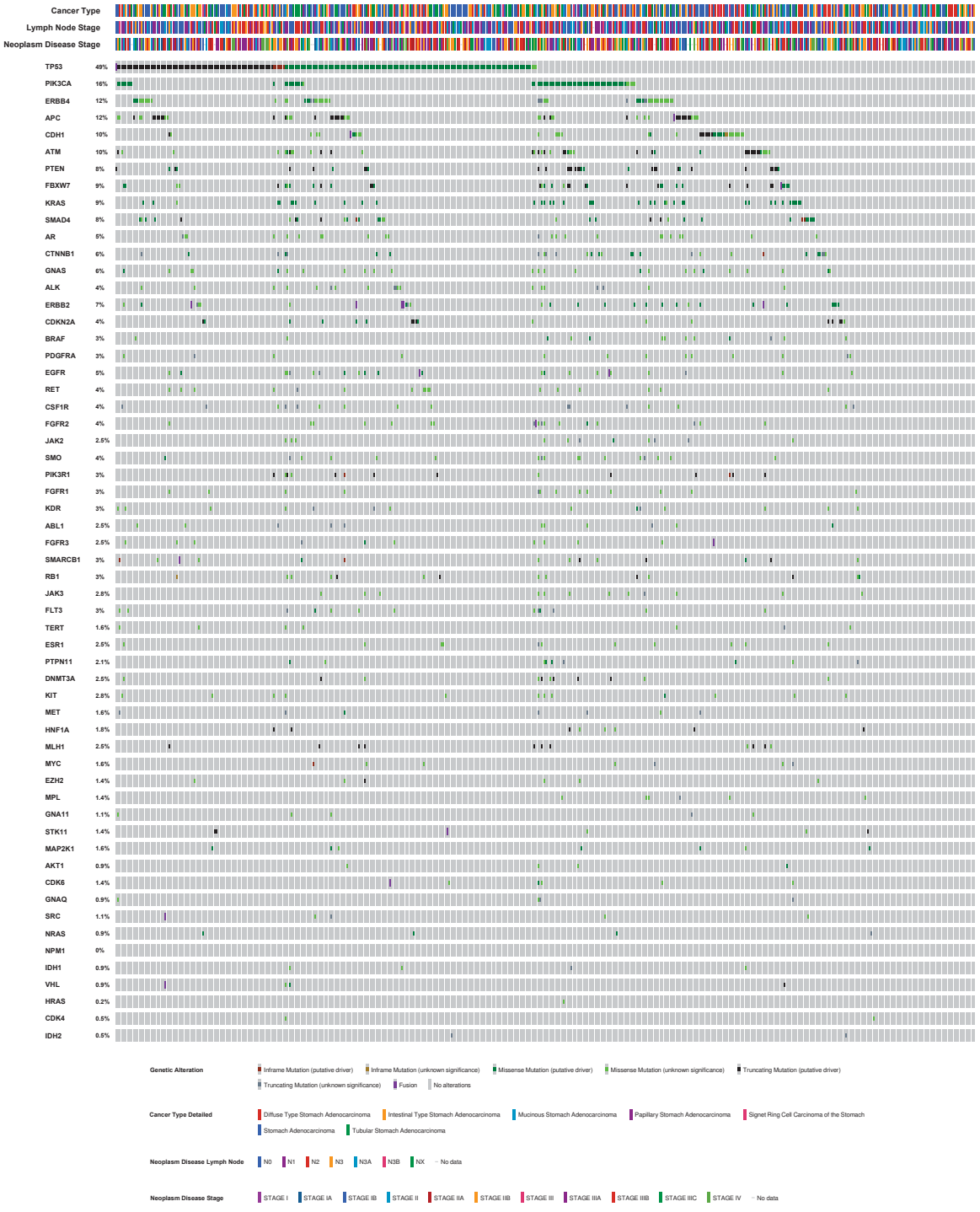


Figure 3.3. Theoretical sensitivity of detection of ultrasensitive NGS approach in gastric cancer. Analyses of TCGA Pan-Cancer Atlas gastric adenocarcinoma cohort showed a theoretical sensitivity of 88 % for the 58-gene panel (81 Kb) used in this study, with 385 out of 436 cases potentially identified using this approach.

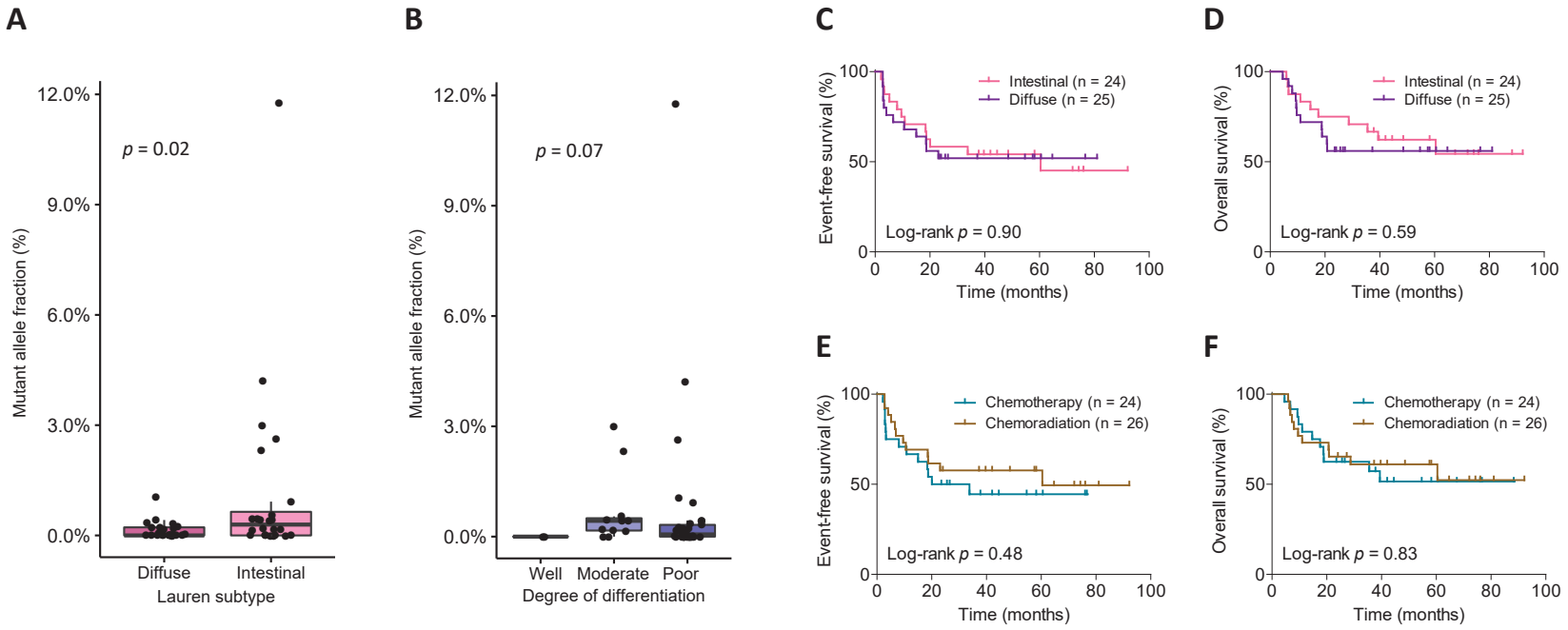


Figure 3.4. Pathological features and ctDNA levels of gastric cancers analyzed. A, Mutant allele fractions of ctDNA at base line in patients with diffuse and intestinal subtype s (Wilcoxon rank sum test, p= 0. 02). B, Mutant allele fractions of ctDNA at baseline in patients with well, moderately, and poorly differentiate d tumors (Kruskal -Wallis test, p= 0.07). C - D, Kaplan-Meier estimates for event- free survival [Log-rank p = 0.90; HR = 1.0 (95% CI = 0.4-2.1)] (C) and overall survival [Log-rank p = 0.59; HR = 0.8 [(95% CI = 0.3-1.9)] (D) of patients with intestinal and diffuse subtype s. E-F, Kaplan-Meier estimates for e vent-free survival [Log-rank p = 0.48; HR = 1.3 (95% CI = 0.6-3. 0)] (E) and overall survival [Log-rank p = 0.83; HR = 1.1 (95% CI = 0.5-2.5)] (F) of patients treated with adjuvant chemotherapy or chemoradiotherapy.

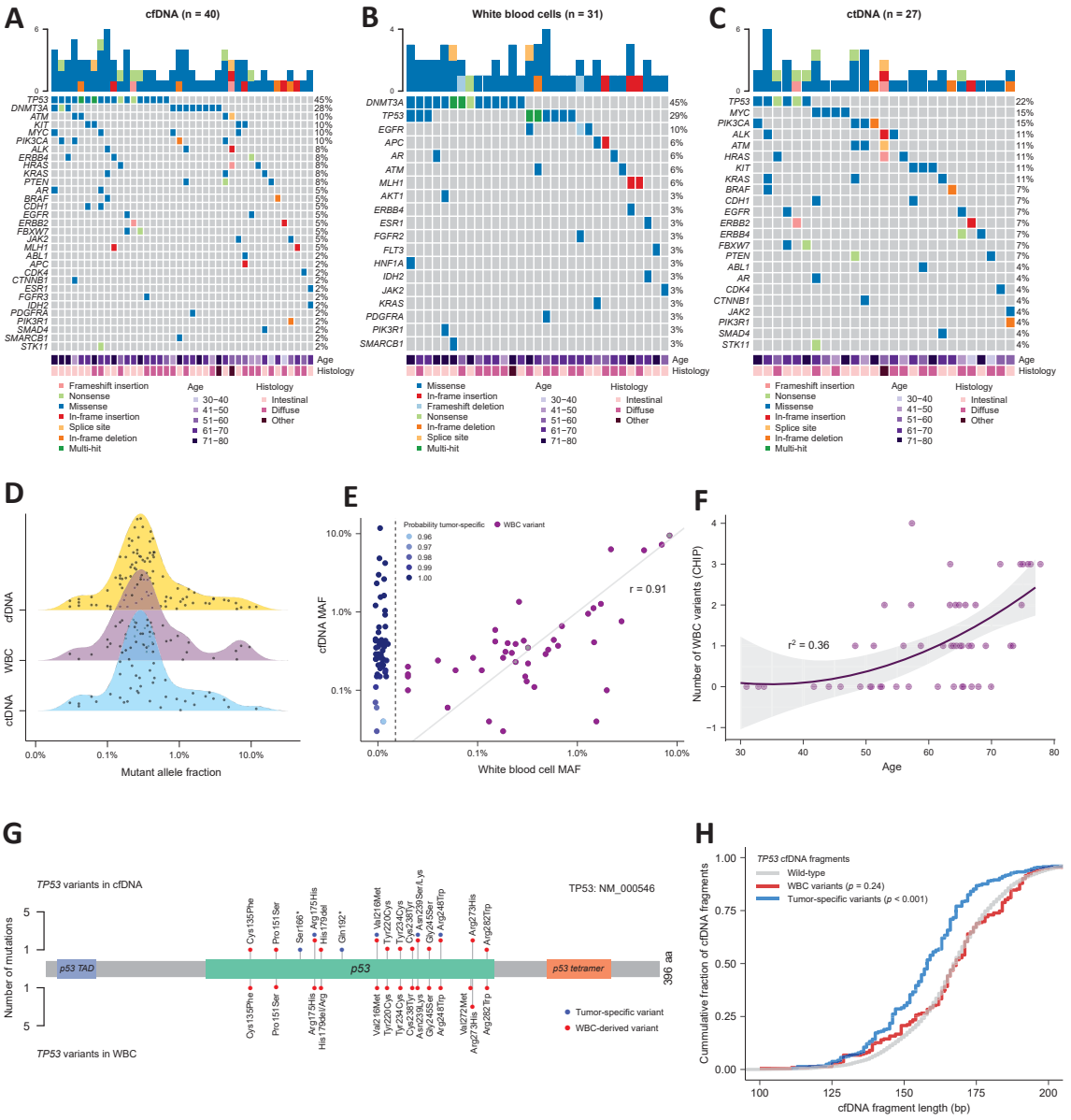


Figure 3.5. Identification of white blood cell and ctDNA variants in cfDNA of patients with localized gastric cancer. A-B, Ultrasensitive targeted sequencing were used to detect mutations in cfDNA (A) and WBCs (B) in 50 patients, with only those cases having alterations indicated. C, Tumor-specific mutations in ctDNA were identified in 27 individuals after subtraction of WBC derived variants in cfDNA. D, Density plots showing the mutant allele fraction distribution of cfDNA variants (top, yellow), WBC variants (middle, purple), and resulting ctDNA variants (bottom, blue). E, Levels of mutant allele fractions in WBCs (horizontal axis) and their correspondent levels in cfDNA (vertical axis) suggest that WBC alterations are identified at similar levels in cfDNA (Pearson correlation coefficient = 0.91, $p < 0.001$). The probability that an identified variant is tumor-derived when the alteration is not detected in WBCs is indicated by the shading of the blue dots. F, Association between age (horizontal axis) and absolute number of WBC variants detected in each patient (vertical axis) suggests that the number of WBC alterations increase with age ($r2 = 0.36$, exponential correlation). G, Positions and frequencies of mutations in TP53 detected in cfDNA (top plot) and WBCs (bottom plot) demonstrate that the majority of TP53 alterations in cfDNA are from WBCs. One TP53 splice site mutation detected in both datasets is not shown. H, Cumulative fraction of cfDNA fragments based on cfDNA fragment length (bp) shows an altered distribution for cfDNA fragments harboring tumor-derived TP53 alterations (blue) compared to WBC TP53 variants (red) and wild-type TP53 sequences ($p < 0.001$, Kolmogorov-Smirnov test)

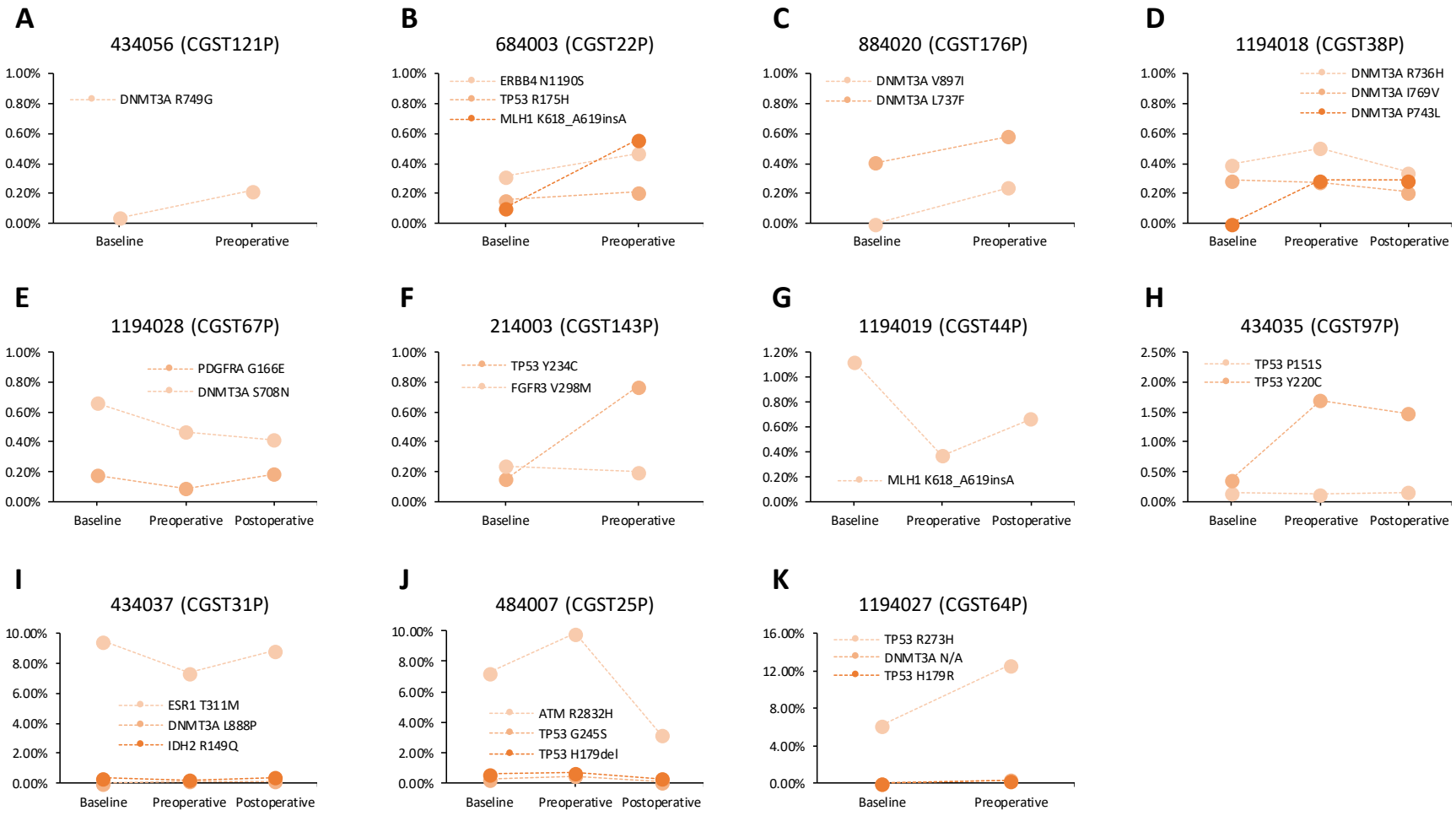


Figure 3.6. Longitudinal detection of white blood cell (WBC) sequence alterations in patients with gastric cancer. A-K, Mutant allele fractions of WBC variants identified in cfDNA in patients without tumor-specific mutations.

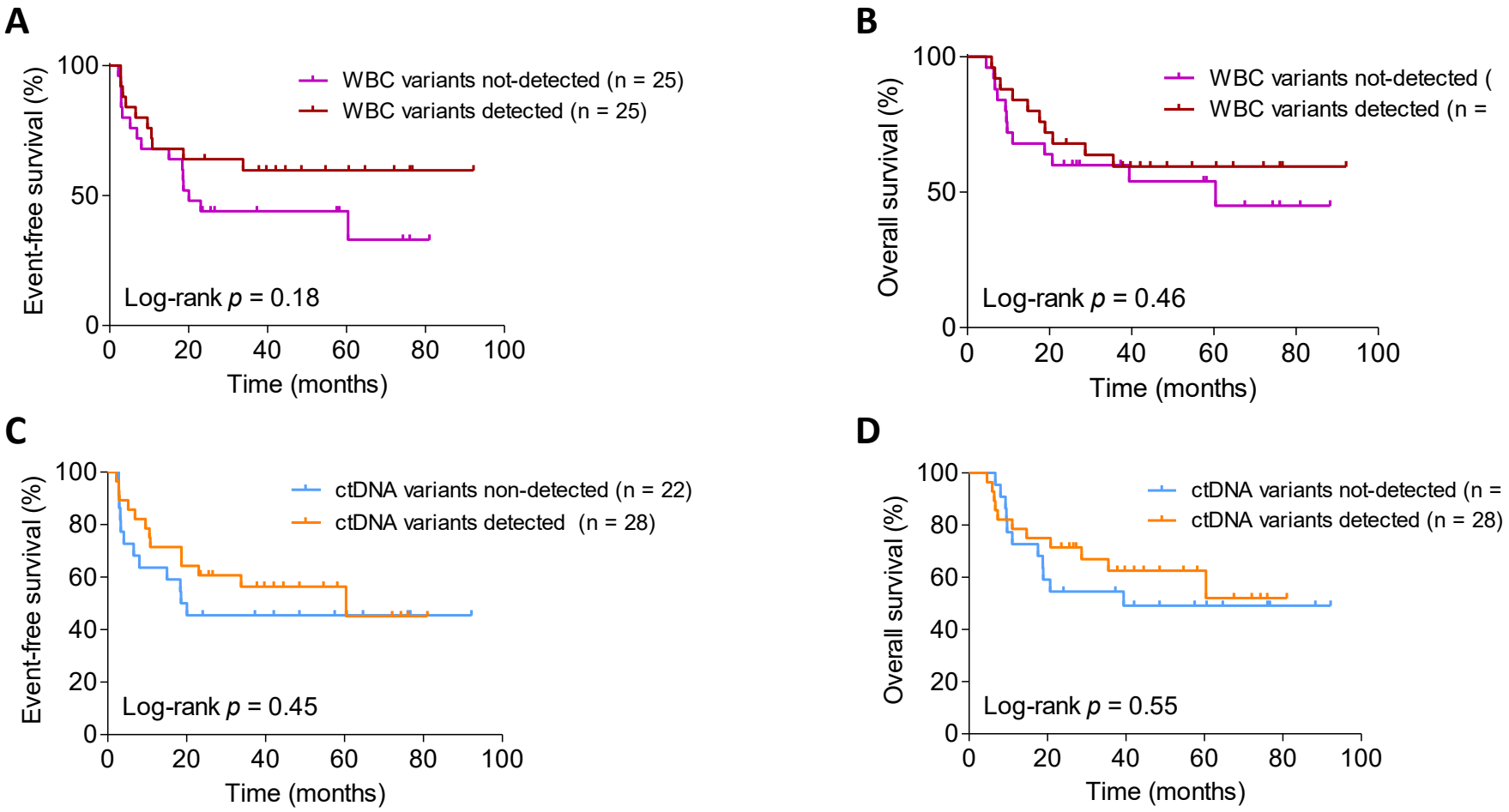


Figure 3.7. Survival outcomes based on WBC variants or tumor-specific alterations in cfDNA at the baseline timepoint. A-B, Kaplan-Meier estimates for event-free survival [Log-rank p = 0.18; HR = 1.7 (95% CI = 0.8-3.8)] (A) and overall survival [Log-rank p = 0.46; HR = 1.4 (95% CI = 0.6-3.2)] (B) of patients with or without WBCs variants in cfDNA at the time of study enrollment. C-D, Kaplan-Meier estimates for event -free survival [Log-rank p = 0.45; HR = 1.4 (95% CI = 0.6-3.0)] (C) and overall survival [Log-rank p = 0.55; HR = 1.3 (95% CI = 0.6-3.0)] (D) of patients with or without ctDNA detected at the time of study enrollment.

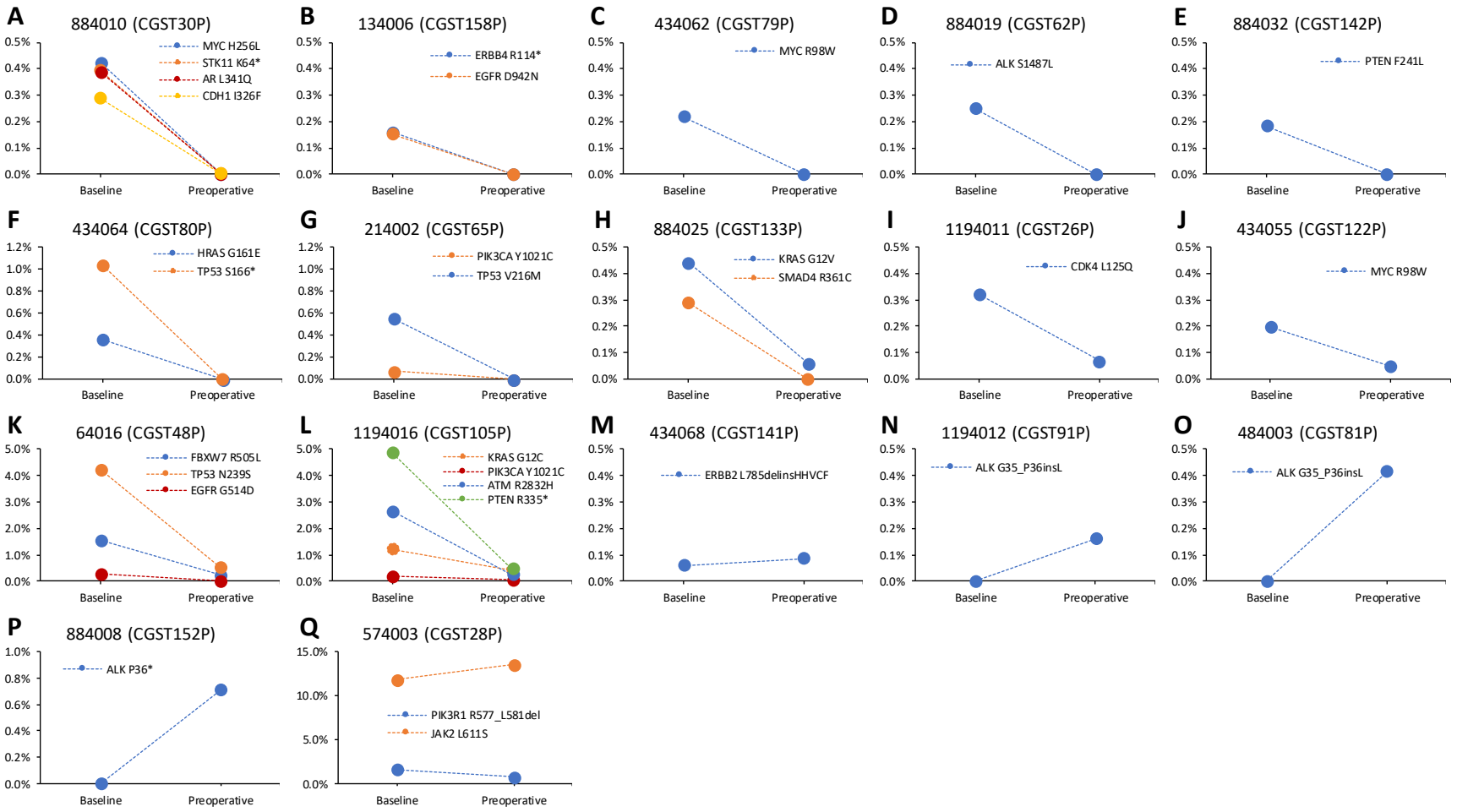


Figure 3.8. Dynamic changes in ctDNA during the preoperative chemotherapy interval. A-Q, ctDNA alterations in each patient were detected during the preoperative chemotherapy interval after removing WBC variants observed in cfDNA.

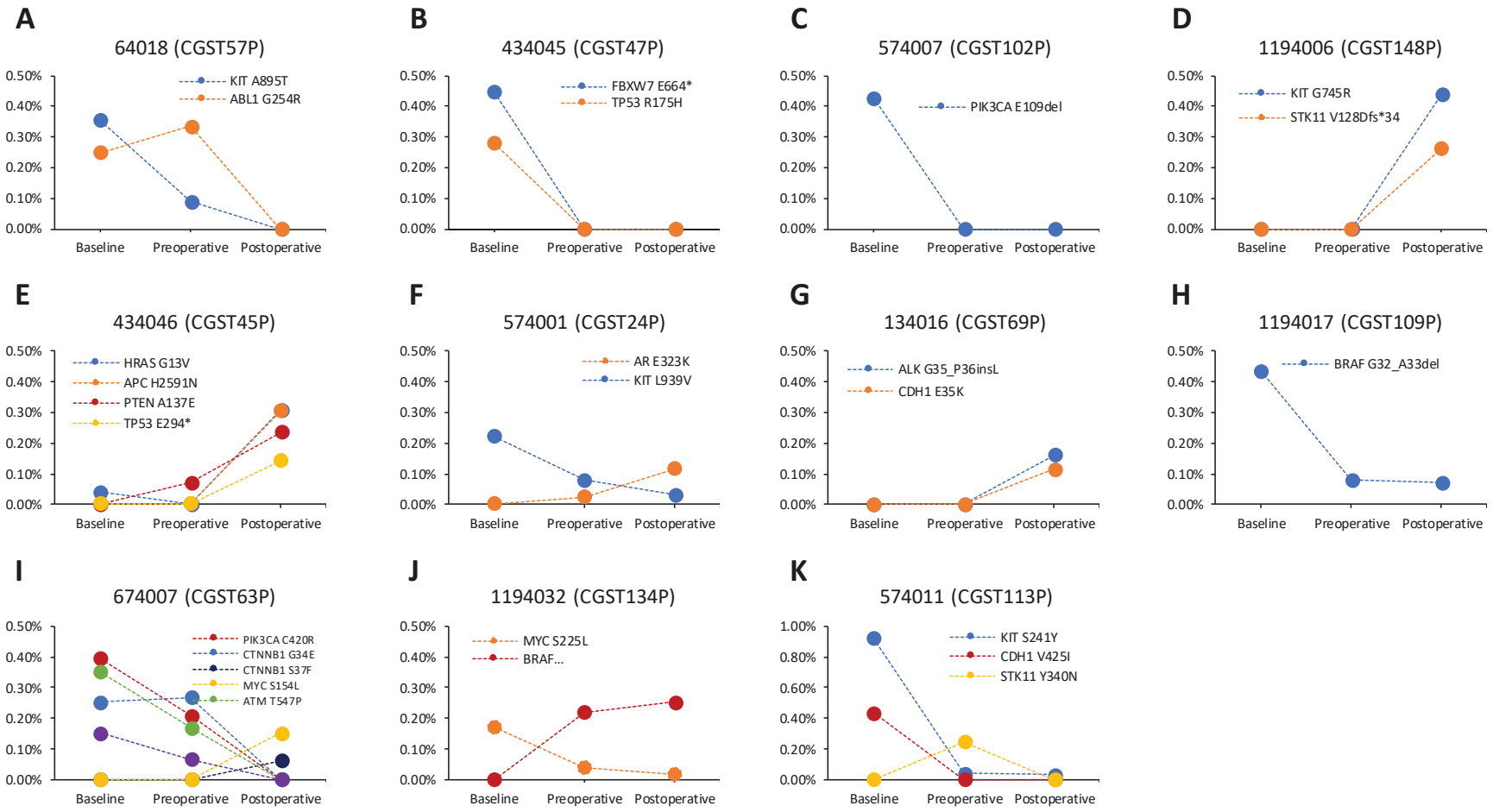


Figure 3.9. Dynamic changes in ctDNA before and after surgery. A-K, ctDNA alterations observed for each patient were detected from baseline through postoperative timepoints after removing WBC variants observed in cfDNA.

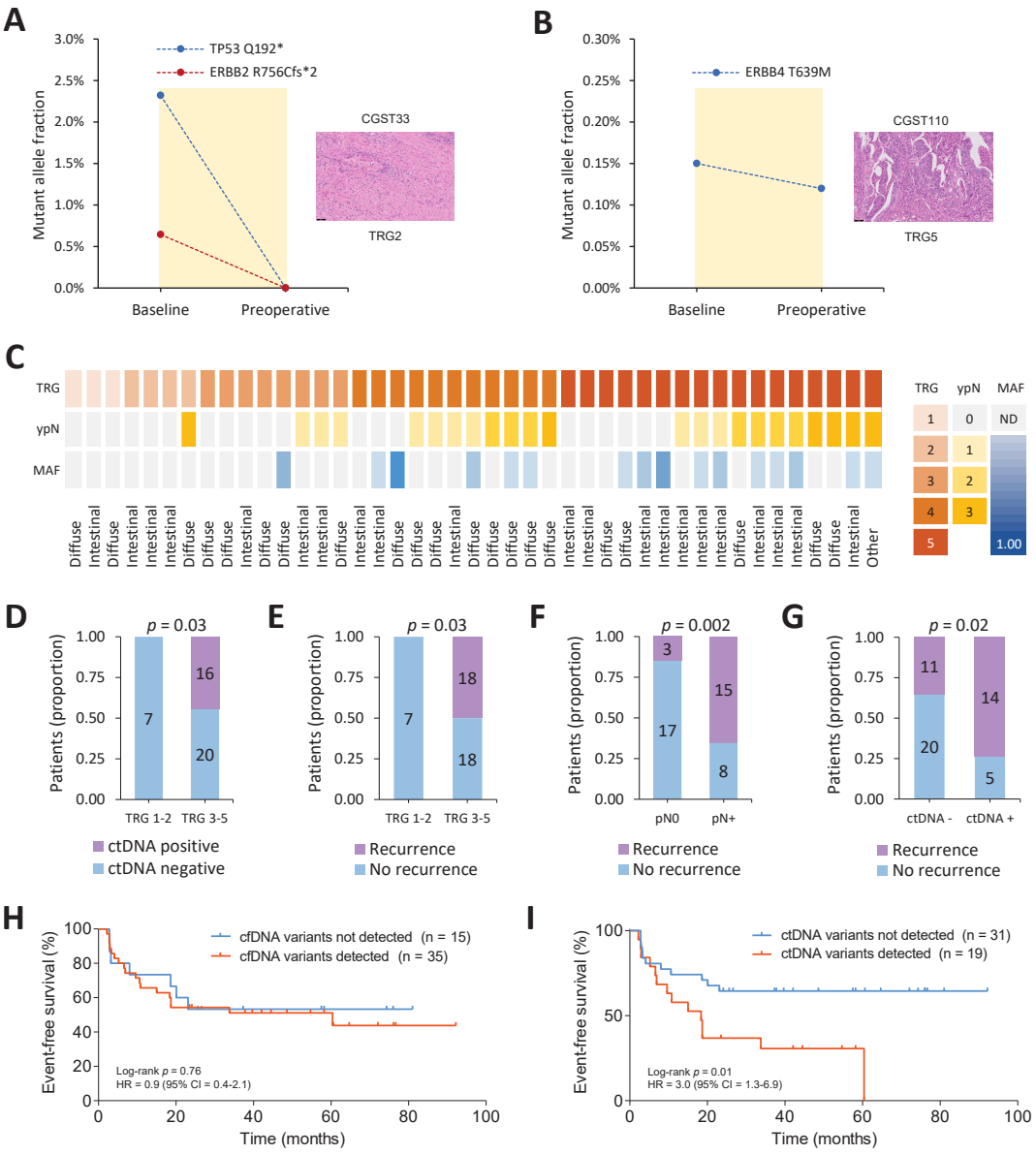


Figure 3.10. Preoperative ctDNA as a biomarker for pathologic response and clinical outcome in gastric cancer. A-B, Levels of ctDNA variants at baseline and the preoperative timepoint in a molecular responder (CGST33) (A) and in a non-responder (CGST110) (B). Variant MAFs in the molecular responder show elimination of ctDNA, while ctDNA levels are relatively unchanged in the molecular non-responder. A representative H&E image (20X) depicting Mandard's tumor regression grade is shown for each case on the right. C, Heatmap representing the pathological features (TRG and lymph node status) and highest mutant allele fraction detected for each of the 43 patients that underwent surgical resection. Lauren's classifications are depicted in the bottom for each case. D, Dichotomized association between degree of tumor regression and ctDNA status at the preoperative timepoint (p = 0.03, Fisher's exact test), E, between degree of tumor regression and disease recurrence (p = 0.03, Fisher's exact test), F, between pathological lymph node status and disease recurrence (p = 0.002, Fisher's exact test), and G, between ctDNA status at the preoperative timepoint and disease recurrence (p = 0.02, Fisher's exact test). H-I, Kaplan-Meier estimates for event-free survival of patients with detected versus non-detected variants at the preoperative timepoint using all cfDNA sequence changes (Log-rank p = 0.76; HR = 0.9; 95% CI = 0.4-2.1) (H) or using only ctDNA alterations identified from the WBC-filtered approach (Log-rank p = 0.01; HR = 3.0; 95% CI = 1.3-6.9) (I).

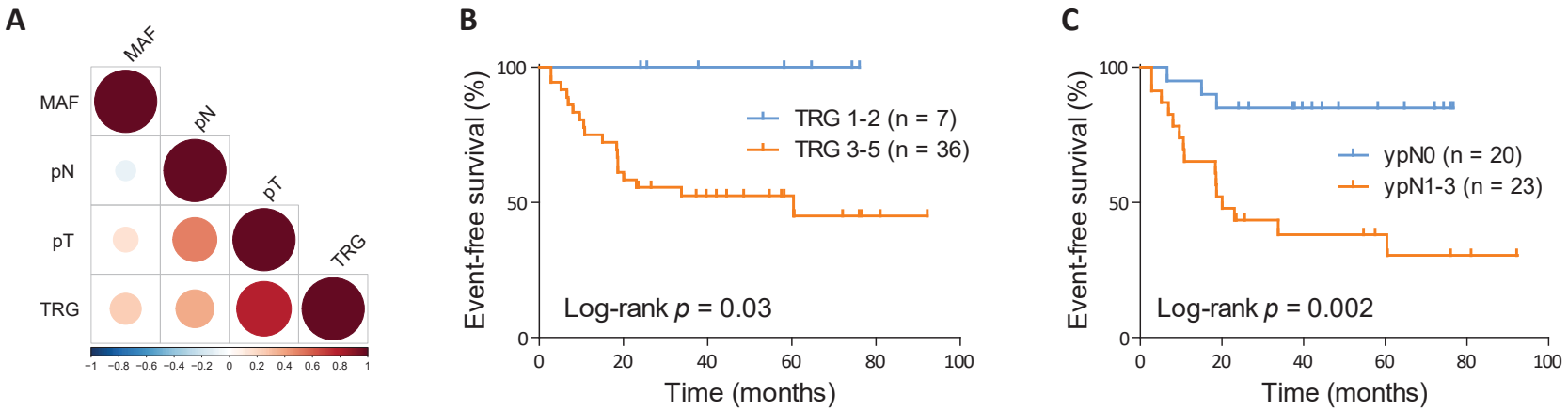


Figure 3.11. Pathological response at the preoperative timepoint and survival outcomes. A, Heatmap showing the Spearman's rank correlation coefficients between mutant allele fractions at the preoperative timepoint and pathological features after surgery (ypN, pathological lymph node assessment; ypT, pathological tumor assessment; TRG, tumor regression grade). B, Kaplan-Meier estimates for event-free survival of patients with minor or no pathological response (TRG 3-5) and major pathological responses (TRG 1-2) to preoperative chemotherapy [Log-rank p = 0.03; HR = 3.6 (95% CI = 1.1-11.3)]. C, Kaplan-Meier estimates for event-free survival of patients with (ypN1-3) and without (ypN0) lymph node tumor infiltration [Log-rank p = 0.002; HR = 4.5 (95% CI = 1.8-11.6)].

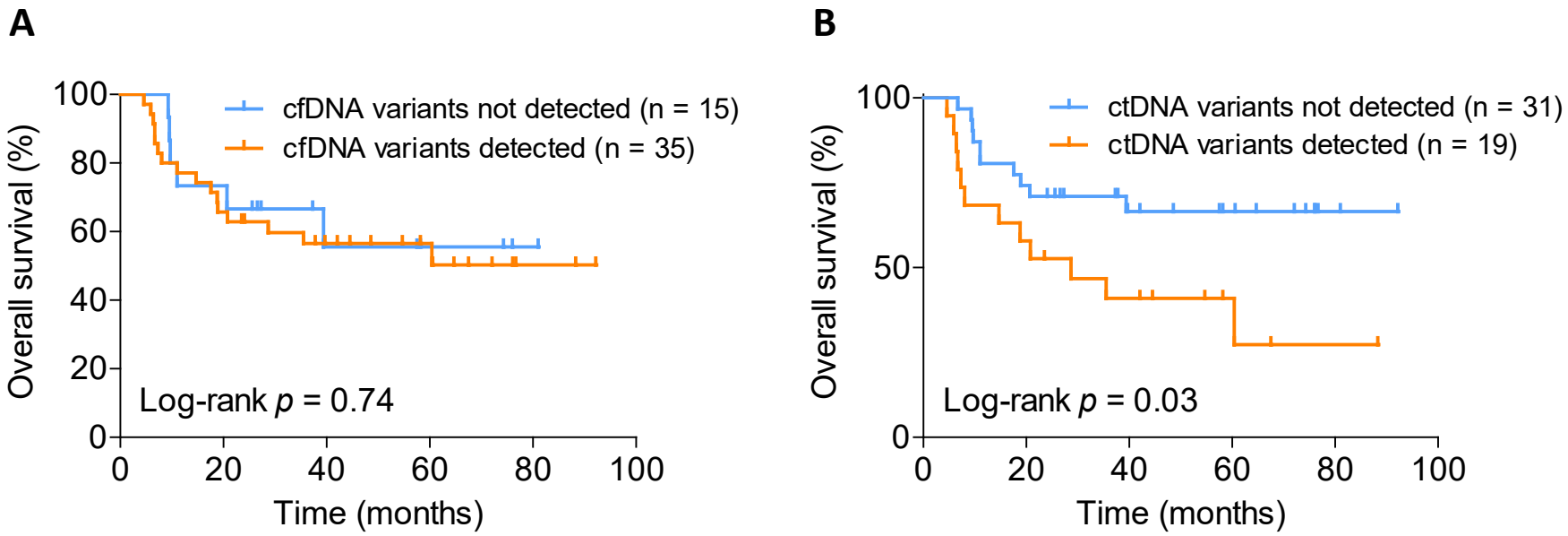


Figure 3.12. Detection of cfDNA and ctDNA variants at the preoperative timepoint and overall survival. A-B, Kaplan-Meier estimates for overall survival of patients with detected versus non-detected variants at the preoperative timepoint using all cfDNA sequence changes [Log-rank p = 0.74; HR = 0.9 (95% CI = 0.4-2.1)] (A) or using only ctDNA alterations identified from the WBC-filtered approach [Log-rank p = 0.03; HR = 2.7 (95 % CI = 1.1-6.7)] (B).

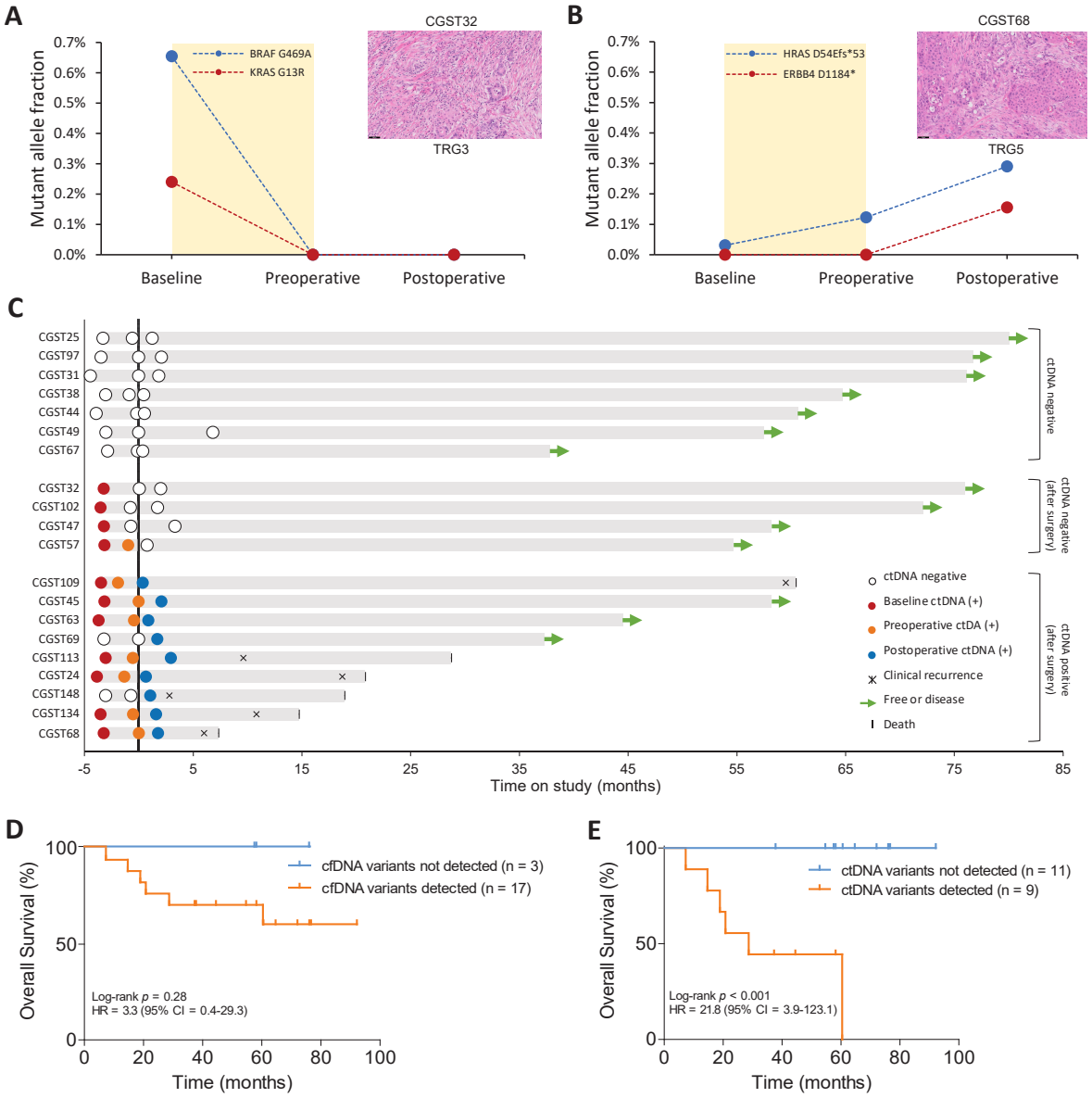


Figure 3.13. Assessment of ctDNA as a minimal residual disease biomarker in resectable gastric cancer. A-B, Levels of ctDNA variants from baseline to postoperative timepoint in a molecular responder (CGST32) (A) and in a non-responder (CGST68) (B). Variant MAFs in the molecular responder show elimination of ctDNA, while ctDNA levels continue to rise in the molecular non-responder. A representative H&E image (20X magnification) depicting Mandard's tumor regression grade is shown for each case on the right. C, Longitudinal representation of ctDNA results from 20 patients with a postoperative timepoint available. Black vertical line represents the time of surgery. Green arrows depict patients with no evidence of disease at last follow-up. D-E, Kaplan-Meier estimates for overall survival of patients with detected versus non-detected variants at the postoperative timepoint using all cfDNA sequence changes (Log-rank p = 0.28; HR = 3.3; 95% CI = 0.4-29) (D) or using only ctDNA alterations identified from the WBC-filtered approach (Log-rank p = 0.001; HR = 21.8; 95% CI = 3.9-123.1) (E).

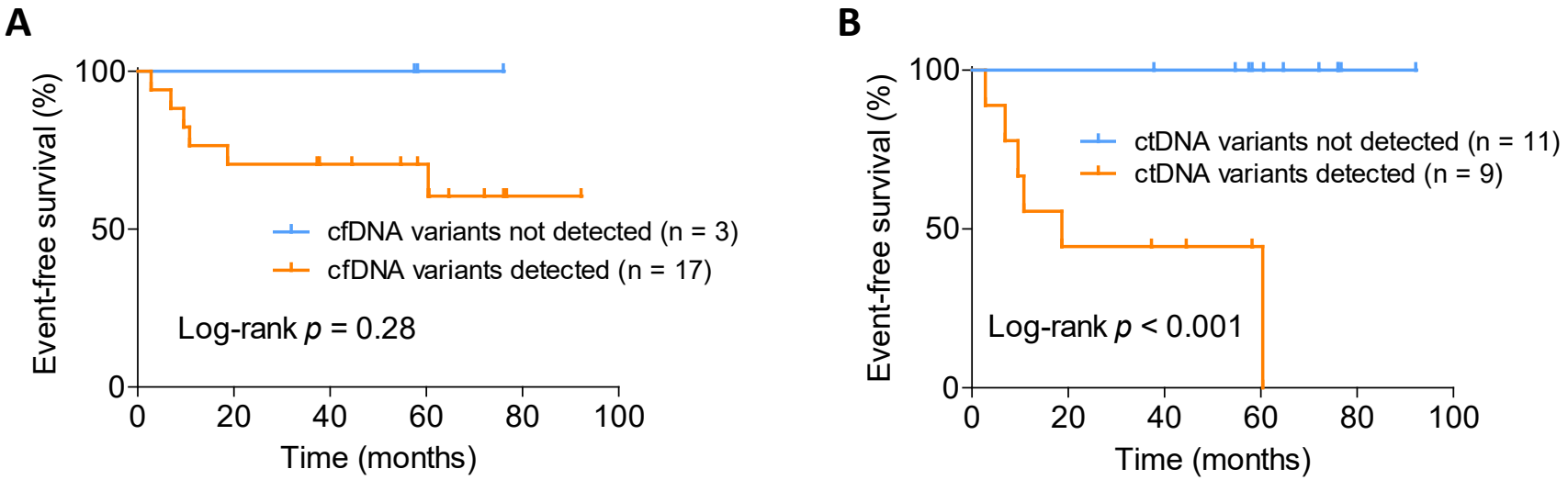


Figure 3.14. Detection of cfDNA and ctDNA variants at the postoperative timepoint and event-free survival. A-B, Kaplan-Meier estimates for event-free survival of patients with detected versus non-detected variants at the postoperative timepoint using all cfDNA sequence data [Log-rank p = 0.28; HR = 3.3 (95% CI = 0.4-29.3)] (A) or using only ctDNA alterations identified from the WBC-filtered approach [Log-rank p < 0.001; HR = 21.8 (95% CI = 3.9-123.1)] (B).

Table 3.1. Summary of clinical characteristics of patients analyzed.

Patient ID	Age	Gender	Preoperative Treatment	Type of Surgery	Postoperative Treatment	Lauren Subtype	ypT	ypN	ypM	MMR Status	EBV Status	Pathological Stage	Resection margins	TRG (Mandard)	Residual Tumor Burden
CGST102	76	Female	3x ECC	Distal gastrectomy	45Gy + 5w CC	Intestinal	ypT3	ypN0	ypM0	MSI	negative	IIA	Negative	TRG 5	0%
CGST105	66	Female	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT3	ypN0	ypM0	MSI	negative	IIA	Negative	TRG 5	0%
CGST114	65	Male	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT4a	ypN1	ypM0	MSS	negative	IIIA	Negative	TRG 4	10-19%
CGST121	75	Male	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT1b	ypN0	ypM0	MSS	negative	IA	Negative	TRG 3	80-89%
CGST122	56	Male	3x ECC	Distal gastrectomy	45Gy + 5w CC	Intestinal	ypT1a	ypN0	ypM0	MSS	negative	IA	Negative	TRG 4	20-29%
CGST134	74	Male	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT3	ypN1	ypM0	MSS	negative	IIB	Negative	TRG 5	0%
CGST143	67	Female	3x ECC	Distal gastrectomy	45Gy + 5w CC	Diffuse	ypT0	ypN0	ypM0	NA	NA	0	Negative	TRG 1	100%
CGST148	49	Female	3x ECC	Distal gastrectomy	3x ECC	Diffuse	ypT4a	ypN2	ypMX	MSS	negative	IIIB	Positive	TRG 5	1-9%
CGST24	76	Female	3x ECC	Distal gastrectomy	45Gy + 5w CC	Diffuse	ypT3	ypN2	ypM0	MSS	negative	IIIA	Positive	TRG 4	30-39%
CGST38	71	Female	3x ECC	Distal gastrectomy	45Gy + 5w CC	Diffuse	ypT0	ypN0	ypM0	NA	negative	0	Negative	TRG 1	100%
CGST44	66	Male	3x ECC	Distal gastrectomy	3x ECC	Diffuse	ypT3	ypN1 (mi)	ypM0	MSS	negative	IIB	Negative	TRG 3	50-59%
CGST47	74	Female	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT1a	ypN0	ypM0	MSS	negative	IA	Negative	TRG 2	90-99%
CGST49	30	Female	3x ECC	Distal gastrectomy	45Gy + 5w CC	Diffuse	ypT2	ypN1	ypM0	MSS	negative	IIA	Negative	TRG 4	40-49%
CGST57	51	Male	3x ECC	Distal gastrectomy	3x ECC	Diffuse	ypT1b	ypN1 (mi)	ypM0	MSS	negative	IB	Negative	TRG 4	10-19%
CGST62	63	Male	3x ECC	Distal gastrectomy	45Gy + 5w CC	Diffuse	ypT4a	ypN0	ypMX	NA	NA	IIB	Negative	TRG 5	0%
CGST67	69	Male	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT1b	ypN0	ypM0	MSS	negative	IA	Negative	TRG 2	90-99%
CGST68	53	Male	3x ECC	Distal gastrectomy	45Gy + 5w CC	Other*	ypT4a	ypN3a	ypM1	MSS	negative	IV	Negative	TRG 5	0%
CGST69	53	Male	3x ECC	Distal gastrectomy	45Gy + 5w CC	Diffuse	ypT2	ypN0	ypM0	MSS	negative	IB	Negative	TRG 3	50-59%
CGST79	45	Male	3x ECC	Distal gastrectomy	3x ECC	Diffuse	ypT2	ypN0	ypM0	MSS	negative	IB	Negative	TRG 3	60-69%

CGST80	58	Male	3x ECC	Distal gastrectomy	3x ECC	Diffuse	ypT3	ypN3a	ypM0	NA	NA	IIIB	Negative	TRG 2	90-99%
CGST91	56	Male	3x ECC	Distal gastrectomy	3x ECC	Intestinal	ypT3	ypN2	ypM0	MSS	negative	IIIA	Negative	TRG 5	0%
CGST113	64	Male	3x ECC	Esophagocardial resection	45Gy + 5w CC	Intestinal	ypT3	ypN2	ypM0	MSS	NA	IIIA	Negative	TRG 5	0%
CGST176	66	Male	3x ECC	Esophagocardial resection	45Gy + 5w CC	Intestinal	ypT3	ypN0	ypMX	NA	NA	IIA	Negative	TRG 4	10-19%
CGST30	64	Female	3x ECC	Esophagocardial resection	45Gy + 5w CC	Diffuse	ypT3	ypN2	ypM0	NA	NA	IIIA	Positive	TRG 4	10-19%
CGST33	61	Male	3x ECC	Esophagocardial resection	45Gy + 5w CC	Intestinal	ypT2	ypN0	ypM0	MSS	negative	IB	Negative	TRG 2	90-99%
CGST28	55	Male	3x ECC	Not performed	3x ECC	Intestinal	ypTx	ypNx	ypMX	MSS	positive	X	No resection	No resection	No resection
CGST22	75	Male	3x ECC	Exploratory laparotomy	3x ECC	Intestinal	ypTx	ypNx	ypM1	MSS	negative	IV	No resection	No resection	No resection
CGST26	51	Male	3x ECC	Exploratory laparotomy	3x ECC	Diffuse	ypTx	ypNx	ypM1	MSS	negative	IV	No resection	No resection	No resection
CGST39	51	Male	3x ECC	Exploratory laparotomy	3x ECC	Diffuse	ypTx	ypNx	ypM1	NA	NA	IV	No resection	No resection	No resection
CGST41	66	Female	3x ECC	Exploratory laparotomy	3x ECC	Diffuse	ypTx	ypNX	ypM1	NA	NA	IV	No resection	No resection	No resection
CGST48	62	Male	3x ECC	Exploratory laparotomy	45Gy + 5w CC	Intestinal	ypTx	ypNx	ypM1	MSS	negative	IV	No resection	No resection	No resection
CGST64	58	Male	3x ECC	Exploratory laparotomy	45Gy + 5w CC	Diffuse	ypTx	ypNx	ypM1	NA	negative	IV	No resection	No resection	No resection
CGST158	45	Male	3x ECC	Proximal gastrectomy	45Gy + 5w CC	Diffuse	ypT3	ypN1	ypM0	MSS	negative	IIB	Negative	TRG 4	40-49%
CGST109	63	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Intestinal	ypT3	ypN2	ypM0	MSS	negative	IIIA	Negative	TRG 5	0%
CGST110	77	Male	3x ECC	Total gastrectomy	3x ECC	Intestinal	ypT4a	ypN3a	ypM0	MSS	NA	IIIC	Negative	TRG 5	0%
CGST131	63	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Diffuse	ypT2	ypN3a	ypM0	MSS	negative	IIIA	Negative	TRG 4	40-49%
CGST133	70	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Intestinal	ypT4b	ypN1	ypM1	NA	NA	IV	Negative	TRG 5	0%
CGST141	33	Female	3x ECC	Total gastrectomy	3x ECC	Diffuse	ypT3	ypN2	ypM0	MSS	negative	IIIA	Negative	TRG 4	20-29%
CGST142	33	Female	3x ECC	Total gastrectomy	45Gy + 5w CC	Diffuse	ypT4a	ypN3a	ypM0	MSS	negative	IIIC	Negative	TRG 5	0%
CGST152	65	Male	3x ECC	Total gastrectomy	3x ECC	Diffuse	ypT4a	ypN0	ypMX	NA	NA	IIB	Positive	TRG 4	30-39%
CGST25	64	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Intestinal	ypT3	ypN1 (mi)	ypM0	MSS	negative	IIB	Negative	TRG 3	70-79%
CGST31	64	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Intestinal	ypT0	ypN0	ypM0	MSS	negative	0	Negative	TRG 1	100%

CGST32	67	Male	3x ECC	Total gastrectomy	3x ECC	Intestinal	ypT3	ypN1	ypM0	MSS	negative	IIB	Negative	TRG 3	60-69%
CGST45	41	Female	3x ECC	Total gastrectomy	45Gy + 5w CC	Diffuse	ypT3	ypN0	ypM0	MSS	negative	IIA	Negative	TRG 5	0%
CGST58	58	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Diffuse	ypT4a	ypN3b	ypM0	MSS	negative	IIIC	Negative	TRG 5	10-19%
CGST63	50	Male	3x ECC	Total gastrectomy	3x ECC	Intestinal	ypT3	ypN0	ypM0	MSS	positive	IIA	Negative	TRG 5	0%
CGST65	73	Male	3x ECC	Total gastrectomy	45Gy + 5w CC	Intestinal	ypT3	ypN0	ypM0	MSS	negative	IIA	Negative	TRG 5	0%
CGST71	53	Male	3x ECC	Total gastrectomy	3x ECC	Intestinal	ypT3	ypN1	ypM0	MSS	negative	IIB	Positive	TRG 5	0%
CGST81	64	Female	3x ECC	Total gastrectomy	45Gy + 5w CC	Diffuse	ypT2	ypN0	ypMX	MSS	negative	IB	Negative	TRG 3	60-69%
CGST97	65	Male	3x ECC	Total gastrectomy	3x ECC	Diffuse	ypT2	ypN0	ypM0	MSS	positive	IB	Negative	TRG 3	70-79%

ECC, epirubicin, cisplatin, capecitabine; CC, cisplatin, capecitabine; MMR, mismatch repair; EBV, Epstein Barr virus; TRG, tumor regression grade, *adenosquamous carcinoma

Table 3.2. Summary of serial timepoints analyzed.

Patient ID	Patient Timepoint	Significance of Timepoint	Sample Type	Sample Volume (ml)	cfDNA Extracted (ng)	cfDNA Input (ng)
CGST102	CGST102P	Baseline	Plasma	4.1	32.9	32.92
CGST102	CGST102N	Baseline	Buffy Coat	0.1	1351.6	75.00
CGST102	CGST102P2	Postoperative	Plasma	4.1	19.9	19.95
CGST102	CGST102P1	Preoperative	Plasma	3.9	29.3	29.33
CGST105	CGST105P	Baseline	Plasma	4.0	68.7	68.73
CGST105	CGST105N	Baseline	Buffy Coat	0.1	1324.8	75.00
CGST105	CGST105P1	Preoperative	Plasma	4.0	151.1	125.00
CGST109	CGST109P	Baseline	Plasma	4.0	98.5	98.49
CGST109	CGST109N	Baseline	Buffy Coat	0.1	2194.4	75.00
CGST109	CGST109P2	Postoperative	Plasma	3.7	246.3	125.00
CGST109	CGST109P1	Preoperative	Plasma	4.0	196.2	125.00
CGST110	CGST110P	Baseline	Plasma	3.8	19.0	19.01
CGST110	CGST110N	Baseline	Buffy Coat	0.1	915.6	75.00
CGST110	CGST110P1	Preoperative	Plasma	4.4	89.9	89.92
CGST113	CGST113P	Baseline	Plasma	3.5	41.3	41.29
CGST113	CGST113N	Baseline	Buffy Coat	0.1	891.0	75.00
CGST113	CGST113P2	Postoperative	Plasma	2.9	31.8	31.84
CGST113	CGST113P1	Preoperative	Plasma	3.8	82.5	82.55
CGST114	CGST114P	Baseline	Plasma	4.4	45.5	45.54
CGST114	CGST114N	Baseline	Buffy Coat	0.1	1947.0	75.00
CGST114	CGST114P1	Preoperative	Plasma	4.5	118.4	118.40
CGST121	CGST121P	Baseline	Plasma	3.8	22.8	22.83
CGST121	CGST121N	Baseline	Buffy Coat	0.1	983.7	75.00

CGST121	CGST121P1	Preoperative	Plasma	3.6	39.6	39.56
CGST122	CGST122P	Baseline	Plasma	3.5	59.2	59.15
CGST122	CGST122N	Baseline	Buffy Coat	0.1	704.2	75.00
CGST122	CGST122P1	Preoperative	Plasma	3.5	128.4	125.00
CGST131	CGST131P	Baseline	Plasma	4.0	17.1	17.13
CGST131	CGST131N	Baseline	Buffy Coat	0.1	2484.0	75.00
CGST131	CGST131P1	Preoperative	Plasma	4.4	131.2	125.00
CGST133	CGST133P	Baseline	Plasma	4.5	182.2	125.00
CGST133	CGST133N	Baseline	Buffy Coat	0.1	891.5	75.00
CGST133	CGST133P1	Preoperative	Plasma	4.5	43.7	43.65
CGST134	CGST134P	Baseline	Plasma	4.5	46.1	46.12
CGST134	CGST134N	Baseline	Buffy Coat	0.1	1056.8	75.00
CGST134	CGST134P2	Postoperative	Plasma	4.7	229.8	125.00
CGST134	CGST134P1	Preoperative	Plasma	4.0	32.6	32.63
CGST141	CGST141P	Baseline	Plasma	4.4	47.7	47.67
CGST141	CGST141N	Baseline	Buffy Coat	0.1	700.0	75.00
CGST141	CGST141P1	Preoperative	Plasma	4.4	69.9	69.94
CGST142	CGST142P	Baseline	Plasma	4.0	10.2	10.19
CGST142	CGST142N	Baseline	Buffy Coat	0.1	942.5	75.00
CGST142	CGST142P1	Preoperative	Plasma	4.5	42.7	42.74
CGST143	CGST143P	Baseline	Plasma	4.4	21.6	21.64
CGST143	CGST143N	Baseline	Buffy Coat	0.1	946.8	75.00
CGST143	CGST143P1	Preoperative	Plasma	4.2	47.7	47.65
CGST148	CGST148P	Baseline	Plasma	2.5	9.9	9.86
CGST148	CGST148N	Baseline	Buffy Coat	0.1	1190.4	75.00
CGST148	CGST148P2	Postoperative	Plasma	4.1	45.1	45.15
CGST148	CGST148P1	Preoperative	Plasma	2.0	21.4	21.42
CGST152	CGST152P	Baseline	Plasma	3.0	59.6	59.64

CGST152	CGST152N	Baseline	Buffy Coat	0.1	1091.2	75.00
CGST152	CGST152P1	Preoperative	Plasma	3.8	257.2	125.00
CGST158	CGST158P	Baseline	Plasma	4.0	89.5	89.48
CGST158	CGST158N	Baseline	Buffy Coat	0.1	1036.8	75.00
CGST158	CGST158P1	Preoperative	Plasma	4.5	49.6	49.62
CGST176	CGST176P	Baseline	Plasma	3.0	40.3	40.26
CGST176	CGST176N	Baseline	Buffy Coat	0.1	543.7	75.00
CGST176	CGST176P1	Preoperative	Plasma	3.4	45.2	45.19
CGST22	CGST22P	Baseline	Plasma	2.5	31.3	31.33
CGST22	CGST22N	Baseline	Buffy Coat	0.1	877.2	75.00
CGST22	CGST22P1	Preoperative	Plasma	2.5	31.3	31.33
CGST24	CGST24P	Baseline	Plasma	4.0	119.9	119.93
CGST24	CGST24N	Baseline	Buffy Coat	0.1	1258.0	75.00
CGST24	CGST24P2	Postoperative	Plasma	4.0	144.9	125.00
CGST24	CGST24P1	Preoperative	Plasma	3.8	194.9	125.00
CGST25	CGST25P	Baseline	Plasma	3.0	14.0	14.04
CGST25	CGST25N	Baseline	Buffy Coat	0.1	734.7	75.00
CGST25	CGST25P2	Postoperative	Plasma	4.1	138.7	125.00
CGST25	CGST25P1	Preoperative	Plasma	3.9	40.4	40.42
CGST26	CGST26P	Baseline	Plasma	3.5	19.5	19.46
CGST26	CGST26N	Baseline	Buffy Coat	0.1	995.7	75.00
CGST26	CGST26P1	Preoperative	Plasma	2.5	46.0	45.96
CGST28	CGST28P	Baseline	Plasma	4.0	23.5	23.45
CGST28	CGST28N	Baseline	Buffy Coat	0.1	1900.0	75.00
CGST28	CGST28P1	Preoperative	Plasma	4.0	33.6	33.62
CGST30	CGST30P	Baseline	Plasma	3.0	12.7	12.66
CGST30	CGST30N	Baseline	Buffy Coat	0.1	1254.4	75.00
CGST30	CGST30P1	Preoperative	Plasma	3.5	72.7	72.65

CGST31	CGST31P	Baseline	Plasma	4.0	103.0	102.99
CGST31	CGST31N	Baseline	Buffy Coat	0.1	1831.8	75.00
CGST31	CGST31P2	Postoperative	Plasma	4.0	57.5	57.46
CGST31	CGST31P1	Preoperative	Plasma	3.5	28.4	28.45
CGST32	CGST32P	Baseline	Plasma	4.0	46.0	45.96
CGST32	CGST32N	Baseline	Buffy Coat	0.1	2219.6	75.00
CGST32	CGST32P2	Postoperative	Plasma	4.0	17.3	17.26
CGST32	CGST32P1	Preoperative	Plasma	3.5	147.8	125.00
CGST33	CGST33P	Baseline	Plasma	3.5	20.0	19.98
CGST33	CGST33N	Baseline	Buffy Coat	0.1	1776.0	75.00
CGST33	CGST33P1	Preoperative	Plasma	4.0	34.8	34.84
CGST38	CGST38P	Baseline	Plasma	4.0	46.0	45.96
CGST38	CGST38N	Baseline	Buffy Coat	0.1	837.4	75.00
CGST38	CGST38P2	Postoperative	Plasma	4.0	49.6	49.63
CGST38	CGST38P1	Preoperative	Plasma	4.5	17.0	16.95
CGST39	CGST39P	Baseline	Plasma	3.5	72.4	72.42
CGST39	CGST39N	Baseline	Buffy Coat	0.1	1064.0	75.00
CGST39	CGST39P1	Preoperative	Plasma	4.5	28.3	28.35
CGST41	CGST41P	Baseline	Plasma	3.5	27.4	27.42
CGST41	CGST41N	Baseline	Buffy Coat	0.1	864.0	75.00
CGST41	CGST41P1	Preoperative	Plasma	4.0	46.4	46.35
CGST44	CGST44P	Baseline	Plasma	3.5	76.0	76.01
CGST44	CGST44N	Baseline	Buffy Coat	0.1	693.6	75.00
CGST44	CGST44P2	Postoperative	Plasma	3.2	75.8	75.76
CGST44	CGST44P1	Preoperative	Plasma	5.0	124.7	124.71
CGST45	CGST45P	Baseline	Plasma	3.8	27.1	27.15
CGST45	CGST45N	Baseline	Buffy Coat	0.1	1159.2	75.00
CGST45	CGST45P2	Postoperative	Plasma	4.5	43.9	43.90

CGST45	CGST45P1	Preoperative	Plasma	3.5	30.9	30.91
CGST47	CGST47P	Baseline	Plasma	4.0	18.2	18.22
CGST47	CGST47N	Baseline	Buffy Coat	0.1	652.1	75.00
CGST47	CGST47P2	Postoperative	Plasma	3.8	65.8	65.76
CGST47	CGST47P1	Preoperative	Plasma	3.5	26.1	26.06
CGST48	CGST48P	Baseline	Plasma	4.5	39.5	39.54
CGST48	CGST48N	Baseline	Buffy Coat	0.1	924.0	75.00
CGST48	CGST48P1	Preoperative	Plasma	3.8	111.4	111.39
CGST49	CGST49P	Baseline	Plasma	4.0	53.8	53.81
CGST49	CGST49N	Baseline	Buffy Coat	0.1	2189.0	75.00
CGST49	CGST49P2	Postoperative	Plasma	4.5	17.8	17.80
CGST49	CGST49P1	Preoperative	Plasma	4.0	23.8	23.83
CGST57	CGST57P	Baseline	Plasma	4.0	30.0	30.05
CGST57	CGST57N	Baseline	Buffy Coat	0.1	703.1	75.00
CGST57	CGST57P2	Postoperative	Plasma	4.5	44.2	44.15
CGST57	CGST57P1	Preoperative	Plasma	4.5	82.5	82.46
CGST58	CGST58P	Baseline	Plasma	3.8	75.3	75.29
CGST58	CGST58N	Baseline	Buffy Coat	0.1	1688.4	75.00
CGST58	CGST58P1	Preoperative	Plasma	4.0	179.2	125.00
CGST62	CGST62P	Baseline	Plasma	3.7	41.4	41.43
CGST62	CGST62N	Baseline	Buffy Coat	0.1	482.2	75.00
CGST62	CGST62P1	Preoperative	Plasma	4.0	45.0	44.98
CGST63	CGST63P	Baseline	Plasma	4.0	32.3	32.31
CGST63	CGST63N	Baseline	Buffy Coat	0.1	1242.0	75.00
CGST63	CGST63P2	Postoperative	Plasma	4.1	413.6	125.00
CGST63	CGST63P1	Preoperative	Plasma	3.8	230.3	125.00
CGST64	CGST64P	Baseline	Plasma	3.0	29.0	29.02
CGST64	CGST64N	Baseline	Buffy Coat	0.1	746.8	75.00

CGST64	CGST64P1	Preoperative	Plasma	4.5	43.7	43.67
CGST65	CGST65P	Baseline	Plasma	4.5	283.1	125.00
CGST65	CGST65N	Baseline	Buffy Coat	0.1	1421.4	75.00
CGST65	CGST65P1	Preoperative	Plasma	4.0	136.7	125.00
CGST67	CGST67P	Baseline	Plasma	3.0	69.0	69.02
CGST67	CGST67N	Baseline	Buffy Coat	0.1	1460.0	75.00
CGST67	CGST67P2	Postoperative	Plasma	4.5	479.9	125.00
CGST67	CGST67P1	Preoperative	Plasma	4.5	245.0	125.00
CGST68	CGST68P	Baseline	Plasma	3.5	169.2	125.00
CGST68	CGST68N	Baseline	Buffy Coat	0.1	2714.0	75.00
CGST68	CGST68P2	Postoperative	Plasma	4.5	39.9	39.94
CGST68	CGST68P1	Preoperative	Plasma	4.5	8.4	8.38
CGST69	CGST69P	Baseline	Plasma	4.0	20.4	20.35
CGST69	CGST69N	Baseline	Buffy Coat	0.1	1402.2	75.00
CGST69	CGST69P2	Postoperative	Plasma	4.5	21.0	20.97
CGST69	CGST69P1	Preoperative	Plasma	4.5	64.0	64.00
CGST71	CGST71P	Baseline	Plasma	4.0	43.4	43.43
CGST71	CGST71N	Baseline	Buffy Coat	0.1	1531.2	75.00
CGST71	CGST71P1	Preoperative	Plasma	4.5	35.9	35.94
CGST79	CGST79P	Baseline	Plasma	4.5	20.2	20.16
CGST79	CGST79P1	Preoperative	Plasma	4.2	55.9	55.86
CGST80	CGST80P	Baseline	Plasma	4.5	38.5	38.51
CGST80	CGST80N	Baseline	Buffy Coat	0.1	1078.8	75.00
CGST80	CGST80P1	Preoperative	Plasma	4.3	46.0	45.96
CGST81	CGST81P	Baseline	Plasma	3.5	130.6	125.00
CGST81	CGST81N	Baseline	Buffy Coat	0.1	1918.4	75.00
CGST81	CGST81P1	Preoperative	Plasma	2.5	307.5	125.00
CGST91	CGST91P	Baseline	Plasma	4.0	147.8	125.00

CGST91	CGST91N	Baseline	Buffy Coat	0.1	555.3	75.00
CGST91	CGST91P1	Preoperative	Plasma	4.0	348.8	125.00
CGST97	CGST97P	Baseline	Plasma	4.4	76.8	76.75
CGST97	CGST97N	Baseline	Buffy Coat	0.1	1895.4	75.00
CGST97	CGST97P2	Postoperative	Plasma	3.0	35.3	35.28
CGST97	CGST97P1	Preoperative	Plasma	4.0	213.1	125.00

Table 3.3. Summary of genes analyzed.

Gene	Region Analyzed	Gene Category
ABL1	Specific Exons	Cancer Driver Gene
AKT1	Specific Exons	Cancer Driver Gene
ALK	Full Coding Region	Cancer Driver Gene
APC	Specific Exons	Cancer Driver Gene
AR	Full Coding Region	Cancer Driver Gene
ATM	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
BRAF	Full Coding Region	Cancer Driver Gene
CDH1	Specific Exons	Cancer Driver Gene
CDK4	Full Coding Region	Cancer Driver Gene
CDK6	Full Coding Region	Cancer Driver Gene
CDKN2A	Specific Exons	Cancer Driver Gene
CSF1R	Specific Exons	Cancer Driver Gene
CTNNB1	Specific Exons	Cancer Driver Gene
DNMT3A	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
EGFR	Full Coding Region	Cancer Driver Gene
ERBB2	Specific Exons	Cancer Driver Gene
ERBB4	Full Coding Region	Cancer Driver Gene
ESR1	Full Coding Region	Cancer Driver Gene
EZH2	Specific Exons	Cancer Driver Gene
FBXW7	Specific Exons	Cancer Driver Gene
FGFR1	Specific Exons	Cancer Driver Gene
FGFR2	Specific Exons	Cancer Driver Gene
FGFR3	Specific Exons	Cancer Driver Gene
FLT3	Specific Exons	Cancer Driver Gene
GNA11	Specific Exons	Cancer Driver Gene
GNAQ	Specific Exons	Cancer Driver Gene
GNAS	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
HNF1A	Specific Exons	Cancer Driver Gene
HRAS	Full Coding Region	Cancer Driver Gene
IDH1	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
IDH2	Specific Exons	Cancer Driver and Clonal Hematopoiesis Gene
JAK2	Full Coding Region	Cancer Driver and Clonal Hematopoiesis Gene
JAK3	Specific Exons	Cancer Driver Gene
KDR	Specific Exons	Cancer Driver Gene
KIT	Full Coding Region	Cancer Driver Gene
KRAS	Full Coding Region	Cancer Driver Gene
MAP2K1	Specific Exons	Cancer Driver Gene
MET	Specific Exons	Cancer Driver Gene

MLH1	Specific Exons	Cancer Driver Gene
MPL	Specific Exons	Cancer Driver Gene
MYC	Specific Exons	Cancer Driver Gene
NPM1	Specific Exons	Cancer Driver Gene
NRAS	Full Coding Region	Cancer Driver Gene
PDGFRA	Full Coding Region	Cancer Driver Gene
PIK3CA	Full Coding Region	Cancer Driver Gene
PIK3R1	Specific Exons	Cancer Driver Gene
PTEN	Full Coding Region	Cancer Driver Gene
PTPN11	Specific Exons	Cancer Driver Gene
RB1	Specific Exons	Cancer Driver Gene
RET	Specific Exons	Cancer Driver Gene
SMAD4	Specific Exons	Cancer Driver Gene
SMARCB1	Specific Exons	Cancer Driver Gene
SMO	Specific Exons	Cancer Driver Gene
SRC	Specific Exons	Cancer Driver Gene
STK11	Full Coding Region	Cancer Driver Gene
TERT	Specific Exons	Cancer Driver Gene
TP53	Full Coding Region	Cancer Driver Gene
VHL	Specific Exons	Cancer Driver Gene

Table 3.4. Summary of genomic analyses of plasma samples.

Patient ID	Patient Timepoint	Analysis Type	Read Length	Bases Mapped to Genome	Bases in Target Region	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage of Target Regions	Distinct Coverage of Target Regions
CGST102	CGST102P	TEC-Seq	100	5,715,504,500	80930	2,644,902,854	46%	31,309	4,503
CGST102	CGST102P1	TEC-Seq	100	5,998,109,300	80930	2,987,328,937	50%	35,356	4,709
CGST102	CGST102P2	TEC-Seq	100	6,793,240,800	80930	3,123,029,034	46%	37,211	4,632
CGST105	CGST105P	TEC-Seq	100	5,860,142,600	80930	2,920,684,685	50%	34,346	6,943
CGST105	CGST105P1	TEC-Seq	100	5,904,082,100	80930	3,055,802,485	52%	35,916	6,585
CGST109	CGST109P	TEC-Seq	100	6,295,967,400	80930	3,248,425,068	52%	38,199	7,053
CGST109	CGST109P1	TEC-Seq	100	6,013,317,300	80930	2,815,835,970	47%	33,100	9,321
CGST109	CGST109P2	TEC-Seq	100	6,619,965,600	80930	2,951,306,546	45%	35,132	9,595
CGST110	CGST110P	TEC-Seq	100	9,179,291,500	80,930	4,298,269,268	47%	51,666	3,873
CGST110	CGST110P1	TEC-Seq	100	8,406,412,800	80,930	4,142,725,047	49%	49,829	7,358
CGST113	CGST113P	TEC-Seq	100	7,800,665,800	80930	1,225,827,874	16%	14,534	2,850
CGST113	CGST113P1	TEC-Seq	100	3,847,385,800	80930	1,796,935,810	47%	20,617	4,527
CGST113	CGST113P2	TEC-Seq	100	6,489,592,600	80930	2,839,487,561	44%	33,777	4,334
CGST114	CGST114P	TEC-Seq	100	7,151,572,200	80,930	3,254,967,293	46%	38,496	4,839
CGST114	CGST114P1	TEC-Seq	100	7,470,020,200	80,930	3,979,321,082	53%	47,176	8,923
CGST121	CGST121P	TEC-Seq	100	5,017,934,500	80,930	2,207,136,971	44%	26,020	5,472
CGST121	CGST121P1	TEC-Seq	100	5,941,381,100	80,930	2,349,841,475	40%	27,709	5,746
CGST122	CGST122P	TEC-Seq	100	5,928,880,500	80,930	2,281,502,089	38%	26,935	8,859
CGST122	CGST122P1	TEC-Seq	100	5,955,730,600	80,930	2,488,111,598	42%	29,306	11,127
CGST131	CGST131P	TEC-Seq	100	6,040,318,900	80,930	2,670,580,911	44%	31,516	4,859
CGST131	CGST131P1	TEC-Seq	100	6,894,739,500	80,930	3,634,605,240	53%	43,086	8,516
CGST133	CGST133P	TEC-Seq	100	4,519,145,400	80930	1,569,298,193	35%	18,034	4,361
CGST133	CGST133P1	TEC-Seq	100	3,778,347,400	80930	1,740,693,788	46%	19,974	7,148
CGST134	CGST134P	TEC-Seq	100	4,762,925,800	80930	2,182,666,734	46%	25,777	6,351

CGST134	CGST134P1	TEC-Seq	100	6,909,633,600	80930	1,625,372,101	24%	19,223	9,958
CGST134	CGST134P2	TEC-Seq	100	5,926,486,300	80930	2,833,507,638	48%	33,929	7,896
CGST141	CGST141P	TEC-Seq	100	6,781,001,300	80930	3,440,927,391	51%	40,762	5,404
CGST141	CGST141P1	TEC-Seq	100	6,712,701,900	80930	3,385,290,681	50%	40,037	7,747
CGST142	CGST142P	TEC-Seq	100	7,361,933,400	80930	3,522,503,790	48%	40,655	5,564
CGST142	CGST142P1	TEC-Seq	100	3,901,705,000	80930	1,635,312,539	42%	18,877	3,406
CGST143	CGST143P	TEC-Seq	100	6,554,500,600	80,930	1,484,918,070	23%	17,583	2,495
CGST143	CGST143P1	TEC-Seq	100	6,315,804,700	80,930	2,921,644,628	46%	34,571	4,683
CGST148	CGST148P	TEC-Seq	100	3,846,279,100	80930	1,452,859,818	38%	16,792	2,005
CGST148	CGST148P1	TEC-Seq	100	4,137,104,400	80930	1,722,641,701	42%	19,861	1,866
CGST148	CGST148P2	TEC-Seq	100	8,115,750,600	80930	3,180,887,811	39%	38,458	6,766
CGST152	CGST152P	TEC-Seq	100	3,353,885,300	80930	1,526,513,135	46%	17,631	3,667
CGST152	CGST152P1	TEC-Seq	100	6,154,888,700	80930	2,411,352,498	39%	27,781	8,626
CGST158	CGST158P	TEC-Seq	100	5,147,112,700	80,930	2,295,516,038	45%	27,138	5,233
CGST158	CGST158P1	TEC-Seq	100	6,006,041,400	80,930	1,552,248,828	26%	15,109	4,181
CGST176	CGST176P	TEC-Seq	100	5,277,972,500	80930	2,287,430,177	43%	26,266	8,093
CGST176	CGST176P1	TEC-Seq	100	4,649,933,000	80930	1,736,286,998	37%	19,916	5,790
CGST22	CGST22P	TEC-Seq	100	5,887,803,000	80930	2,449,271,468	42%	28,702	3,601
CGST22	CGST22P1	TEC-Seq	100	3,809,398,300	80930	1,305,798,697	34%	15,073	3,839
CGST24	CGST24P	TEC-Seq	100	9,043,109,900	80930	4,151,550,042	46%	50,067	10,317
CGST24	CGST24P1	TEC-Seq	100	6,571,692,600	80930	2,841,136,771	43%	34,030	3,327
CGST24	CGST24P2	TEC-Seq	100	4,263,908,500	80930	2,198,635,683	52%	25,136	7,992
CGST25	CGST25P	TEC-Seq	100	6,914,308,700	80930	3,008,397,120	44%	35,837	4,451
CGST25	CGST25P1	TEC-Seq	100	5,138,989,000	80930	2,212,593,275	43%	26,099	8,343
CGST25	CGST25P2	TEC-Seq	100	6,583,579,300	80930	2,964,750,497	45%	35,208	9,462
CGST26	CGST26P	TEC-Seq	100	5,197,445,200	80930	2,241,760,526	43%	26,834	2,764
CGST26	CGST26P1	TEC-Seq	100	5,026,542,800	80930	1,342,021,803	27%	15,184	2,278
CGST28	CGST28P	TEC-Seq	100	6,288,486,100	80930	2,884,997,993	46%	34,538	2,586

CGST28	CGST28P1	TEC-Seq	100	6,937,938,400	80930	1,635,435,940	24%	19,404	1,561
CGST30	CGST30P	TEC-Seq	100	6,141,213,100	80930	3,109,994,564	51%	37,194	2,555
CGST30	CGST30P1	TEC-Seq	100	4,309,015,500	80930	1,981,934,757	46%	22,849	4,840
CGST31	CGST31P	TEC-Seq	100	5,630,437,800	80,930	2,042,169,995	36%	24,282	1,220
CGST31	CGST31P1	TEC-Seq	100	6,716,001,300	80,930	3,196,877,907	48%	37,990	8,384
CGST31	CGST31P2	TEC-Seq	100	7,178,183,100	80,930	3,672,017,873	51%	43,634	7,429
CGST32	CGST32P	TEC-Seq	100	6,969,139,300	80,930	3,099,120,469	44%	36,726	3,935
CGST32	CGST32P1	TEC-Seq	100	6,739,502,000	80,930	3,545,231,854	53%	42,170	9,073
CGST32	CGST32P2	TEC-Seq	100	6,114,722,100	80,930	1,310,653,630	21%	15,542	2,413
CGST33	CGST33P	TEC-Seq	100	6,560,309,400	80,930	3,168,371,917	48%	37,916	4,597
CGST33	CGST33P1	TEC-Seq	100	6,109,550,400	80,930	2,383,268,213	39%	27,743	6,622
CGST38	CGST38P	TEC-Seq	100	6,914,087,800	80930	3,364,615,563	49%	39,918	2,669
CGST38	CGST38P1	TEC-Seq	100	6,792,524,700	80930	3,453,432,793	51%	41,040	3,184
CGST38	CGST38P2	TEC-Seq	100	7,077,217,200	80930	3,690,973,158	52%	43,827	4,771
CGST39	CGST39P	TEC-Seq	100	7,043,791,400	80930	2,992,801,875	42%	35,620	6,737
CGST39	CGST39P1	TEC-Seq	100	7,190,291,400	80930	3,676,474,263	51%	43,674	4,221
CGST41	CGST41P	TEC-Seq	100	6,975,053,100	80,930	3,224,065,662	46%	38,300	4,016
CGST41	CGST41P1	TEC-Seq	100	5,053,505,000	80,930	2,630,170,488	52%	31,538	4,523
CGST44	CGST44P	TEC-Seq	100	6,617,597,800	80930	2,819,442,093	43%	33,500	5,086
CGST44	CGST44P1	TEC-Seq	100	6,599,597,300	80930	1,996,464,970	30%	23,365	10,484
CGST44	CGST44P2	TEC-Seq	100	6,559,486,700	80930	1,882,852,044	29%	22,374	6,462
CGST45	CGST45P	TEC-Seq	100	6,130,812,200	80,930	2,944,524,278	48%	35,264	4,745
CGST45	CGST45P1	TEC-Seq	100	5,141,669,800	80,930	2,517,511,584	49%	30,257	4,063
CGST45	CGST45P2	TEC-Seq	100	5,058,317,000	80,930	2,836,133,105	56%	34,129	3,173
CGST47	CGST47P	TEC-Seq	100	5,961,400,000	80,930	3,083,523,351	52%	37,008	3,112
CGST47	CGST47P1	TEC-Seq	100	5,512,507,200	80,930	2,739,158,303	50%	32,912	3,827
CGST47	CGST47P2	TEC-Seq	100	3,767,665,100	80,930	1,661,884,444	44%	19,699	4,936
CGST48	CGST48P	TEC-Seq	100	6,418,652,700	80,930	1,497,230,327	23%	17,782	2,410

CGST48	CGST48P1	TEC-Seq	100	6,383,392,100	80,930	3,459,431,552	54%	41,093	9,184
CGST49	CGST49P	TEC-Seq	100	5,472,227,600	80,930	2,370,408,567	43%	28,332	2,383
CGST49	CGST49P1	TEC-Seq	100	5,908,475,400	80,930	3,032,025,653	51%	36,455	3,802
CGST49	CGST49P2	TEC-Seq	100	5,659,634,300	80,930	1,822,487,750	32%	21,945	3,037
CGST57	CGST57P	TEC-Seq	100	4,348,848,500	80,930	2,146,269,880	49%	25,722	2,261
CGST57	CGST57P1	TEC-Seq	100	5,885,101,900	80,930	1,555,343,429	26%	18,522	2,964
CGST57	CGST57P2	TEC-Seq	100	6,246,025,500	80,930	1,758,717,326	28%	21,153	3,139
CGST58	CGST58P	TEC-Seq	100	5,818,344,500	80,930	1,274,708,429	22%	15,281	2,924
CGST58	CGST58P1	TEC-Seq	100	6,317,592,400	80,930	3,085,307,789	49%	35,909	13,524
CGST62	CGST62P	TEC-Seq	100	5,893,688,000	80930	2,468,833,173	42%	29,637	4,878
CGST62	CGST62P1	TEC-Seq	100	5,532,879,600	80930	2,459,461,654	44%	28,276	6,522
CGST63	CGST63P	TEC-Seq	100	9,691,297,400	80930	4,263,233,224	44%	51,805	4,578
CGST63	CGST63P1	TEC-Seq	100	4,267,392,400	80930	1,358,856,933	32%	15,787	6,039
CGST63	CGST63P2	TEC-Seq	100	7,800,940,600	80930	3,694,883,659	47%	44,200	13,580
CGST64	CGST64P	TEC-Seq	100	1,039,325,300	80930	491,124,993	47%	5,805	569
CGST64	CGST64P1	TEC-Seq	100	4,481,165,500	80930	1,873,316,247	42%	22,100	6,413
CGST65	CGST65P	TEC-Seq	100	6,623,122,300	80,930	3,354,942,634	51%	40,340	8,129
CGST65	CGST65P1	TEC-Seq	100	5,461,226,100	80,930	2,183,094,789	40%	25,833	11,395
CGST67	CGST67P	TEC-Seq	100	5,268,060,800	80930	2,636,276,768	50%	31,722	3,769
CGST67	CGST67P1	TEC-Seq	100	6,612,674,300	80930	3,000,041,572	45%	35,719	6,228
CGST67	CGST67P2	TEC-Seq	100	6,525,344,900	80930	1,547,996,128	24%	18,443	4,647
CGST68	CGST68P	TEC-Seq	100	7,460,521,500	80,930	2,483,281,621	33%	29,734	5,351
CGST68	CGST68P1	TEC-Seq	100	7,539,795,800	80,930	3,745,488,233	50%	44,815	3,096
CGST68	CGST68P2	TEC-Seq	100	8,234,458,000	80,930	4,134,050,485	50%	49,372	7,134
CGST69	CGST69P	TEC-Seq	100	7,181,374,600	80,930	1,659,017,269	23%	19,729	2,859
CGST69	CGST69P1	TEC-Seq	100	7,692,923,500	80,930	3,149,678,548	41%	37,595	7,021
CGST69	CGST69P2	TEC-Seq	100	7,695,301,500	80,930	3,738,347,074	49%	43,959	6,196
CGST71	CGST71P	TEC-Seq	100	6,920,751,100	80930	2,676,513,996	39%	31,859	3,982

CGST71	CGST71P1	TEC-Seq	100	4,806,898,600	80930	2,010,702,082	42%	23,755	6,087
CGST79	CGST79P	TEC-Seq	100	5,751,410,700	80,930	2,857,360,446	50%	34,355	4,059
CGST79	CGST79P1	TEC-Seq	100	4,608,100,300	80930	2,351,565,191	51%	27,744	9,023
CGST80	CGST80P	TEC-Seq	100	6,368,064,600	80930	3,298,497,188	52%	39,692	5,280
CGST80	CGST80P1	TEC-Seq	100	4,644,341,200	80930	1,924,333,584	41%	22,613	547
CGST81	CGST81P	TEC-Seq	100	8,655,691,400	80930	1,519,121,452	18%	17,988	6,419
CGST81	CGST81P1	TEC-Seq	100	6,299,242,900	80930	2,904,512,762	46%	34,274	10,293
CGST91	CGST91P	TEC-Seq	100	5,792,398,700	80930	2,326,866,089	40%	26,358	5,654
CGST91	CGST91P1	TEC-Seq	100	5,274,928,600	80930	2,005,984,185	38%	22,722	8,176
CGST97	CGST97P	TEC-Seq	100	596,719,000	80,930	297,518,719	50%	3,524	894
CGST97	CGST97P1	TEC-Seq	100	7,564,129,200	80,930	2,350,459,556	31%	27,883	5,481
CGST97	CGST97P2	TEC-Seq	100	6,578,254,800	80,930	2,953,292,992	45%	35,098	5,902

Table 3.5. Summary of genomic analyses of white blood cell samples.

Patient ID	Patient Timepoint	Analysis Type	Read Length	Bases Mapped to Genome	Bases in Target Region	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage of Target Regions	Distinct Coverage of Target Regions
CGST102	CGST102N	Targeted NGS	100	6,195,634,700	80,930	2,863,951,939	46%	34,359	5,536
CGST105	CGST105N	Targeted NGS	100	6,284,700,700	80,930	2,925,783,638	47%	34,939	5,403
CGST109	CGST109N	Targeted NGS	100	7,820,998,800	80,930	3,840,198,215	49%	45,909	7,261
CGST110	CGST110N	Targeted NGS	100	7,235,895,300	80,930	3,176,811,726	44%	37,828	6,013
CGST113	CGST113N	Targeted NGS	100	6,730,493,500	80,930	3,049,171,631	45%	36,327	5,595
CGST114	CGST114N	Targeted NGS	100	7,389,659,000	80,930	3,550,259,484	48%	42,347	5,852
CGST121	CGST121N	Targeted NGS	100	7,294,075,400	80,930	3,595,800,814	49%	42,878	5,256
CGST122	CGST122N	Targeted NGS	100	7,218,344,200	80,930	3,191,080,807	44%	38,087	4,115
CGST131	CGST131N	Targeted NGS	100	6,391,134,300	80,930	2,637,110,909	41%	31,673	5,115
CGST133	CGST133N	Targeted NGS	100	7,516,524,800	80,930	3,478,702,025	46%	41,402	5,710
CGST134	CGST134N	Targeted NGS	100	6,970,616,400	80,930	3,161,421,788	45%	37,556	5,589
CGST141	CGST141N	Targeted NGS	100	6,806,738,800	80,930	2,903,065,706	43%	34,532	4,966
CGST142	CGST142N	Targeted NGS	100	7,802,988,500	80,930	3,473,339,304	45%	41,413	5,131
CGST143	CGST143N	Targeted NGS	100	7,214,764,900	80,930	2,840,601,982	39%	33,713	4,597
CGST148	CGST148N	Targeted NGS	100	6,381,761,000	80,930	3,012,876,406	47%	35,988	5,380
CGST152	CGST152N	Targeted NGS	100	7,536,990,700	80,930	3,346,738,961	44%	40,271	5,850
CGST158	CGST158N	Targeted NGS	100	6,575,033,600	80,930	2,941,340,317	45%	34,952	6,131
CGST176	CGST176N	Targeted NGS	100	7,408,525,500	80,930	3,568,504,771	48%	42,451	5,899
CGST22	CGST22N	Targeted NGS	100	7,017,843,200	80,930	3,046,997,907	43%	36,555	5,758
CGST24	CGST24N	Targeted NGS	100	6,031,439,500	80,930	2,600,962,106	43%	31,116	4,629
CGST25	CGST25N	Targeted NGS	100	7,628,153,000	80,930	2,867,232,470	38%	34,509	5,252
CGST26	CGST26N	Targeted NGS	100	6,848,908,800	80,930	3,010,566,003	44%	35,769	5,851
CGST28	CGST28N	Targeted NGS	100	7,088,090,300	80,930	1,860,318,810	26%	22,093	4,936

CGST30	CGST30N	Targeted NGS	100	6,443,455,500	80,930	2,408,385,115	37%	28,497	5,139
CGST31	CGST31N	Targeted NGS	100	7,391,554,100	80,930	1,995,510,669	27%	23,806	4,907
CGST32	CGST32N	Targeted NGS	100	6,602,195,900	80,930	3,047,662,118	46%	36,222	6,165
CGST33	CGST33N	Targeted NGS	100	6,528,986,900	80,930	3,141,629,807	48%	37,298	5,441
CGST38	CGST38N	Targeted NGS	100	7,641,335,900	80,930	3,221,456,102	42%	38,339	5,592
CGST39	CGST39N	Targeted NGS	100	7,240,196,600	80,930	3,318,695,433	46%	39,607	6,715
CGST41	CGST41N	Targeted NGS	100	7,533,950,900	80,930	3,465,686,126	46%	41,253	6,348
CGST44	CGST44N	Targeted NGS	100	7,254,063,600	80,930	2,005,128,421	28%	23,889	5,797
CGST45	CGST45N	Targeted NGS	100	6,257,089,600	80,930	2,949,372,085	47%	35,166	5,670
CGST47	CGST47N	Targeted NGS	100	7,348,319,800	80,930	3,266,126,327	44%	38,867	6,146
CGST48	CGST48N	Targeted NGS	100	6,846,646,900	80,930	3,150,453,485	46%	37,532	6,130
CGST49	CGST49N	Targeted NGS	100	8,539,596,100	80,930	3,408,355,429	40%	40,448	4,317
CGST57	CGST57N	Targeted NGS	100	6,039,413,200	80,930	2,953,736,278	49%	35,127	4,995
CGST58	CGST58N	Targeted NGS	100	6,930,306,600	80,930	3,298,094,768	48%	39,172	5,684
CGST62	CGST62N	Targeted NGS	100	7,369,061,300	80,930	3,566,181,334	48%	42,380	5,631
CGST63	CGST63N	Targeted NGS	100	7,061,323,300	80,930	2,297,686,683	33%	27,334	5,445
CGST64	CGST64N	Targeted NGS	100	7,281,306,400	80,930	2,165,252,030	30%	25,867	4,143
CGST65	CGST65N	Targeted NGS	100	6,914,494,900	80,930	3,417,164,449	49%	40,861	4,737
CGST67	CGST67N	Targeted NGS	100	6,813,029,900	80,930	2,675,216,687	39%	31,866	4,427
CGST68	CGST68N	Targeted NGS	100	6,674,736,700	80,930	3,293,565,113	49%	39,316	4,607
CGST69	CGST69N	Targeted NGS	100	6,865,458,700	80,930	2,803,579,545	41%	33,489	6,562
CGST71	CGST71N	Targeted NGS	100	7,345,327,200	80,930	3,398,613,398	46%	40,390	5,379
CGST80	CGST80N	Targeted NGS	100	7,781,481,700	80,930	3,472,259,854	45%	41,285	5,414
CGST81	CGST81N	Targeted NGS	100	8,329,032,000	80,930	3,923,705,794	47%	46,682	7,299
CGST91	CGST91N	Targeted NGS	100	7,107,909,300	80,930	3,324,593,160	47%	39,586	5,275
CGST97	CGST97N	Targeted NGS	100	6,859,313,400	80,930	3,192,573,607	47%	37,876	5,732

Table 3.6. Summary of sequence alterations detected in cfDNA.

Patient ID	Patient Timepoint	Timepoint Significance	Gene Symbol	Amino Acid (Protein)	Transcript Accession	Mutation Type	Consequence	Origin	Mutant Allele Fraction	Total Distinct Coverage	Distinct Mutant Coverage	Hotspot Alteration
CGST148	CGST148P2	Postoperative	STK11	V128Dfs*34	CCDS45896.1	Deletion	Frameshift	ctDNA	0.26%	1924	5	No
CGST152	CGST152P1	Preoperative	ALK	P36*	CCDS33172.1	Insertion	Frameshift	ctDNA	0.71%	983	7	No
CGST33	CGST33P	Baseline	ERBB2	R756Cfs*2	CCDS32642.1	Insertion	Frameshift	ctDNA	0.64%	2331	15	No
CGST68	CGST68P	Baseline	HRAS	D54Efs*53	CCDS7698.1	Insertion	Frameshift	ctDNA	0.03%	3174	1	No
CGST68	CGST68P2	Postoperative	ERBB4	D1184*	CCDS2394.1	Insertion	Frameshift	ctDNA	0.16%	3857	6	No
CGST68	CGST68P2	Postoperative	HRAS	D54Efs*53	CCDS7698.1	Insertion	Frameshift	ctDNA	0.29%	5856	17	No
CGST102	CGST102P	Baseline	PIK3CA	E109del	CCDS43171.1	Deletion	In-frame deletion	ctDNA	0.43%	2577	11	No
CGST109	CGST109P	Baseline	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	ctDNA	0.43%	1380	6	No
CGST109	CGST109P2	Postoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	ctDNA	0.07%	1456	1	No
CGST109	CGST109P1	Preoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	ctDNA	0.08%	1250	1	No
CGST134	CGST134P2	Postoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	ctDNA	0.25%	2384	6	No
CGST134	CGST134P1	Preoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	ctDNA	0.22%	459	1	No
CGST25	CGST25P	Baseline	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	CHIP	0.59%	3029	18	No
CGST25	CGST25P2	Postoperative	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	CHIP	0.28%	6442	18	No
CGST25	CGST25P1	Preoperative	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	CHIP	0.66%	3325	22	No
CGST28	CGST28P	Baseline	PIK3R1	R577_L581del	CCDS3993.1	Deletion	In-frame deletion	ctDNA	1.62%	1170	19	No
CGST28	CGST28P1	Preoperative	PIK3R1	R577_L581del	CCDS3993.1	Deletion	In-frame deletion	ctDNA	0.70%	712	5	No
CGST141	CGST141P	Baseline	ERBB2	L785delinsHHVCF	CCDS32642.1	Insertion	In-frame insertion	ctDNA	0.06%	4903	3	No
CGST141	CGST141P1	Preoperative	ERBB2	L785delinsHHVCF	CCDS32642.1	Insertion	In-frame insertion	ctDNA	0.09%	7024	6	No
CGST22	CGST22P	Baseline	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	CHIP	0.10%	1918	2	No
CGST22	CGST22P1	Preoperative	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	CHIP	0.56%	2325	13	No
CGST44	CGST44P	Baseline	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	CHIP	1.12%	3380	38	No
CGST44	CGST44P2	Postoperative	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	CHIP	0.67%	3154	21	No

CGST44	CGST44P1	Preoperative	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	CHIP	0.37%	3208	12	No
CGST57	CGST57P	Baseline	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	CHIP	0.76%	1048	8	No
CGST57	CGST57P2	Postoperative	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	CHIP	1.78%	1962	35	No
CGST57	CGST57P1	Preoperative	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	CHIP	2.22%	1804	40	No
CGST68	CGST68P	Baseline	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	ctDNA	0.04%	2619	1	No
CGST68	CGST68P2	Postoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	ctDNA	0.56%	2522	14	No
CGST68	CGST68P1	Preoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	ctDNA	0.04%	2230	1	No
CGST68	CGST68P1	Preoperative	HRAS	D54Efs*53	CCDS7698.1	Insertion	In-frame insertion	ctDNA	0.12%	2443	3	No
CGST69	CGST69P2	Postoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	ctDNA	0.16%	3732	6	No
CGST81	CGST81P1	Preoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	ctDNA	0.41%	2413	10	No
CGST91	CGST91P1	Preoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	ctDNA	0.16%	3734	6	No
CGST105	CGST105P	Baseline	PTEN	R335*	CCDS31238.1	Substitution	Nonsense	ctDNA	4.85%	1959	95	Yes
CGST105	CGST105P1	Preoperative	PTEN	R335*	CCDS31238.1	Substitution	Nonsense	ctDNA	0.46%	1954	9	Yes
CGST158	CGST158P	Baseline	ERBB4	R114*	CCDS2394.1	Substitution	Nonsense	ctDNA	0.16%	4412	7	No
CGST30	CGST30P	Baseline	STK11	K64*	CCDS45896.1	Substitution	Nonsense	ctDNA	0.39%	1281	5	No
CGST33	CGST33P	Baseline	TP53	Q192*	CCDS11118.1	Substitution	Nonsense	ctDNA	2.32%	2628	61	Yes
CGST45	CGST45P2	Postoperative	TP53	E294*	CCDS11118.1	Substitution	Nonsense	ctDNA	0.14%	2787	4	Yes
CGST47	CGST47P	Baseline	FBXW7	E664*	CCDS3777.1	Substitution	Nonsense	ctDNA	0.45%	2015	9	No
CGST65	CGST65P	Baseline	DNMT3A	R771*	CCDS33157.1	Substitution	Nonsense	CHIP	0.33%	4611	15	No
CGST65	CGST65P1	Preoperative	DNMT3A	R771*	CCDS33157.1	Substitution	Nonsense	CHIP	0.11%	2828	3	No
CGST80	CGST80P	Baseline	TP53	S166*	CCDS11118.1	Substitution	Nonsense	ctDNA	1.04%	4823	50	No
CGST102	CGST102P	Baseline	DNMT3A	V895L	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.24%	2879	7	No
CGST102	CGST102P	Baseline	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	CHIP	0.40%	3214	13	No
CGST102	CGST102P	Baseline	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	CHIP	1.27%	2677	34	No
CGST102	CGST102P2	Postoperative	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.50%	2788	14	No
CGST102	CGST102P2	Postoperative	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	CHIP	0.71%	2943	21	No
CGST102	CGST102P1	Preoperative	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	CHIP	0.54%	3326	18	No
CGST102	CGST102P1	Preoperative	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.85%	2957	25	No

CGST105	CGST105P	Baseline	PIK3CA	Y1021C	CCDS43171.1	Substitution	Nonsynonymous	ctDNA	0.19%	5304	10	Yes
CGST105	CGST105P	Baseline	KRAS	G12C	NM_033360	Substitution	Nonsynonymous	ctDNA	1.21%	2561	31	Yes
CGST105	CGST105P	Baseline	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	ctDNA	2.63%	2736	72	No
CGST105	CGST105P1	Preoperative	PIK3CA	Y1021C	CCDS43171.1	Substitution	Nonsynonymous	ctDNA	0.04%	4910	2	Yes
CGST105	CGST105P1	Preoperative	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	ctDNA	0.24%	2482	6	No
CGST105	CGST105P1	Preoperative	KRAS	G12C	NM_033360	Substitution	Nonsynonymous	ctDNA	0.42%	2646	11	Yes
CGST109	CGST109P2	Postoperative	TP53	R267W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.07%	4195	3	Yes
CGST110	CGST110P	Baseline	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.04%	2763	1	Yes
CGST110	CGST110P	Baseline	DNMT3A	H873R	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.03%	3207	1	No
CGST110	CGST110P	Baseline	ERBB4	T639M	CCDS2394.1	Substitution	Nonsynonymous	ctDNA	0.15%	2697	4	No
CGST110	CGST110P1	Preoperative	DNMT3A	H873R	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.10%	5871	6	No
CGST110	CGST110P1	Preoperative	ERBB4	T639M	CCDS2394.1	Substitution	Nonsynonymous	ctDNA	0.12%	5089	6	No
CGST110	CGST110P1	Preoperative	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.07%	5600	4	Yes
CGST113	CGST113P	Baseline	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	1.35%	1699	23	Yes
CGST113	CGST113P	Baseline	CDH1	V425I	CCDS10869.1	Substitution	Nonsynonymous	ctDNA	0.43%	1845	8	No
CGST113	CGST113P	Baseline	KIT	S241Y	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.92%	1625	15	No
CGST113	CGST113P2	Postoperative	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	1.41%	2898	41	Yes
CGST113	CGST113P2	Postoperative	KIT	S241Y	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.03%	3005	1	Yes
CGST113	CGST113P1	Preoperative	KIT	S241Y	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.04%	2735	1	No
CGST113	CGST113P1	Preoperative	STK11	Y340N	CCDS45896.1	Substitution	Nonsynonymous	ctDNA	0.25%	2038	5	No
CGST113	CGST113P1	Preoperative	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	1.16%	2161	25	Yes
CGST121	CGST121P	Baseline	DNMT3A	R749G	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.04%	2695	1	No
CGST121	CGST121P1	Preoperative	DNMT3A	R749G	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.22%	2742	6	No
CGST122	CGST122P	Baseline	KIT	P733S	CCDS3496.1	Substitution	Nonsynonymous	CHIP	0.18%	4981	9	No
CGST122	CGST122P	Baseline	MYC	R98W	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.20%	3506	7	No
CGST122	CGST122P	Baseline	JAK2	V617F	CCDS6457.1	Substitution	Nonsynonymous	CHIP	6.32%	2293	145	Yes
CGST122	CGST122P1	Preoperative	MYC	R98W	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.05%	4000	2	No
CGST122	CGST122P1	Preoperative	JAK2	V617F	CCDS6457.1	Substitution	Nonsynonymous	CHIP	0.63%	1897	12	Yes

CGST133	CGST133P	Baseline	SMAD4	R361C	CCDS11950.1	Substitution	Nonsynonymous	ctDNA	0.29%	2761	8	Yes
CGST133	CGST133P	Baseline	KRAS	G12V	NM_033360	Substitution	Nonsynonymous	ctDNA	0.44%	1806	8	Yes
CGST133	CGST133P1	Preoperative	KRAS	G12V	NM_033360	Substitution	Nonsynonymous	ctDNA	0.06%	1802	1	Yes
CGST134	CGST134P	Baseline	TP53	R282W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.06%	3634	2	Yes
CGST134	CGST134P	Baseline	MYC	S225L	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.17%	3536	6	No
CGST134	CGST134P	Baseline	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	CHIP	0.44%	1836	8	No
CGST134	CGST134P	Baseline	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.95%	3773	36	No
CGST134	CGST134P2	Postoperative	TP53	R282W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.12%	6029	7	Yes
CGST134	CGST134P2	Postoperative	MYC	S225L	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.02%	5746	1	No
CGST134	CGST134P2	Postoperative	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	CHIP	0.60%	3337	20	No
CGST134	CGST134P2	Postoperative	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.88%	6217	55	No
CGST134	CGST134P1	Preoperative	MYC	S225L	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.04%	2687	1	No
CGST134	CGST134P1	Preoperative	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	CHIP	0.08%	1259	4	No
CGST134	CGST134P1	Preoperative	TP53	R282W	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.03%	3183	1	Yes
CGST134	CGST134P1	Preoperative	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.48%	2724	13	No
CGST142	CGST142P	Baseline	PTEN	F241L	CCDS31238.1	Substitution	Nonsynonymous	ctDNA	0.18%	3290	6	No
CGST143	CGST143P	Baseline	TP53	Y234C	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.15%	1314	2	Yes
CGST143	CGST143P	Baseline	FGFR3	V298M	CCDS3353.1	Substitution	Nonsynonymous	CHIP	0.24%	1655	4	No
CGST143	CGST143P1	Preoperative	FGFR3	V298M	CCDS3353.1	Substitution	Nonsynonymous	CHIP	0.20%	3033	6	No
CGST143	CGST143P1	Preoperative	TP53	Y234C	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.77%	2081	16	Yes
CGST148	CGST148P	Baseline	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.13%	780	1	Yes
CGST148	CGST148P2	Postoperative	KIT	G745R	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.44%	5023	22	No
CGST148	CGST148P2	Postoperative	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.49%	4271	21	Yes
CGST148	CGST148P1	Preoperative	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.11%	925	1	Yes
CGST158	CGST158P	Baseline	EGFR	D942N	CCDS5514.1	Substitution	Nonsynonymous	ctDNA	0.15%	3972	6	No
CGST176	CGST176P	Baseline	DNMT3A	L737F	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.41%	2202	9	No
CGST176	CGST176P1	Preoperative	DNMT3A	V897I	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.24%	2079	5	No
CGST176	CGST176P1	Preoperative	DNMT3A	L737F	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.58%	2054	12	No

CGST22	CGST22P	Baseline	TP53	R175H	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.16%	1930	3	Yes
CGST22	CGST22P	Baseline	ERBB4	N1190S	CCDS2394.1	Substitution	Nonsynonymous	CHIP	0.31%	2235	7	No
CGST22	CGST22P1	Preoperative	ERBB4	N1190S	CCDS2394.1	Substitution	Nonsynonymous	CHIP	0.47%	2349	11	No
CGST22	CGST22P1	Preoperative	TP53	R175H	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.21%	1896	4	Yes
CGST24	CGST24P	Baseline	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.30%	1690	5	Yes
CGST24	CGST24P	Baseline	KIT	L939V	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.22%	2244	5	No
CGST24	CGST24P2	Postoperative	KIT	L939V	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.03%	6498	2	No
CGST24	CGST24P2	Postoperative	AR	E323K	CCDS14387.1	Substitution	Nonsynonymous	ctDNA	0.12%	8506	10	No
CGST24	CGST24P2	Postoperative	EGFR	D1175G	CCDS5514.1	Substitution	Nonsynonymous	CHIP	0.16%	8145	13	No
CGST24	CGST24P2	Postoperative	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.21%	6721	14	Yes
CGST24	CGST24P1	Preoperative	AR	E323K	CCDS14387.1	Substitution	Nonsynonymous	ctDNA	0.02%	4408	1	Yes
CGST24	CGST24P1	Preoperative	KIT	L939V	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.08%	3829	3	Yes
CGST24	CGST24P1	Preoperative	EGFR	D1175G	CCDS5514.1	Substitution	Nonsynonymous	CHIP	0.10%	4997	5	No
CGST24	CGST24P1	Preoperative	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.41%	2709	11	Yes
CGST25	CGST25P	Baseline	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.26%	1934	5	Yes
CGST25	CGST25P	Baseline	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	CHIP	7.25%	2040	148	No
CGST25	CGST25P2	Postoperative	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.06%	4965	3	Yes
CGST25	CGST25P2	Postoperative	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	CHIP	3.17%	2744	87	No
CGST25	CGST25P1	Preoperative	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	CHIP	9.84%	2856	281	No
CGST25	CGST25P1	Preoperative	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.45%	2215	10	Yes
CGST26	CGST26P	Baseline	CDK4	L125Q	CCDS8953.1	Substitution	Nonsynonymous	ctDNA	0.32%	1551	5	No
CGST26	CGST26P1	Preoperative	CDK4	L125Q	CCDS8953.1	Substitution	Nonsynonymous	ctDNA	0.07%	1429	1	No
CGST28	CGST28P	Baseline	JAK2	L611S	CCDS6457.1	Substitution	Nonsynonymous	ctDNA	11.77%	1775	209	No
CGST28	CGST28P1	Preoperative	JAK2	L611S	CCDS6457.1	Substitution	Nonsynonymous	ctDNA	13.50%	1030	139	No
CGST30	CGST30P	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.31%	1590	5	Yes
CGST30	CGST30P	Baseline	CDH1	I326F	CCDS10869.1	Substitution	Nonsynonymous	ctDNA	0.29%	1754	5	No
CGST30	CGST30P	Baseline	AR	L341Q	CCDS14387.1	Substitution	Nonsynonymous	ctDNA	0.39%	1291	5	No
CGST30	CGST30P	Baseline	MYC	H256L	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.42%	1420	6	No

CGST30	CGST30P1	Preoperative	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.20%	2503	5	Yes
CGST31	CGST31P	Baseline	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	CHIP	0.35%	579	2	No
CGST31	CGST31P	Baseline	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	CHIP	9.47%	602	57	No
CGST31	CGST31P2	Postoperative	DNMT3A	L888P	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.10%	5911	6	No
CGST31	CGST31P2	Postoperative	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	CHIP	0.39%	4389	17	No
CGST31	CGST31P2	Postoperative	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	CHIP	8.88%	5115	454	No
CGST31	CGST31P1	Preoperative	DNMT3A	L888P	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.13%	5932	8	No
CGST31	CGST31P1	Preoperative	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	CHIP	0.20%	4938	10	No
CGST31	CGST31P1	Preoperative	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	CHIP	7.36%	5478	403	No
CGST32	CGST32P	Baseline	ALK	N1497I	CCDS33172.1	Substitution	Nonsynonymous	ctDNA	0.21%	2855	6	No
CGST32	CGST32P	Baseline	ALK	E172V	CCDS33172.1	Substitution	Nonsynonymous	ctDNA	0.21%	2807	6	No
CGST32	CGST32P	Baseline	KRAS	G13R	NM_033360	Substitution	Nonsynonymous	ctDNA	0.24%	2080	5	Yes
CGST32	CGST32P	Baseline	ALK	L347Q	CCDS33172.1	Substitution	Nonsynonymous	ctDNA	0.26%	1918	5	No
CGST32	CGST32P	Baseline	BRAF	G469A	CCDS5863.1	Substitution	Nonsynonymous	ctDNA	0.65%	2445	16	Yes
CGST32	CGST32P	Baseline	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	ctDNA	2.99%	2138	64	Yes
CGST38	CGST38P	Baseline	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.29%	1724	5	No
CGST38	CGST38P	Baseline	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.39%	1778	7	No
CGST38	CGST38P2	Postoperative	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.21%	3368	7	No
CGST38	CGST38P2	Postoperative	DNMT3A	P743L	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.29%	3827	11	No
CGST38	CGST38P2	Postoperative	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.34%	3498	12	No
CGST38	CGST38P1	Preoperative	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.28%	2163	6	No
CGST38	CGST38P1	Preoperative	DNMT3A	P743L	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.29%	2413	7	No
CGST38	CGST38P1	Preoperative	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.50%	2184	11	No
CGST45	CGST45P	Baseline	HRAS	G13V	CCDS7698.1	Substitution	Nonsynonymous	ctDNA	0.04%	2226	1	Yes
CGST45	CGST45P2	Postoperative	PTEN	A137E	CCDS31238.1	Substitution	Nonsynonymous	ctDNA	0.24%	2552	6	No
CGST45	CGST45P2	Postoperative	APC	H2591N	CCDS4107.1	Substitution	Nonsynonymous	ctDNA	0.30%	1645	5	No
CGST45	CGST45P2	Postoperative	HRAS	G13V	CCDS7698.1	Substitution	Nonsynonymous	ctDNA	0.31%	1624	5	Yes
CGST45	CGST45P1	Preoperative	PTEN	A137E	CCDS31238.1	Substitution	Nonsynonymous	ctDNA	0.07%	3001	2	No

CGST47	CGST47P	Baseline	TP53	R175H	CCDS11118.1	Substitution	Nonsynonymous	ctDNA	0.28%	1431	4	Yes
CGST48	CGST48P	Baseline	EGFR	G514D	CCDS5514.1	Substitution	Nonsynonymous	ctDNA	0.27%	2230	6	No
CGST48	CGST48P	Baseline	EGFR	L417F	CCDS5514.1	Substitution	Nonsynonymous	CHIP	0.43%	1872	8	No
CGST48	CGST48P	Baseline	FBXW7	R505L	CCDS3777.1	Substitution	Nonsynonymous	ctDNA	1.55%	1806	28	No
CGST48	CGST48P	Baseline	TP53	N239S	CCDS11118.1	Substitution	Nonsynonymous	ctDNA	4.21%	1259	53	Yes
CGST48	CGST48P1	Preoperative	EGFR	L417F	CCDS5514.1	Substitution	Nonsynonymous	CHIP	0.10%	7003	7	No
CGST48	CGST48P1	Preoperative	FBXW7	R505L	CCDS3777.1	Substitution	Nonsynonymous	ctDNA	0.23%	5603	13	No
CGST48	CGST48P1	Preoperative	TP53	N239S	CCDS11118.1	Substitution	Nonsynonymous	ctDNA	0.50%	4396	22	Yes
CGST57	CGST57P	Baseline	ABL1	G254R	CCDS35166.1	Substitution	Nonsynonymous	ctDNA	0.25%	1217	3	No
CGST57	CGST57P	Baseline	KIT	A895T	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.36%	1406	5	No
CGST57	CGST57P1	Preoperative	KIT	A895T	CCDS3496.1	Substitution	Nonsynonymous	ctDNA	0.09%	2277	2	No
CGST57	CGST57P1	Preoperative	ABL1	G254R	CCDS35166.1	Substitution	Nonsynonymous	ctDNA	0.33%	2095	7	No
CGST62	CGST62P	Baseline	DNMT3A	F732I	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.11%	1747	2	No
CGST62	CGST62P	Baseline	PTEN	R130Q	CCDS31238.1	Substitution	Nonsynonymous	CHIP	0.10%	3091	3	Yes
CGST62	CGST62P	Baseline	ALK	S1487L	CCDS33172.1	Substitution	Nonsynonymous	ctDNA	0.25%	3613	9	No
CGST62	CGST62P	Baseline	DNMT3A	R882L	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.26%	2701	7	No
CGST62	CGST62P1	Preoperative	PTEN	R130Q	CCDS31238.1	Substitution	Nonsynonymous	CHIP	0.02%	5000	1	Yes
CGST62	CGST62P1	Preoperative	DNMT3A	R882L	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.16%	2579	4	No
CGST62	CGST62P1	Preoperative	DNMT3A	F732I	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.39%	2297	9	No
CGST63	CGST63P	Baseline	TP53	N239K	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.23%	3522	8	No
CGST63	CGST63P	Baseline	ATM	K3043R	CCDS31669.1	Substitution	Nonsynonymous	ctDNA	0.15%	4120	6	No
CGST63	CGST63P	Baseline	CTNNB1	G34E	CCDS2694.1	Substitution	Nonsynonymous	ctDNA	0.25%	3964	10	Yes
CGST63	CGST63P	Baseline	ATM	T547P	CCDS31669.1	Substitution	Nonsynonymous	ctDNA	0.35%	3125	11	No
CGST63	CGST63P	Baseline	PIK3CA	C420R	CCDS43171.1	Substitution	Nonsynonymous	ctDNA	0.39%	2788	11	Yes
CGST63	CGST63P2	Postoperative	TP53	N239K	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.12%	5799	7	No
CGST63	CGST63P2	Postoperative	CTNNB1	S37F	CCDS2694.1	Substitution	Nonsynonymous	ctDNA	0.06%	6340	4	Yes
CGST63	CGST63P2	Postoperative	MYC	S154L	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.15%	9254	14	No
CGST63	CGST63P1	Preoperative	ATM	K3043R	CCDS31669.1	Substitution	Nonsynonymous	ctDNA	0.06%	3091	2	No

CGST63	CGST63P1	Preoperative	ATM	T547P	CCDS31669.1	Substitution	Nonsynonymous	ctDNA	0.17%	1786	3	No
CGST63	CGST63P1	Preoperative	PIK3CA	C420R	CCDS43171.1	Substitution	Nonsynonymous	ctDNA	0.21%	1436	3	Yes
CGST63	CGST63P1	Preoperative	CTNNB1	G34E	CCDS2694.1	Substitution	Nonsynonymous	ctDNA	0.27%	2620	7	Yes
CGST63	CGST63P1	Preoperative	TP53	N239K	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.29%	1752	5	No
CGST64	CGST64P	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	CHIP	6.14%	293	18	Yes
CGST64	CGST64P1	Preoperative	TP53	H179R	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.25%	3640	9	Yes
CGST64	CGST64P1	Preoperative	TP53	V272M	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.77%	2970	23	Yes
CGST64	CGST64P1	Preoperative	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	CHIP	12.59%	3184	401	Yes
CGST65	CGST65P	Baseline	PIK3CA	Y1021C	CCDS43171.1	Substitution	Nonsynonymous	ctDNA	0.07%	5704	4	Yes
CGST65	CGST65P	Baseline	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	ctDNA	0.55%	5987	33	Yes
CGST67	CGST67P	Baseline	PDGFRA	G166E	CCDS3495.1	Substitution	Nonsynonymous	CHIP	0.18%	2778	5	No
CGST67	CGST67P	Baseline	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.66%	2573	17	No
CGST67	CGST67P2	Postoperative	PDGFRA	G166E	CCDS3495.1	Substitution	Nonsynonymous	CHIP	0.19%	3749	7	No
CGST67	CGST67P2	Postoperative	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.42%	3846	16	No
CGST67	CGST67P1	Preoperative	PDGFRA	G166E	CCDS3495.1	Substitution	Nonsynonymous	CHIP	0.09%	5556	5	No
CGST67	CGST67P1	Preoperative	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	CHIP	0.47%	5555	26	No
CGST69	CGST69P2	Postoperative	CDH1	E35K	CCDS10869.1	Substitution	Nonsynonymous	ctDNA	0.12%	5212	6	No
CGST79	CGST79P	Baseline	MYC	R98W	CCDS6359.2	Substitution	Nonsynonymous	ctDNA	0.22%	2745	6	No
CGST80	CGST80P	Baseline	HRAS	G161E	CCDS7698.1	Substitution	Nonsynonymous	ctDNA	0.36%	3059	11	No
CGST81	CGST81P	Baseline	TP53	C135F	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.20%	3509	7	Yes
CGST97	CGST97P	Baseline	TP53	P151S	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.15%	682	1	Yes
CGST97	CGST97P	Baseline	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.37%	539	2	Yes
CGST97	CGST97P2	Postoperative	TP53	P151S	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.16%	3783	6	Yes
CGST97	CGST97P2	Postoperative	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	CHIP	1.48%	3443	51	Yes
CGST97	CGST97P1	Preoperative	TP53	P151S	CCDS11118.1	Substitution	Nonsynonymous	CHIP	0.12%	4015	5	Yes
CGST97	CGST97P1	Preoperative	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	CHIP	1.70%	3596	61	Yes
CGST24	CGST24P	Baseline	TP53	NA	CCDS11118.1	Substitution	Splice site acceptor	CHIP	0.22%	2296	5	Yes
CGST24	CGST24P2	Postoperative	TP53	NA	CCDS11118.1	Substitution	Splice site acceptor	CHIP	0.22%	6922	15	Yes

CGST24	CGST24P1	Preoperative	TP53	NA	CCDS11118.1	Substitution	Splice site acceptor	CHIP	0.10%	4149	4	Yes
CGST64	CGST64P1	Preoperative	DNMT3A	N/A	CCDS33157.1	Deletion	Splice site acceptor	CHIP	0.35%	3417	12	No
CGST68	CGST68P	Baseline	ATM	N/A	CCDS31669.1	Substitution	Splice site donor	ctDNA	0.11%	2683	3	No
CGST68	CGST68P2	Postoperative	ATM	N/A	CCDS31669.1	Substitution	Splice site donor	ctDNA	0.18%	3318	6	No
CGST68	CGST68P1	Preoperative	ATM	N/A	CCDS31669.1	Substitution	Splice site donor	ctDNA	0.06%	1585	1	No

Table 3.7. Summary of sequence alterations detected in WBCs.

Patient ID	Timepoint Significance	Gene Symbol	Amino Acid (Protein)	Transcript Accession	Mutation Type	Consequence	Mutant Allele Fraction	Total Distinct Coverage	Distinct Mutant Coverage	Hot-spot Alteration*
CGST58	Baseline	DNMT3A	S714Hfs*19	CCDS33157.1	Deletion	Frameshift	0.16%	4904	8	No
CGST81	Baseline	EGFR	G632Vfs*73	CCDS5514.1	Deletion	Frameshift	0.19%	3611	7	No
CGST25	Baseline	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	0.15%	4707	7	No
CGST22	Baseline	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	1.97%	3849	76	No
CGST44	Baseline	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	1.45%	3460	50	No
CGST57	Baseline	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	2.77%	3682	102	No
CGST65	Baseline	DNMT3A	R771*	CCDS33157.1	Substitution	Nonsense	0.51%	3533	18	No
CGST102	Baseline	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	1.72%	3537	61	No
CGST102	Baseline	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	0.20%	4028	8	No
CGST110	Baseline	DNMT3A	H873R	CCDS33157.1	Substitution	Nonsynonymous	0.18%	3833	7	No
CGST110	Baseline	HNF1A	G151D	CCDS9209.1	Substitution	Nonsynonymous	0.35%	5080	18	No
CGST110	Baseline	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	0.13%	4485	6	Yes
CGST113	Baseline	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	0.26%	3799	10	Yes
CGST121	Baseline	AKT1	E17K	CCDS9994.1	Substitution	Nonsynonymous	0.15%	4073	6	Yes
CGST121	Baseline	DNMT3A	R749G	CCDS33157.1	Substitution	Nonsynonymous	1.55%	3995	62	No
CGST121	Baseline	PIK3R1	N564K	CCDS3993.1	Substitution	Nonsynonymous	0.23%	3449	8	No
CGST122	Baseline	JAK2	V617F	CCDS6457.1	Substitution	Nonsynonymous	2.17%	2808	61	Yes
CGST131	Baseline	AR	R775C	CCDS14387.1	Substitution	Nonsynonymous	0.54%	1863	10	No
CGST134	Baseline	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	0.58%	2074	12	No
CGST134	Baseline	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	1.28%	4135	53	No
CGST143	Baseline	DNMT3A	Y735C	CCDS33157.1	Substitution	Nonsynonymous	0.42%	2842	12	No
CGST143	Baseline	TP53	Y234C	CCDS11118.1	Substitution	Nonsynonymous	0.30%	2990	9	Yes
CGST148	Baseline	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	0.31%	3845	12	Yes

CGST152	Baseline	DNMT3A	R882C	CCDS33157.1	Substitution	Nonsynonymous	0.12%	4268	5	Yes
CGST176	Baseline	DNMT3A	L737F	CCDS33157.1	Substitution	Nonsynonymous	1.47%	3603	53	No
CGST176	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	0.06%	5223	3	Yes
CGST22	Baseline	ERBB4	N1190S	CCDS2394.1	Substitution	Nonsynonymous	0.19%	4215	8	No
CGST22	Baseline	ERBB4	V673F	CCDS2394.1	Substitution	Nonsynonymous	0.24%	2919	7	No
CGST24	Baseline	EGFR	D1175G	CCDS5514.1	Substitution	Nonsynonymous	0.22%	4010	9	No
CGST24	Baseline	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	0.22%	3237	7	Yes
CGST25	Baseline	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	7.01%	2467	173	No
CGST25	Baseline	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	0.18%	3793	7	Yes
CGST30	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	0.15%	4096	6	Yes
CGST31	Baseline	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	8.40%	3073	258	No
CGST31	Baseline	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	0.32%	3141	10	No
CGST38	Baseline	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	0.24%	3360	8	No
CGST38	Baseline	DNMT3A	P743L	CCDS33157.1	Substitution	Nonsynonymous	0.48%	3527	17	No
CGST38	Baseline	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	0.48%	3725	18	No
CGST41	Baseline	ATM	A2040P	CCDS31669.1	Substitution	Nonsynonymous	0.14%	4300	6	No
CGST47	Baseline	FLT3	S585L	CCDS31953.1	Substitution	Nonsynonymous	0.53%	2635	14	No
CGST48	Baseline	EGFR	L417F	CCDS5514.1	Substitution	Nonsynonymous	0.29%	4822	14	No
CGST58	Baseline	DNMT3A	D876Y	CCDS33157.1	Substitution	Nonsynonymous	0.17%	4089	7	No
CGST62	Baseline	DNMT3A	I705T	CCDS33157.1	Substitution	Nonsynonymous	0.29%	4764	14	No
CGST62	Baseline	DNMT3A	F732I	CCDS33157.1	Substitution	Nonsynonymous	0.37%	3477	13	No
CGST64	Baseline	PDGFRA	T1052M	CCDS3495.1	Substitution	Nonsynonymous	0.24%	4089	10	No
CGST64	Baseline	TP53	H179R	CCDS11118.1	Substitution	Nonsynonymous	0.07%	4213	3	Yes
CGST64	Baseline	TP53	V272M	CCDS11118.1	Substitution	Nonsynonymous	0.13%	3889	5	Yes
CGST64	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	4.66%	3884	181	Yes
CGST67	Baseline	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	0.70%	3885	27	No
CGST71	Baseline	APC	T1493A	CCDS4107.1	Substitution	Nonsynonymous	0.26%	4178	11	No
CGST71	Baseline	KRAS	G13D	NM_033360	Substitution	Nonsynonymous	0.10%	3105	3	Yes

CGST80	Baseline	DNMT3A	R882C	CCDS33157.1	Substitution	Nonsynonymous	0.08%	3873	3	Yes
CGST81	Baseline	FGFR2	S282I	CCDS31298.1	Substitution	Nonsynonymous	0.16%	4905	8	No
CGST97	Baseline	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	0.64%	4823	31	Yes
CGST24	Baseline	TP53	N/A	CCDS11118.1	Substitution	Splice site acceptor	0.32%	4022	13	Yes
CGST102	Baseline	DNMT3A	N/A	CCDS33157.1	Substitution	Splice site donor	0.18%	3983	7	Yes

Table 3.8. Summary of sequence alterations detected in ctDNA.

Patient ID	Patient Timepoint	Timepoint Significance	Gene Symbol	Amino Acid (Protein)	Transcript Accession	Mutation Type	Consequence	Mutant Allele Fraction	Total Distinct Coverage	Distinct Mutant Coverage	Hotspot Alteration
CGST33	CGST33P	Baseline	ERBB2	R756Cfs*2	CCDS32642.1	Insertion	Frameshift	0.64%	2331	15	No
CGST68	CGST68P	Baseline	HRAS	D54Efs*53	CCDS7698.1	Insertion	Frameshift	0.03%	3174	1	No
CGST148	CGST148P2	Postoperative	STK11	V128Dfs*34	CCDS45896.1	Deletion	Frameshift	0.26%	1924	5	No
CGST68	CGST68P2	Postoperative	ERBB4	D1184*	CCDS2394.1	Insertion	Frameshift	0.16%	3857	6	No
CGST68	CGST68P2	Postoperative	HRAS	D54Efs*53	CCDS7698.1	Insertion	Frameshift	0.29%	5856	17	No
CGST152	CGST152P1	Preoperative	ALK	P36*	CCDS33172.1	Insertion	Frameshift	0.71%	983	7	No
CGST102	CGST102P	Baseline	PIK3CA	E109del	CCDS43171.1	Deletion	In-frame deletion	0.43%	2577	11	No
CGST109	CGST109P	Baseline	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	0.43%	1380	6	No
CGST28	CGST28P	Baseline	PIK3R1	R577_L581del	CCDS3993.1	Deletion	In-frame deletion	1.62%	1170	19	No
CGST109	CGST109P2	Postoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	0.07%	1456	1	No
CGST134	CGST134P2	Postoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	0.25%	2384	6	No
CGST109	CGST109P1	Preoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	0.08%	1250	1	No
CGST134	CGST134P1	Preoperative	BRAF	G32_A33del	CCDS5863.1	Deletion	In-frame deletion	0.22%	459	1	No
CGST28	CGST28P1	Preoperative	PIK3R1	R577_L581del	CCDS3993.1	Deletion	In-frame deletion	0.70%	712	5	No
CGST141	CGST141P	Baseline	ERBB2	L785delinsHHVCF	CCDS32642.1	Insertion	In-frame insertion	0.06%	4903	3	No
CGST68	CGST68P	Baseline	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	0.04%	2619	1	No
CGST68	CGST68P2	Postoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	0.56%	2522	14	No
CGST69	CGST69P2	Postoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	0.16%	3732	6	No
CGST141	CGST141P1	Preoperative	ERBB2	L785delinsHHVCF	CCDS32642.1	Insertion	In-frame insertion	0.09%	7024	6	No
CGST68	CGST68P1	Preoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	0.04%	2230	1	No
CGST68	CGST68P1	Preoperative	HRAS	D54Efs*53	CCDS7698.1	Insertion	In-frame insertion	0.12%	2443	3	No
CGST81	CGST81P1	Preoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	0.41%	2413	10	No
CGST91	CGST91P1	Preoperative	ALK	G35_P36insL	CCDS33172.1	Insertion	In-frame insertion	0.16%	3734	6	No
CGST105	CGST105P	Baseline	PTEN	R335*	CCDS31238.1	Substitution	Nonsense	4.85%	1959	95	Yes

CGST158	CGST158P	Baseline	ERBB4	R114*	CCDS2394.1	Substitution	Nonsense	0.16%	4412	7	No
CGST30	CGST30P	Baseline	STK11	K64*	CCDS45896.1	Substitution	Nonsense	0.39%	1281	5	No
CGST33	CGST33P	Baseline	TP53	Q192*	CCDS11118.1	Substitution	Nonsense	2.32%	2628	61	Yes
CGST47	CGST47P	Baseline	FBXW7	E664*	CCDS3777.1	Substitution	Nonsense	0.45%	2015	9	No
CGST80	CGST80P	Baseline	TP53	S166*	CCDS11118.1	Substitution	Nonsense	1.04%	4823	50	No
CGST45	CGST45P2	Postoperative	TP53	E294*	CCDS11118.1	Substitution	Nonsense	0.14%	2787	4	Yes
CGST105	CGST105P1	Preoperative	PTEN	R335*	CCDS31238.1	Substitution	Nonsense	0.46%	1954	9	Yes
CGST105	CGST105P	Baseline	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	2.63%	2736	72	No
CGST105	CGST105P	Baseline	KRAS	G12C	NM_033360	Substitution	Nonsynonymous	1.21%	2561	31	Yes
CGST105	CGST105P	Baseline	PIK3CA	Y1021C	CCDS43171.1	Substitution	Nonsynonymous	0.19%	5304	10	Yes
CGST110	CGST110P	Baseline	ERBB4	T639M	CCDS2394.1	Substitution	Nonsynonymous	0.15%	2697	4	No
CGST113	CGST113P	Baseline	CDH1	V425I	CCDS10869.1	Substitution	Nonsynonymous	0.43%	1845	8	No
CGST113	CGST113P	Baseline	KIT	S241Y	CCDS3496.1	Substitution	Nonsynonymous	0.92%	1625	15	No
CGST122	CGST122P	Baseline	MYC	R98W	CCDS6359.2	Substitution	Nonsynonymous	0.20%	3506	7	No
CGST133	CGST133P	Baseline	KRAS	G12V	NM_033360	Substitution	Nonsynonymous	0.44%	1806	8	Yes
CGST133	CGST133P	Baseline	SMAD4	R361C	CCDS11950.1	Substitution	Nonsynonymous	0.29%	2761	8	Yes
CGST134	CGST134P	Baseline	MYC	S225L	CCDS6359.2	Substitution	Nonsynonymous	0.17%	3536	6	No
CGST142	CGST142P	Baseline	PTEN	F241L	CCDS31238.1	Substitution	Nonsynonymous	0.18%	3290	6	No
CGST158	CGST158P	Baseline	EGFR	D942N	CCDS5514.1	Substitution	Nonsynonymous	0.15%	3972	6	No
CGST24	CGST24P	Baseline	KIT	L939V	CCDS3496.1	Substitution	Nonsynonymous	0.22%	2244	5	No
CGST26	CGST26P	Baseline	CDK4	L125Q	CCDS8953.1	Substitution	Nonsynonymous	0.32%	1551	5	No
CGST28	CGST28P	Baseline	JAK2	L611S	CCDS6457.1	Substitution	Nonsynonymous	11.77%	1775	209	No
CGST30	CGST30P	Baseline	AR	L341Q	CCDS14387.1	Substitution	Nonsynonymous	0.39%	1291	5	No
CGST30	CGST30P	Baseline	CDH1	I326F	CCDS10869.1	Substitution	Nonsynonymous	0.29%	1754	5	No
CGST30	CGST30P	Baseline	MYC	H256L	CCDS6359.2	Substitution	Nonsynonymous	0.42%	1420	6	No
CGST32	CGST32P	Baseline	ALK	L347Q	CCDS33172.1	Substitution	Nonsynonymous	0.26%	1918	5	No
CGST32	CGST32P	Baseline	ALK	N1497I	CCDS33172.1	Substitution	Nonsynonymous	0.21%	2855	6	No
CGST32	CGST32P	Baseline	ALK	E172V	CCDS33172.1	Substitution	Nonsynonymous	0.21%	2807	6	No
CGST32	CGST32P	Baseline	BRAF	G469A	CCDS5863.1	Substitution	Nonsynonymous	0.65%	2445	16	Yes

CGST32	CGST32P	Baseline	KRAS	G13R	NM_033360	Substitution	Nonsynonymous	0.24%	2080	5	Yes
CGST32	CGST32P	Baseline	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	2.99%	2138	64	Yes
CGST45	CGST45P	Baseline	HRAS	G13V	CCDS7698.1	Substitution	Nonsynonymous	0.04%	2226	1	Yes
CGST47	CGST47P	Baseline	TP53	R175H	CCDS11118.1	Substitution	Nonsynonymous	0.28%	1431	4	Yes
CGST48	CGST48P	Baseline	EGFR	G514D	CCDS5514.1	Substitution	Nonsynonymous	0.27%	2230	6	No
CGST48	CGST48P	Baseline	FBXW7	R505L	CCDS3777.1	Substitution	Nonsynonymous	1.55%	1806	28	No
CGST48	CGST48P	Baseline	TP53	N239S	CCDS11118.1	Substitution	Nonsynonymous	4.21%	1259	53	Yes
CGST57	CGST57P	Baseline	ABL1	G254R	CCDS35166.1	Substitution	Nonsynonymous	0.25%	1217	3	No
CGST57	CGST57P	Baseline	KIT	A895T	CCDS3496.1	Substitution	Nonsynonymous	0.36%	1406	5	No
CGST62	CGST62P	Baseline	ALK	S1487L	CCDS33172.1	Substitution	Nonsynonymous	0.25%	3613	9	No
CGST63	CGST63P	Baseline	ATM	K3043R	CCDS31669.1	Substitution	Nonsynonymous	0.15%	4120	6	No
CGST63	CGST63P	Baseline	ATM	T547P	CCDS31669.1	Substitution	Nonsynonymous	0.35%	3125	11	No
CGST63	CGST63P	Baseline	CTNNB1	G34E	CCDS2694.1	Substitution	Nonsynonymous	0.25%	3964	10	Yes
CGST63	CGST63P	Baseline	PIK3CA	C420R	CCDS43171.1	Substitution	Nonsynonymous	0.39%	2788	11	Yes
CGST65	CGST65P	Baseline	PIK3CA	Y1021C	CCDS43171.1	Substitution	Nonsynonymous	0.07%	5704	4	Yes
CGST65	CGST65P	Baseline	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	0.55%	5987	33	Yes
CGST79	CGST79P	Baseline	MYC	R98W	CCDS6359.2	Substitution	Nonsynonymous	0.22%	2745	6	No
CGST80	CGST80P	Baseline	HRAS	G161E	CCDS7698.1	Substitution	Nonsynonymous	0.36%	3059	11	No
CGST113	CGST113P2	Postoperative	KIT	S241Y	CCDS3496.1	Substitution	Nonsynonymous	0.03%	3005	1	Yes
CGST134	CGST134P2	Postoperative	MYC	S225L	CCDS6359.2	Substitution	Nonsynonymous	0.02%	5746	1	No
CGST148	CGST148P2	Postoperative	KIT	G745R	CCDS3496.1	Substitution	Nonsynonymous	0.44%	5023	22	No
CGST24	CGST24P2	Postoperative	KIT	L939V	CCDS3496.1	Substitution	Nonsynonymous	0.03%	6498	2	No
CGST24	CGST24P2	Postoperative	AR	E323K	CCDS14387.1	Substitution	Nonsynonymous	0.12%	8506	10	No
CGST45	CGST45P2	Postoperative	APC	H2591N	CCDS4107.1	Substitution	Nonsynonymous	0.30%	1645	5	No
CGST45	CGST45P2	Postoperative	HRAS	G13V	CCDS7698.1	Substitution	Nonsynonymous	0.31%	1624	5	Yes
CGST45	CGST45P2	Postoperative	PTEN	A137E	CCDS31238.1	Substitution	Nonsynonymous	0.24%	2552	6	No
CGST63	CGST63P2	Postoperative	CTNNB1	S37F	CCDS2694.1	Substitution	Nonsynonymous	0.06%	6340	4	Yes
CGST63	CGST63P2	Postoperative	MYC	S154L	CCDS6359.2	Substitution	Nonsynonymous	0.15%	9254	14	No
CGST69	CGST69P2	Postoperative	CDH1	E35K	CCDS10869.1	Substitution	Nonsynonymous	0.12%	5212	6	No

CGST105	CGST105P1	Preoperative	PIK3CA	Y1021C	CCDS43171.1	Substitution	Nonsynonymous	0.04%	4910	2	Yes
CGST105	CGST105P1	Preoperative	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	0.24%	2482	6	No
CGST105	CGST105P1	Preoperative	KRAS	G12C	NM_033360	Substitution	Nonsynonymous	0.42%	2646	11	Yes
CGST110	CGST110P1	Preoperative	ERBB4	T639M	CCDS2394.1	Substitution	Nonsynonymous	0.12%	5089	6	No
CGST113	CGST113P1	Preoperative	KIT	S241Y	CCDS3496.1	Substitution	Nonsynonymous	0.04%	2735	1	No
CGST113	CGST113P1	Preoperative	STK11	Y340N	CCDS45896.1	Substitution	Nonsynonymous	0.25%	2038	5	No
CGST122	CGST122P1	Preoperative	MYC	R98W	CCDS6359.2	Substitution	Nonsynonymous	0.05%	4000	2	No
CGST133	CGST133P1	Preoperative	KRAS	G12V	NM_033360	Substitution	Nonsynonymous	0.06%	1802	1	Yes
CGST134	CGST134P1	Preoperative	MYC	S225L	CCDS6359.2	Substitution	Nonsynonymous	0.04%	2687	1	No
CGST24	CGST24P1	Preoperative	AR	E323K	CCDS14387.1	Substitution	Nonsynonymous	0.02%	4408	1	Yes
CGST24	CGST24P1	Preoperative	KIT	L939V	CCDS3496.1	Substitution	Nonsynonymous	0.08%	3829	3	Yes
CGST26	CGST26P1	Preoperative	CDK4	L125Q	CCDS8953.1	Substitution	Nonsynonymous	0.07%	1429	1	No
CGST28	CGST28P1	Preoperative	JAK2	L611S	CCDS6457.1	Substitution	Nonsynonymous	13.50%	1030	139	No
CGST45	CGST45P1	Preoperative	PTEN	A137E	CCDS31238.1	Substitution	Nonsynonymous	0.07%	3001	2	No
CGST48	CGST48P1	Preoperative	FBXW7	R505L	CCDS3777.1	Substitution	Nonsynonymous	0.23%	5603	13	No
CGST48	CGST48P1	Preoperative	TP53	N239S	CCDS11118.1	Substitution	Nonsynonymous	0.50%	4396	22	Yes
CGST57	CGST57P1	Preoperative	KIT	A895T	CCDS3496.1	Substitution	Nonsynonymous	0.09%	2277	2	No
CGST57	CGST57P1	Preoperative	ABL1	G254R	CCDS35166.1	Substitution	Nonsynonymous	0.33%	2095	7	No
CGST63	CGST63P1	Preoperative	ATM	K3043R	CCDS31669.1	Substitution	Nonsynonymous	0.06%	3091	2	No
CGST63	CGST63P1	Preoperative	ATM	T547P	CCDS31669.1	Substitution	Nonsynonymous	0.17%	1786	3	No
CGST63	CGST63P1	Preoperative	PIK3CA	C420R	CCDS43171.1	Substitution	Nonsynonymous	0.21%	1436	3	Yes
CGST63	CGST63P1	Preoperative	CTNNB1	G34E	CCDS2694.1	Substitution	Nonsynonymous	0.27%	2620	7	Yes
CGST68	CGST68P	Baseline	ATM	N/A	CCDS31669.1	Substitution	Splice site donor	0.11%	2683	3	No
CGST68	CGST68P2	Postoperative	ATM	N/A	CCDS31669.1	Substitution	Splice site donor	0.18%	3318	6	No
CGST68	CGST68P1	Preoperative	ATM	N/A	CCDS31669.1	Substitution	Splice site donor	0.06%	1585	1	No

Table 3.9. Summary of white blood cells sequence alterations detected in cfDNA.

Patient ID	Patient Timepoint	Timepoint Significance	Gene Symbol	Amino Acid (Protein)	Transcript Accession	Mutation Type	Consequence	Mutant Allele Fraction	Total Distinct Coverage	Distinct Mutant Coverage	Hot-spot Alteration*
CGST25	CGST25P	Baseline	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	0.59%	3029	18	No
CGST25	CGST25P2	Postoperative	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	0.28%	6442	18	No
CGST25	CGST25P1	Preoperative	TP53	H179del	CCDS11118.1	Deletion	In-frame deletion	0.66%	3325	22	No
CGST22	CGST22P	Baseline	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	0.10%	1918	2	No
CGST22	CGST22P1	Preoperative	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	0.56%	2325	13	No
CGST44	CGST44P	Baseline	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	1.12%	3380	38	No
CGST44	CGST44P2	Postoperative	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	0.67%	3154	21	No
CGST44	CGST44P1	Preoperative	MLH1	K618_A619insA	CCDS2663.1	Insertion	In-frame insertion	0.37%	3208	12	No
CGST57	CGST57P	Baseline	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	0.76%	1048	8	No
CGST57	CGST57P2	Postoperative	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	1.78%	1962	35	No
CGST57	CGST57P1	Preoperative	APC	A1755_S1756insS	CCDS4107.1	Insertion	In-frame insertion	2.22%	1804	40	No
CGST65	CGST65P	Baseline	DNMT3A	R771*	CCDS33157.1	Substitution	Nonsense	0.33%	4611	15	No
CGST65	CGST65P1	Preoperative	DNMT3A	R771*	CCDS33157.1	Substitution	Nonsense	0.11%	2828	3	No
CGST102	CGST102P	Baseline	DNMT3A	V895L	CCDS33157.1	Substitution	Nonsynonymous	0.24%	2879	7	No
CGST102	CGST102P	Baseline	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	1.27%	2677	34	No
CGST102	CGST102P	Baseline	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	0.40%	3214	13	No
CGST102	CGST102P2	Postoperative	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	0.50%	2788	14	No
CGST102	CGST102P2	Postoperative	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	0.71%	2943	21	No
CGST102	CGST102P1	Preoperative	SMARCB1	T214M	CCDS13817.1	Substitution	Nonsynonymous	0.54%	3326	18	No
CGST102	CGST102P1	Preoperative	DNMT3A	C911Y	CCDS33157.1	Substitution	Nonsynonymous	0.85%	2957	25	No
CGST109	CGST109P2	Postoperative	TP53	R267W	CCDS11118.1	Substitution	Nonsynonymous	0.07%	4195	3	Yes
CGST110	CGST110P	Baseline	DNMT3A	H873R	CCDS33157.1	Substitution	Nonsynonymous	0.03%	3207	1	No
CGST110	CGST110P	Baseline	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	0.04%	2763	1	Yes

CGST110	CGST110P1	Preoperative	TP53	V216M	CCDS11118.1	Substitution	Nonsynonymous	0.07%	5600	4	Yes
CGST110	CGST110P1	Preoperative	DNMT3A	H873R	CCDS33157.1	Substitution	Nonsynonymous	0.10%	5871	6	No
CGST113	CGST113P	Baseline	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	1.35%	1699	23	Yes
CGST113	CGST113P2	Postoperative	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	1.41%	2898	41	Yes
CGST113	CGST113P1	Preoperative	TP53	R248W	CCDS11118.1	Substitution	Nonsynonymous	1.16%	2161	25	Yes
CGST121	CGST121P	Baseline	DNMT3A	R749G	CCDS33157.1	Substitution	Nonsynonymous	0.04%	2695	1	No
CGST121	CGST121P1	Preoperative	DNMT3A	R749G	CCDS33157.1	Substitution	Nonsynonymous	0.22%	2742	6	No
CGST122	CGST122P	Baseline	JAK2	V617F	CCDS6457.1	Substitution	Nonsynonymous	6.32%	2293	145	Yes
CGST122	CGST122P	Baseline	KIT	P733S	CCDS3496.1	Substitution	Nonsynonymous	0.18%	4981	9	No
CGST122	CGST122P1	Preoperative	JAK2	V617F	CCDS6457.1	Substitution	Nonsynonymous	0.63%	1897	12	Yes
CGST134	CGST134P	Baseline	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	0.44%	1836	8	No
CGST134	CGST134P	Baseline	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	0.95%	3773	36	No
CGST134	CGST134P	Baseline	TP53	R282W	CCDS11118.1	Substitution	Nonsynonymous	0.06%	3634	2	Yes
CGST134	CGST134P2	Postoperative	TP53	R282W	CCDS11118.1	Substitution	Nonsynonymous	0.12%	6029	7	Yes
CGST134	CGST134P2	Postoperative	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	0.60%	3337	20	No
CGST134	CGST134P2	Postoperative	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	0.88%	6217	55	No
CGST134	CGST134P1	Preoperative	TP53	R282W	CCDS11118.1	Substitution	Nonsynonymous	0.03%	3183	1	Yes
CGST134	CGST134P1	Preoperative	AR	N757S	CCDS14387.1	Substitution	Nonsynonymous	0.08%	1259	4	No
CGST134	CGST134P1	Preoperative	DNMT3A	S714F	CCDS33157.1	Substitution	Nonsynonymous	0.48%	2724	13	No
CGST143	CGST143P	Baseline	FGFR3	V298M	CCDS3353.1	Substitution	Nonsynonymous	0.24%	1655	4	No
CGST143	CGST143P	Baseline	TP53	Y234C	CCDS11118.1	Substitution	Nonsynonymous	0.15%	1314	2	Yes
CGST143	CGST143P1	Preoperative	FGFR3	V298M	CCDS3353.1	Substitution	Nonsynonymous	0.20%	3033	6	No
CGST143	CGST143P1	Preoperative	TP53	Y234C	CCDS11118.1	Substitution	Nonsynonymous	0.77%	2081	16	Yes
CGST148	CGST148P	Baseline	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	0.13%	780	1	Yes
CGST148	CGST148P2	Postoperative	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	0.49%	4271	21	Yes
CGST148	CGST148P1	Preoperative	DNMT3A	R882H	CCDS33157.1	Substitution	Nonsynonymous	0.11%	925	1	Yes
CGST176	CGST176P	Baseline	DNMT3A	L737F	CCDS33157.1	Substitution	Nonsynonymous	0.41%	2202	9	No
CGST176	CGST176P1	Preoperative	DNMT3A	V897I	CCDS33157.1	Substitution	Nonsynonymous	0.24%	2079	5	No

CGST176	CGST176P1	Preoperative	DNMT3A	L737F	CCDS33157.1	Substitution	Nonsynonymous	0.58%	2054	12	No
CGST22	CGST22P	Baseline	ERBB4	N1190S	CCDS2394.1	Substitution	Nonsynonymous	0.31%	2235	7	No
CGST22	CGST22P	Baseline	TP53	R175H	CCDS11118.1	Substitution	Nonsynonymous	0.16%	1930	3	Yes
CGST22	CGST22P1	Preoperative	TP53	R175H	CCDS11118.1	Substitution	Nonsynonymous	0.21%	1896	4	Yes
CGST22	CGST22P1	Preoperative	ERBB4	N1190S	CCDS2394.1	Substitution	Nonsynonymous	0.47%	2349	11	No
CGST24	CGST24P	Baseline	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	0.30%	1690	5	Yes
CGST24	CGST24P2	Postoperative	EGFR	D1175G	CCDS5514.1	Substitution	Nonsynonymous	0.16%	8145	13	No
CGST24	CGST24P2	Postoperative	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	0.21%	6721	14	Yes
CGST24	CGST24P1	Preoperative	EGFR	D1175G	CCDS5514.1	Substitution	Nonsynonymous	0.10%	4997	5	No
CGST24	CGST24P1	Preoperative	TP53	C238Y	CCDS11118.1	Substitution	Nonsynonymous	0.41%	2709	11	Yes
CGST25	CGST25P	Baseline	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	7.25%	2040	148	No
CGST25	CGST25P	Baseline	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	0.26%	1934	5	Yes
CGST25	CGST25P2	Postoperative	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	0.06%	4965	3	Yes
CGST25	CGST25P2	Postoperative	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	3.17%	2744	87	No
CGST25	CGST25P1	Preoperative	TP53	G245S	CCDS11118.1	Substitution	Nonsynonymous	0.45%	2215	10	Yes
CGST25	CGST25P1	Preoperative	ATM	R2832H	CCDS31669.1	Substitution	Nonsynonymous	9.84%	2856	281	No
CGST30	CGST30P	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	0.31%	1590	5	Yes
CGST30	CGST30P1	Preoperative	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	0.20%	2503	5	Yes
CGST31	CGST31P	Baseline	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	9.47%	602	57	No
CGST31	CGST31P	Baseline	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	0.35%	579	2	No
CGST31	CGST31P2	Postoperative	DNMT3A	L888P	CCDS33157.1	Substitution	Nonsynonymous	0.10%	5911	6	No
CGST31	CGST31P2	Postoperative	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	0.39%	4389	17	No
CGST31	CGST31P2	Postoperative	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	8.88%	5115	454	No
CGST31	CGST31P1	Preoperative	DNMT3A	L888P	CCDS33157.1	Substitution	Nonsynonymous	0.13%	5932	8	No
CGST31	CGST31P1	Preoperative	IDH2	R149Q	CCDS10359.1	Substitution	Nonsynonymous	0.20%	4938	10	No
CGST31	CGST31P1	Preoperative	ESR1	T311M	CCDS5234.1	Substitution	Nonsynonymous	7.36%	5478	403	No
CGST38	CGST38P	Baseline	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	0.29%	1724	5	No
CGST38	CGST38P	Baseline	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	0.39%	1778	7	No

CGST38	CGST38P2	Postoperative	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	0.21%	3368	7	No
CGST38	CGST38P2	Postoperative	DNMT3A	P743L	CCDS33157.1	Substitution	Nonsynonymous	0.29%	3827	11	No
CGST38	CGST38P2	Postoperative	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	0.34%	3498	12	No
CGST38	CGST38P1	Preoperative	DNMT3A	I769V	CCDS33157.1	Substitution	Nonsynonymous	0.28%	2163	6	No
CGST38	CGST38P1	Preoperative	DNMT3A	P743L	CCDS33157.1	Substitution	Nonsynonymous	0.29%	2413	7	No
CGST38	CGST38P1	Preoperative	DNMT3A	R736H	CCDS33157.1	Substitution	Nonsynonymous	0.50%	2184	11	No
CGST48	CGST48P	Baseline	EGFR	L417F	CCDS5514.1	Substitution	Nonsynonymous	0.43%	1872	8	No
CGST48	CGST48P1	Preoperative	EGFR	L417F	CCDS5514.1	Substitution	Nonsynonymous	0.10%	7003	7	No
CGST62	CGST62P	Baseline	DNMT3A	F732I	CCDS33157.1	Substitution	Nonsynonymous	0.11%	1747	2	No
CGST62	CGST62P	Baseline	DNMT3A	R882L	CCDS33157.1	Substitution	Nonsynonymous	0.26%	2701	7	No
CGST62	CGST62P	Baseline	PTEN	R130Q	CCDS31238.1	Substitution	Nonsynonymous	0.10%	3091	3	Yes
CGST62	CGST62P1	Preoperative	PTEN	R130Q	CCDS31238.1	Substitution	Nonsynonymous	0.02%	5000	1	Yes
CGST62	CGST62P1	Preoperative	DNMT3A	R882L	CCDS33157.1	Substitution	Nonsynonymous	0.16%	2579	4	No
CGST62	CGST62P1	Preoperative	DNMT3A	F732I	CCDS33157.1	Substitution	Nonsynonymous	0.39%	2297	9	No
CGST63	CGST63P	Baseline	TP53	N239K	CCDS11118.1	Substitution	Nonsynonymous	0.23%	3522	8	No
CGST63	CGST63P2	Postoperative	TP53	N239K	CCDS11118.1	Substitution	Nonsynonymous	0.12%	5799	7	No
CGST63	CGST63P1	Preoperative	TP53	N239K	CCDS11118.1	Substitution	Nonsynonymous	0.29%	1752	5	No
CGST64	CGST64P	Baseline	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	6.14%	293	18	Yes
CGST64	CGST64P1	Preoperative	TP53	H179R	CCDS11118.1	Substitution	Nonsynonymous	0.25%	3640	9	Yes
CGST64	CGST64P1	Preoperative	TP53	V272M	CCDS11118.1	Substitution	Nonsynonymous	0.77%	2970	23	Yes
CGST64	CGST64P1	Preoperative	TP53	R273H	CCDS11118.1	Substitution	Nonsynonymous	12.59%	3184	401	Yes
CGST67	CGST67P	Baseline	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	0.66%	2573	17	No
CGST67	CGST67P	Baseline	PDGFRA	G166E	CCDS3495.1	Substitution	Nonsynonymous	0.18%	2778	5	No
CGST67	CGST67P2	Postoperative	PDGFRA	G166E	CCDS3495.1	Substitution	Nonsynonymous	0.19%	3749	7	No
CGST67	CGST67P2	Postoperative	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	0.42%	3846	16	No
CGST67	CGST67P1	Preoperative	PDGFRA	G166E	CCDS3495.1	Substitution	Nonsynonymous	0.09%	5556	5	No
CGST67	CGST67P1	Preoperative	DNMT3A	S708N	CCDS33157.1	Substitution	Nonsynonymous	0.47%	5555	26	No
CGST81	CGST81P	Baseline	TP53	C135F	CCDS11118.1	Substitution	Nonsynonymous	0.20%	3509	7	Yes

CGST97	CGST97P	Baseline	TP53	P151S	CCDS11118.1	Substitution	Nonsynonymous	0.15%	682	1	Yes
CGST97	CGST97P	Baseline	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	0.37%	539	2	Yes
CGST97	CGST97P2	Postoperative	TP53	P151S	CCDS11118.1	Substitution	Nonsynonymous	0.16%	3783	6	Yes
CGST97	CGST97P2	Postoperative	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	1.48%	3443	51	Yes
CGST97	CGST97P1	Preoperative	TP53	P151S	CCDS11118.1	Substitution	Nonsynonymous	0.12%	4015	5	Yes
CGST97	CGST97P1	Preoperative	TP53	Y220C	CCDS11118.1	Substitution	Nonsynonymous	1.70%	3596	61	Yes
CGST24	CGST24P	Baseline	TP53	NA	CCDS11118.1	Substitution	Splice site acceptor	0.22%	2296	5	Yes
CGST24	CGST24P2	Postoperative	TP53	NA	CCDS11118.1	Substitution	Splice site acceptor	0.22%	6922	15	Yes
CGST24	CGST24P1	Preoperative	TP53	NA	CCDS11118.1	Substitution	Splice site acceptor	0.10%	4149	4	Yes
CGST64	CGST64P1	Preoperative	DNMT3A	N/A	CCDS33157.1	Deletion	Splice site acceptor	0.35%	3417	12	No

CHAPTER 4:

GENOME-WIDE CELL-FREE DNA FRAGMENTATION IN PATIENTS WITH CANCER

METHODS

Source of plasma samples

Plasma samples from healthy individuals and plasma and tissue samples from patients with breast, lung, ovarian, colorectal, bile duct, and gastric cancers were obtained from ILSBio/Bioreclamation, Aarhus University, Herlev Hospital of the University of Copenhagen, Hvidovre Hospital, the University Medical Center of the University of Utrecht, the Academic Medical Center of the University of Amsterdam, the Netherlands Cancer Institute, and the University of California, San Diego. All samples were obtained under Institutional Review Board approved protocols with informed consent for research use at participating institutions. Plasma samples from healthy individuals were obtained at the time of routine screening, including for colonoscopies or Pap smears. Individuals were considered healthy if they had no previous history of cancer and negative screening results.

Plasma samples from individuals with breast, colorectal, gastric, lung, ovarian, pancreatic and bile duct cancer were obtained at the time of diagnosis, prior to tumor resection or therapy. Nineteen lung cancer patients analyzed for change in cfDNA fragmentation profiles across multiple time points were undergoing treatment with anti-EGFR or anti-ERBB2 therapy (19). Clinical data for all patients included in this study are listed in table S1. Gender was confirmed through genomic analyses of X and Y chromosome representation. Pathologic staging of gastric cancer patients was performed after neoadjuvant therapy. Samples where the tumor stage was unknown were indicated as stage X or unknown.

Nucleosomal DNA purification

Viably frozen lymphocytes were elutriated from leukocytes obtained from a healthy male (C0618) and female (D0808-L) (Advanced Biotechnologies Inc., Eldersburg, MD). Aliquots of 1 x 10^6 cells

were used for nucleosomal DNA purification using EZ Nucleosomal DNA Prep Kit (Zymo Research, Irvine, CA). Cells were initially treated with 100µl of Nuclei Prep Buffer and incubated on ice for 5 minutes. After centrifugation at 200*g* for 5 minutes, supernatant was discarded, and pelleted nuclei were treated twice with 100µl of Atlantis Digestion Buffer or with 100µl of micrococcal nuclease (MN) Digestion Buffer. Finally, cellular nucleic DNA was fragmented with 0.5U of Atlantis dsDNase at 42°C for 20 minutes or 1.5U of MNase at 37°C for 20 minutes. Reactions were stopped using 5X MN Stop Buffer and DNA was purified using Zymo-Spin™ IIC Columns. Concentration and quality of eluted cellular nucleic DNA were analyzed using the Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA).

Sample preparation and sequencing of cfDNA

Whole blood was collected in EDTA tubes and processed immediately or within one day after storage at 4°C or were collected in Streck tubes and processed within two days of collection for three cancer patients who were part of the monitoring analysis. Plasma and cellular components were separated by centrifugation at 800g for 10 min at 4°C. Plasma was centrifuged a second time at 18,000g at room temperature to remove any remaining cellular debris and stored at −80°C until the time of DNA extraction. DNA was isolated from plasma using the Qiagen Circulating Nucleic Acids Kit (Qiagen GmbH) and eluted in LoBind tubes (Eppendorf AG). Concentration and quality of cfDNA were assessed using the Bioanalyzer 2100 (Agilent Technologies).

NGS cfDNA libraries were prepared for whole genome sequencing and targeted sequencing using 5 to 250 ng of cfDNA as previously described (15). Briefly, genomic libraries were prepared using the NEBNext DNA Library Prep Kit for Illumina [New England Biolabs (NEB)] with four main modifications to the manufacturer's guidelines: (i) The library purification steps used the on-bead AMPure XP approach to minimize sample loss during elution and tube transfer steps (83); (ii) NEBNext End Repair, A-tailing, and adapter ligation enzyme and buffer volumes were adjusted as

appropriate to accommodate the on-bead AMPure XP purification strategy; (iii) a pool of eight unique Illumina dual index adapters with 8–base pair (bp) barcodes was used in the ligation reaction instead of the standard Illumina single or dual index adapters with 6- or 8-bp barcodes, respectively; and (iv) cfDNA libraries were amplified with Phusion Hot Start Polymerase.

Whole genome libraries were sequenced directly. For targeted libraries, capture was performed using Agilent SureSelect reagents and a custom set of hybridization probes targeting 58 genes (15) per the manufacturer's guidelines. The captured library was amplified with Phusion Hot Start Polymerase (NEB). Concentration and quality of captured cfDNA libraries were assessed on the Bioanalyzer 2100 using theDNA1000 Kit (Agilent Technologies). Targeted libraries were sequenced using 100-bp paired-end runs on the Illumina HiSeq 2000/2500 (Illumina).

Analyses of targeted sequencing data from cfDNA

Analyses of targeted NGS data for cfDNA samples was performed as previously described (15). Briefly, primary processing was completed using Illumina CASAVA (Consensus Assessment of Sequence and Variation) software (version 1.8), including demultiplexing and masking of dual-index adapter sequences. Sequence reads were aligned against the human reference genome (version hg18 or hg19) using NovoAlign with additional realignment of select regions using the Needleman-Wunsch method (71). The positions of sequence alterations we identified have not been affected by the different genome builds. Candidate mutations, consisting of point mutations, small insertions, and deletions, were identified using VariantDx (71) (Personal Genome Diagnostics, Baltimore, MD) across the targeted regions of interest.

To analyze the fragment lengths of cfDNA molecules, we required that each read pair from a cfDNA molecule have a Phred quality score ≥ 30. We removed all duplicate ctDNA fragments, defined as having the same start, end, and index barcode. For each mutation, we only included

fragments for which one or both of the read pairs contained the mutated (or wild-type) base at the given position. This analysis was done using the R packages Rsamtools and GenomicAlignments.

For each genomic locus where a somatic mutation was identified, we compared the lengths of fragments containing the mutant allele to the lengths of fragments with the wild-type allele. If more than 100 mutant fragments were identified, we used Welch's two-sample t-test to compare the mean fragment lengths. For loci with fewer than 100 mutant fragments, we implemented a bootstrap procedure. Specifically, we sampled with replacement N fragments containing the wild-type allele, where N denotes the number of fragments with the mutation. For each bootstrap replicate of wild type fragments, we computed their median length. The p-value was estimated as the fraction of bootstrap replicates with a median wild-type fragment length as or more extreme than the observed median mutant fragment length.

Analyses of whole genome sequencing data from cfDNA

Primary processing of whole genome NGS data for cfDNA samples was performed using Illumina CASAVA (Consensus Assessment of Sequence and Variation) software (version 1.8.2), including demultiplexing and masking of dual-index adapter sequences. Sequence reads were aligned against the human reference genome (version hg19) using ELAND.

Read pairs with a MAPQ score below 30 for either read and PCR duplicates were removed. We tiled the hg19 autosomes into 26,236 adjacent, non-overlapping 100 kb bins. We excluded regions of low mappability based on previous work (84) where 10% of bins with the lowest coverage were removed, and excluded reads falling in the Duke blacklisted regions (http://hgdownload.cse.ucsc.edu/goldenpath/hg19/encodeDCC/wgEncodeMapability/). Using this approach, we excluded 361 Mb (13%) of the hg19 reference genome, including centromeric and telomeric regions. Short fragments were defined as having lengths between 100 and 150 bp and long fragments as having lengths between 151 and 220 bp.

To account for biases in coverage attributable to GC content of the genome, we applied the locally weighted smoother loess with span ¾ to the scatterplot of average fragment GC versus coverage calculated for each 100kb bin. This loess regression was performed separately for short and long fragments to account for possible differences in GC effects on coverage in plasma by fragment length, an approach loosely motivated by Benjamini et al (85). We subtracted the predictions for short and long coverage explained by GC from the loess model, obtaining residuals for short and long that were uncorrelated with GC. We returned the residuals to the original scale by adding back the genome-wide median short and long estimates of coverage. This procedure was repeated for each sample to account for possible differences in GC effects on coverage between samples. To further reduce the feature space and noise, we calculated the total GC-adjusted coverage in 5 Mb bins.

To compare the variability of fragment lengths from healthy subjects to fragments in patients with cancer, we calculated the standard deviation of the short to long fragmentation profiles for each individual. We compared the standard deviations in the two groups by a Wilcoxon rank sum test.

Analyses of chromosome arm copy number changes

To develop arm-level statistics for copy number changes, we adopted a previously described approach for aneuploidy detection in plasma (9). This approach divides the genome into non-overlapping 50KB bins for which GC-corrected log2 read depth was obtained after correction by loess with span 3/4. This loess-based correction is comparable to the approach outlined above but is evaluated on a log2 scale to increase robustness to outliers in the smaller bins and does not stratify by fragment length. To obtain an arm-specific Z-score for copy number changes, the mean GC-adjusted read depth for each arm (GR) was centered and scaled by the average and standard deviation, respectively, of GR scores obtained from an independent set of 50 healthy samples.

Analyses of mitochondrial-aligned reads from cfDNA

Whole genome sequence reads that initially mapped to the mitochondrial genome were extracted from bam files and realigned to the hg19 reference genome in end-to-end mode with Bowtie2 as previously described (86). The resulting aligned reads were filtered such that both mates aligned to the mitochondrial genome with MAPQ >= 30. The number of fragments mapping to the mitochondrial genome was counted and converted to a percentage of the total number of fragments in the original bam files.

Prediction model for cancer classification

To distinguish healthy from cancer patients using fragmentation profiles, we used a stochastic gradient boosting machine (gbm) (87, 88). GC-corrected total and short fragment coverage for all 504 bins were centered and scaled for each sample to have mean 0 and unit standard deviation. Additional features included Z-scores for each of the 39 autosomal arms and mitochondrial representation (log10-transformed proportion of reads mapped to the mitochondria). To estimate the prediction error of this approach, we used 10-fold cross-validation. Feature selection, performed only on the training data in each cross-validation run, removed bins that were highly correlated (correlation > 0.9) or had near zero variance. Stochastic gradient boosted machine learning was implemented using the R package gbm package with parameters n.trees=150, interaction.depth=3, shrinkage=0.1, and n.minobsinside=10. To average over the prediction error from the randomization of patients to folds, we repeated the 10-fold cross validation procedure 10 times. Confidence intervals for sensitivity fixed at 98% and 95% specificity were obtained from 2000 bootstrap replicates.

Prediction model for tumor tissue of origin classification

For samples correctly classified as cancer patients at 90% specificity (n = 174), a separate stochastic gradient boosting model was trained to classify the tissue type. To account for the small number of lung samples used for prediction, we included 18 late stage lung cancer patients from the monitoring analyses of our study, using the cfDNA analyses from the baseline blood samples. Performance characteristics of the model were evaluated by 10-fold cross-validation repeated 10 times. This gbm model was trained using the same features as in the cancer classification model. As previously described, features that displayed correlation above 0.9 to each other or had near zero variance were removed within each training dataset during cross-validation. The tissue class probabilities were averaged across the 10 replicates for each patient and the class with the highest probability was taken as the predicted tissue.

Analyses of nucleosomal DNA from human lymphocytes and cfDNA

From the nuclease treated lymphocytes, fragment sizes were analyzed in 5 Mb bins as described above for whole genome cfDNA analyses. A genome-wide map of nucleosome positions was constructed from the nuclease treated lymphocyte cell-lines. This approach identified local biases in the coverage of circulating fragments, indicating a region protected from degradation. A "Window positioning score" (WPS) was used to score each base pair in the genome (65). Using a sliding window of 60bp centered around each base, the WPS was calculated as the number of fragments completely spanning the window minus the number of fragments with only one end in the window. Since fragments arising from nucleosomes have a median length of 167 bp, a high WPS indicated a possible nucleosomal position. WPS scores were centered at zero using a running median and smoothed using a Kolmogorov-Zurbenko filter (89). For spans of positive WPS between 50 and 450 bp, a nucleosome peak was defined as the set of base pairs with a WPS above the median in that window. The calculation of nucleosome positions for cfDNA from 30 healthy individuals with sequence coverage of 9x was determined in the same manner as for lymphocyte DNA. To ensure that nucleosomes in healthy cfDNA were representative, we defined a consensus

track of nucleosomes consisting only of nucleosomes identified in two or more individuals. Median distances between adjacent nucleosomes were calculated from the consensus track.

Monte Carlo simulation of detection sensitivity

We used Monte Carlo simulation to estimate the probability of detecting a molecule with a tumor-derived alteration (Figure 4.1). Briefly, we generated 1 million molecules from a multinomial distribution. For a simulation with m alterations, wild-type molecules were simulated with probability p and each of the m tumor alterations were simulated with probability $(1-p)/m$. Next, we sampled $g * m$ molecules randomly with replacement, where g denotes the number of genome equivalents in 1 ml of plasma. If a tumor alteration was sampled s or more times, we classified the sample as cancer-derived. We repeated the simulation 1000 times, estimating the probability that the *in silico* sample would be correctly classified as cancer by the mean of the cancer indicator. Setting $g = 2000$ and $s = 5$, we varied the number of tumor alterations by powers of 2 from 1 to 256 and the fraction of tumor-derived molecules from 0.0001% to 1%.

Statistical analyses

All statistical analyses were perform using R version 3.4.3. The R packages caret (version 6.0-79) and gbm (version 2.1-4) were used to implement the classification of healthy versus cancer and tissue of origin. Confidence intervals from the model output were obtained with the pROC (version 1.13) R packages (90). Assuming the prevalence of undiagnosed cancer cases in this population is high (1 or 2 cases per 100 healthy), a genomic assay with a specificity of 0.95 and sensitivity of 0.8 would have useful operating characteristics (positive predictive value of 0.25 and negative predictive value near 1). Power calculations suggest that an analysis of more than 200 cancer patients and an approximately equal number of healthy controls, enable an estimation of the sensitivity with a margin of error of 0.06 at the desired specificity of 0.95 or greater.

RESULTS

As an initial proof of principle, we used 5 Mb windows for evaluating cfDNA fragmentation patterns as this would provide over 20,000 reads per window even at 1-2x genome coverage. Within each window, we examined the coverage and size distribution of cfDNA fragments. We used this approach to evaluate the variation of genome-wide fragmentation profiles in healthy and cancer populations (Table 4.1). The genome-wide pattern from an individual can be compared to reference populations to determine if the pattern is likely healthy or cancer-derived. As genome-wide profiles reveal positional differences associated with specific tissues that may be missed in overall fragment size distributions, these patterns may also indicate the tissue source of cfDNA (Figure 4.2).

We initially focused on the fragmentation size of cfDNA as we found that cancer-derived cfDNA molecules may be more variable in size than cfDNA derived from non-cancer cells. We examined cfDNA fragments from targeted regions that were captured and sequenced at high coverage (43,706 total coverage, 8,044 distinct coverage) from patients with breast, colorectal, lung or ovarian cancer (15) (Tables 4.1, 4.2, 4.3). Analyses of loci containing 165 tumor-specific alterations from 81 patients (range of 1-7 alterations per patient) revealed an average absolute difference of 6.5 bp (95% CI, 5.4-7.6 bp) between lengths of median mutant and wild-type cfDNA fragments (Figure 4.3 and Table 4.3). The median size of mutant cfDNA fragments ranged from 30 bases smaller at chromosome 3 position 41,266,124 to 47 bases larger at chromosome 11 position 108,117,753 than the wild-type sequences at these regions (Table 4.3). GC content was similar for mutated and non-mutated fragments (Figure 4.4 A), and there was no correlation between GC content and fragment length (Figure 4.4 B). Similar analyses of 44 germline alterations from 38 patients identified median cfDNA size differences of less than 1 bp between fragment lengths of different alleles (Figure 4.5 and Table 4.3). Additionally, we identified 41 alterations related to clonal hematopoiesis through a previous sequence comparison of DNA from plasma, buffy coat, and

tumors of the same individuals (15). Unlike tumor-derived fragments, there were no significant differences between fragments with hematopoietic alterations and wild type fragments (Figure 4.6 and Table 4.3). Overall, cancer-derived cfDNA fragment lengths were significantly more variable compared to non-cancer cfDNA fragments at certain genomic regions ($p<0.001$, variance ratio test). We hypothesized that these differences may be due to changes in higher-order chromatin structure as well as other genomic and epigenomic abnormalities in cancer (91, 92) and that cfDNA fragmentation in a position-specific manner could therefore serve as a unique biomarker for cancer detection.

As targeted sequencing only analyzes a limited number of loci, we investigated whether larger-scale genome-wide analyses would detect additional abnormalities in cfDNA fragmentation. In a pilot analysis, we isolated cfDNA from ~4 ml of plasma from 8 lung cancer patients with stage I-III disease as well as from 30 healthy individuals (Tables 4.1, 4.4, and 4.5). We used a high efficiency approach to convert cfDNA to next generation sequencing libraries and performed whole genome sequencing at ~9x coverage (Table 4.4). As expected from previous studies (57, 65, 66), overall cfDNA fragment lengths of healthy individuals were larger, with a median fragment size of 167.3 bp, while patients with cancer had median fragment sizes of 163.8 ($p<0.01$, Welch's t-test) (Table 4.5). To examine differences in fragment size and coverage in a position dependent manner across the genome, we mapped sequenced fragments to their genomic origin and evaluated fragment lengths in 504 windows that were 5 Mb in size, covering ~2.6 Gb of the genome. For each window, we determined the fraction of small cfDNA fragments (100 to 150 bp in length) to larger cfDNA fragments (151 to 220 bp) and overall coverage to obtain genome-wide fragmentation profiles for each sample.

We found that healthy individuals had very similar fragmentation profiles throughout the genome (Figures 4.7 A, 4.7 B, and 4.8 A). To examine the origins of fragmentation patterns normally observed in cfDNA, we isolated nuclei from elutriated lymphocytes of two healthy individuals and

treated these with DNA nucleases to obtain nucleosomal DNA fragments. Analyses of cfDNA patterns in observed healthy individuals revealed a high correlation to lymphocyte nucleosomal DNA fragmentation profiles (Figures 4.7 B and 4.8 B) and nucleosome distances (Figures 4.7 C and 4.8 C). We also found that the median distances between nucleosomes in lymphocytes were correlated to open (A) and closed (B) compartments of lymphoblastoid cells as revealed using the Hi-C method for examining the three-dimensional architecture of genomes (Figure 4.7 C) (84, 93) These analyses suggest that the fragmentation patterns of normal cfDNA are the result of nucleosomal DNA patterns that largely reflect the chromatin structure of normal blood cells.

In contrast to healthy cfDNA, patients with cancer had multiple distinct genomic differences with increases and decreases in fragment sizes at different regions (Figures 4.7 A and 4.7 B). Similar to our observations from targeted analyses, there was also greater variation in fragment lengths genome-wide for patients with cancer compared to healthy individuals. To determine whether cfDNA fragment length patterns could be used to distinguish patients with cancer from healthy individuals, we performed genome-wide correlation analyses of the fraction of short to long cfDNA fragments for each sample compared to the median fragment length profile calculated from healthy individuals (Figures 4.7 A, 4.7 B, 4.8 D). While the profiles of cfDNA fragments were remarkably consistent among healthy individuals (median correlation of 0.99), the median correlation of genome-wide fragment ratios among cancer patients was 0.84 (0.15 lower, 95% CI 0.07-0.50, $p<0.001$, Wilcoxon rank sum test) (Table 4.5). Similar differences were observed when comparing fragmentation profiles of cancer patients to fragmentation profiles or nucleosome distances in healthy lymphocytes (Figures 4.7 C, 4.8 B, 4.8 C). To account for potential biases in the fragmentation profiles attributable to GC content, we applied a locally weighted smoother independently to each sample and found that differences in fragmentation profiles between healthy individuals and cancer patients remained after this adjustment (median correlation of cancer patients to healthy = 0.83) (Table 4.5).

We performed subsampling analyses of whole genome sequence data at 9x coverage from cfDNA of patients with cancer at ~2x, ~1x, ~0.5x, ~0.2x, and ~0.1x genome coverage, and determined that altered fragmentation profiles were readily identified even at 0.5x genome coverage (Figures 4.8 E and 4.8 F). Based on these observations, we performed whole genome sequencing with coverage of 1-2x to evaluate whether fragmentation profiles may change during the course of targeted therapy in a manner similar to monitoring of sequence alterations (19, 20, 56). We evaluated cfDNA from 19 non-small cell lung cancer patients, including 5 with partial radiographic response, 8 with stable disease, 4 with progressive disease, and 2 with non-measureable disease, during the course of anti-EGFR or anti-ERBB2 therapy (Table 4.6). As shown in Figure 4.9, the degree of abnormality in the fragmentation profiles during therapy closely matched levels of EGFR or ERBB2 mutant allele fractions as determined using targeted sequencing (Spearman correlation of mutant allele fractions to fragmentation profiles = 0.74) (19). This correlation is remarkable as genome-wide and mutation-based methods are orthogonal and examine different cfDNA alterations that may be suppressed in these patients due to prior therapy. Notably all cases that had progression free survival of six or more months displayed a drop of or had extremely low levels of ctDNA after initiation of therapy as determined by fragmentation profiles, while cases with poor clinical outcome had increases in ctDNA. These results demonstrate the feasibility of fragmentation analyses for detecting the presence of tumor-derived cfDNA and suggests that such analyses may also be useful for quantitative monitoring of cancer patients during treatment.

As fragmentation profiles would be expected to reflect both epigenomic and genomic alterations, we examined the fragmentation profiles in the context of known copy number changes in a patient where parallel analyses of tumor tissue were obtained. These analyses demonstrated that altered fragmentation profiles were present in regions of the genome that were copy neutral and that these may be further affected in regions with copy number changes (Figures 4.10 A and 4.11 A). Position dependent differences in fragmentation patterns could be used to distinguish cancer-derived cfDNA

from healthy cfDNA in these regions (Figures 4.11 A and 4.11 B), while overall cfDNA fragment size measurements would have missed such differences (Figure 4.11 A).

We extended these analyses to an independent cohort of cancer patients and healthy individuals. We performed whole genome sequencing of cfDNA at 1-2x coverage from a total of 208 patients with cancer, including breast (n=54), colorectal (n=27), lung (n=12), ovarian (n=28), pancreatic (n=34), gastric (n=27), or bile duct cancers (n=26), as well as 215 individuals without cancer (Tables 4.1 and 4.4). All cancer patients were treatment naïve and the majority had resectable disease (n=183). After GC adjustment of short and long cfDNA fragment coverage (Figure 4.12 A), we examined coverage and size characteristics of fragments in windows throughout the genome (Figure 4.10 B and Tables 4.4 and 4.7). Genome-wide correlations of coverage to GC content were limited and we observed no differences in these correlations between cancer patients and healthy individuals ($p = 0.2$, Welch's t-test) (Figure 4.12 B). As we previously observed in the pilot analyses, healthy individuals had highly concordant fragmentation profiles, while patients with cancer had high variability with decreased correlation to the median healthy profile (Table 4.7). An analysis of the most commonly altered fragmentation windows in the genome among cancer patients revealed a median of 60 affected windows across the cancer types analyzed, highlighting the multitude of position dependent alterations in fragmentation of cfDNA in individuals with cancer (Figure 4.10 C).

To determine if position dependent fragmentation changes can be used to detect individuals with cancer, we implemented a gradient tree boosting machine learning model to examine whether cfDNA can be categorized as having characteristics of a cancer patient or healthy individual and estimated performance characteristics of this approach by ten-fold cross validation repeated ten times (87, 88, 94) (Figures 4.13 A, 4.13 B). The machine learning model included GC-adjusted short and long fragment coverage characteristics in windows throughout the genome. We also developed a machine learning classifier for copy number changes from chromosomal arm

dependent features rather than a single score (9, 55) (Figure 4.14 A and Table 4.8) as well as mitochondrial copy number changes (57) (Figure 4.14 B) as these could also help distinguish cancer from healthy individuals. Using this implementation of DELFI, we obtained a score that could be used to classify patients as healthy or having cancer. We detected 152 of the 208 cancer patients (73% sensitivity, 95% CI 67%-79%) while misclassifying four of the 215 healthy individuals (98% specificity) (Table 4.9). At a threshold of 95% specificity, we detected 80% of patients with cancer (95% CI, 74%-85%), including 79% of resectable (stage I – III) patients (145 of 183) and 82% of metastatic (stage IV) patients (18 out of 22) (Table 4.9). Receiver operator characteristic analyses for detection of patients with cancer had an AUC of 0.94 (95% CI 0.92 – 0.96), ranged among cancer types from 0.86 for pancreatic cancer to ≥0.99 for lung and ovarian cancers (Figures 4.15 and 4.16 A), and had AUCs ≥0.92 across all stages (Figure 4.16 B). The DELFI classifier score did not differ with age among either cancer patients or healthy individuals (Table 4.1). To assess the contribution of fragment size and coverage, chromosome arm copy number, or mitochondrial mapping to the predictive accuracy of the model, we implemented the repeated 10-fold cross-validation procedure to assess performance characteristics of these features in isolation. We observed that fragment coverage features alone (AUC = 0.94) were nearly identical to the classifier that combined all features (AUC = 0.94). In contrast, analyses of chromosomal copy number changes had lower performance (AUC = 0.88) but were still more predictive than copy number changes based on individual scores (AUC=0.78) or mitochondrial mapping (AUC = 0.72) (Figure 4.15). These results suggest that fragment coverage is the major contributor to our classifier, but we have included all features in our prediction model as they can be obtained from the same genome sequence data and may contribute in a complementary fashion for detection of patients with cancer.

As fragmentation profiles reveal regional differences in fragmentation that may differ between tissues, we used a similar machine learning approach to examine whether cfDNA patterns could identify the tissue of origin of these tumors. We found that this approach had a 61% accuracy (95%

CI 53%-67%), including 76% for breast, 44% for bile duct, 71% for colorectal, 67% for gastric, 53% for lung, 48% for ovarian, and 50% for pancreatic cancers (Figure 4.16 C and Table 4.10). The accuracy increased to 75% (95% CI 69%-81%) when considering assigning patients with abnormal cfDNA to one of two sites of origin (Table 4.10). For all tumor types the classification of the tissue of origin by DELFI was significantly higher than determined by random assignment ($p<0.01$, binomial test, Table 4.10).

As cancer-specific sequence alterations can also be used to identify patients with cancer, we evaluated whether combining DELFI with this approach could increase the sensitivity of cancer detection (Figure 4.17). We previously analyzed cfDNA from a subset of the treatment naïve cancer patients in this study using targeted error correction sequencing (15). An evaluation of all cases analyzed using both DELFI and targeted sequencing revealed that 82% (103 of 126) of patients had fragmentation profile alterations while 66% (83 of 126) had sequence alterations. Over 89% of cases with mutant allele fractions >1% were detected by DELFI while for cases with mutant allele fractions <1% the fraction detected by DELFI was 80%, including for cases that were undetectable using targeted sequencing (Table 4.7). When these approaches were used together the combined sensitivity of detection increased to 91% (115 of 126 patients) with a specificity of 98% (Figure 4.17).

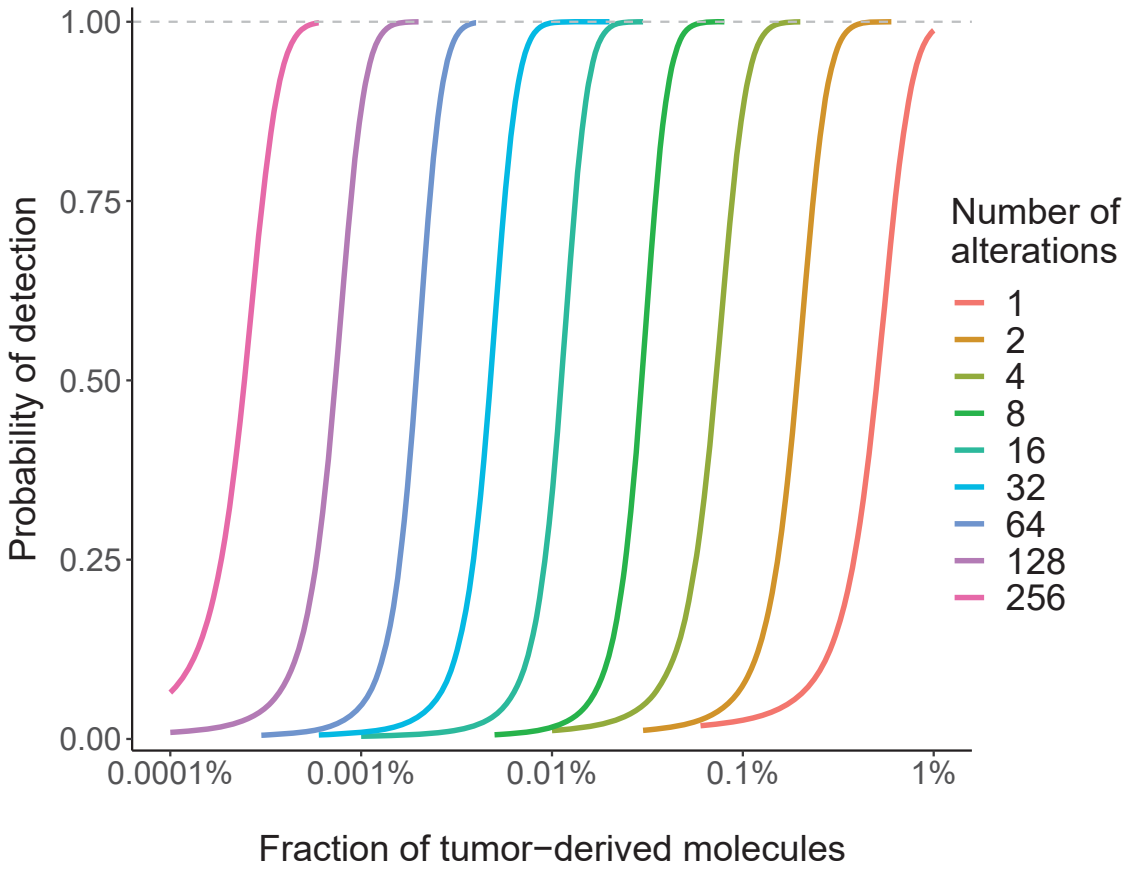


Figure 4.1. Simulations of noninvasive cancer detection based on number of alterations analyzed. Monte Carlo simulations were performed using different numbers of tumor-specific alterations to evaluate the probability of detecting cancer alterations in cfDNA at the indicated fraction of tumor-derived molecules. The simulations were performed assuming an average of 2000 genome equivalents of cfDNA and the requirement of five or more observations of any alteration. These analyses indicate that increasing the number of tumor-specific alterations improves the sensitivity of detection of circulating tumor DNA.

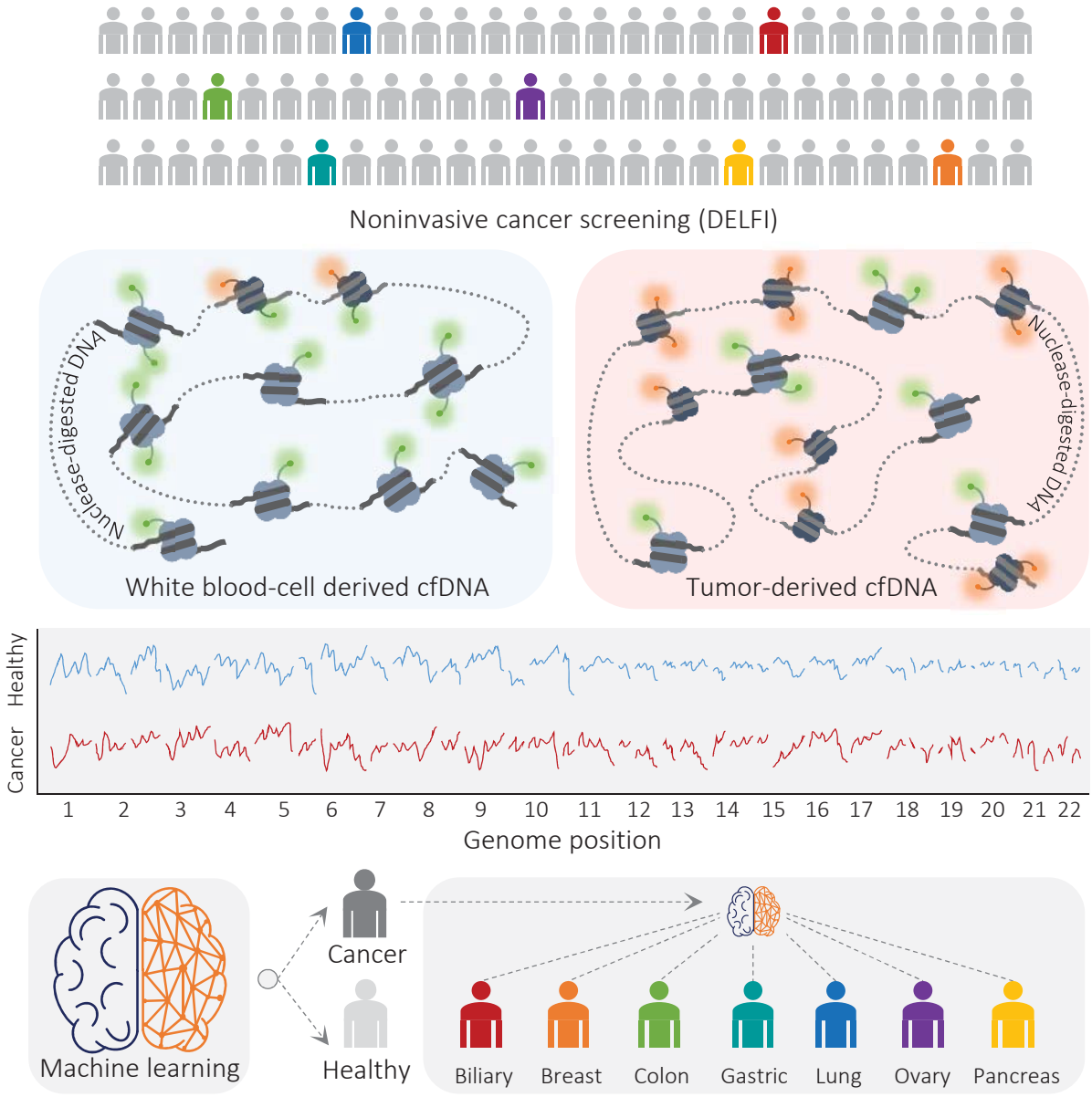


Figure 4.2. Schematic of DELFI approach. Blood is collected from a cohort of healthy individuals and patients with cancer. Nucleosome protected cfDNA is extracted from the plasma fraction, processed into sequencing libraries, examined through whole genome sequencing, mapped to the genome, and analyzed to determine cfDNA fragment profiles in different windows across the genome. Machine learning approaches are used to categorize individuals as healthy or as having cancer and to identify the tumor tissue of origin using genome-wide cfDNA fragmentation patterns.

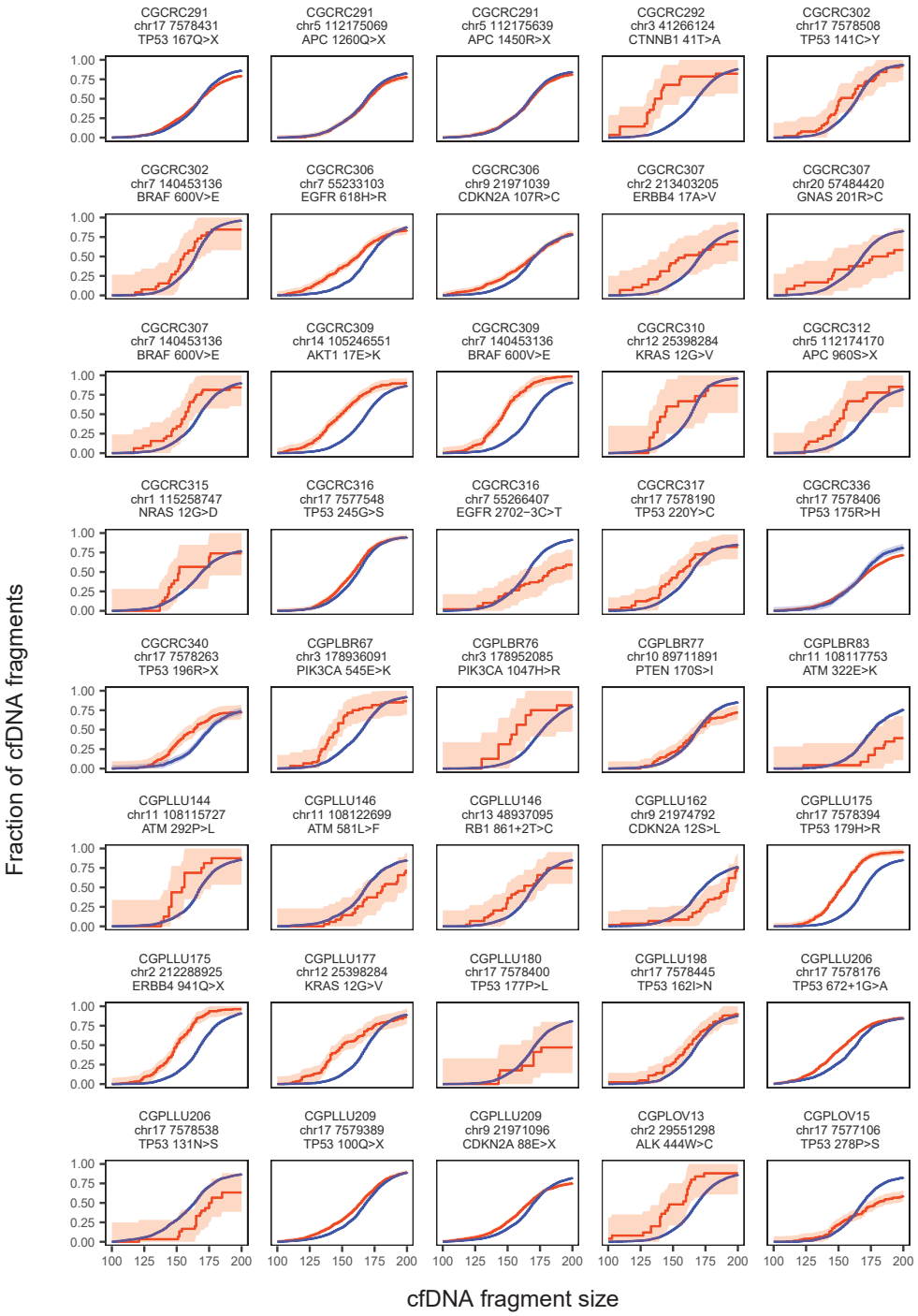


Figure 4.3. Tumor-derived cfDNA fragment distributions. Cumulative density functions of cfDNA fragment lengths of 42 loci containing tumor-specific alterations from 30 patients with breast, colorectal, lung, or ovarian cancer are shown with 95% confidence bands (red). Lengths of mutant cfDNA fragments were significantly different in size compared to wild-type cfDNA fragments (blue) at these loci.

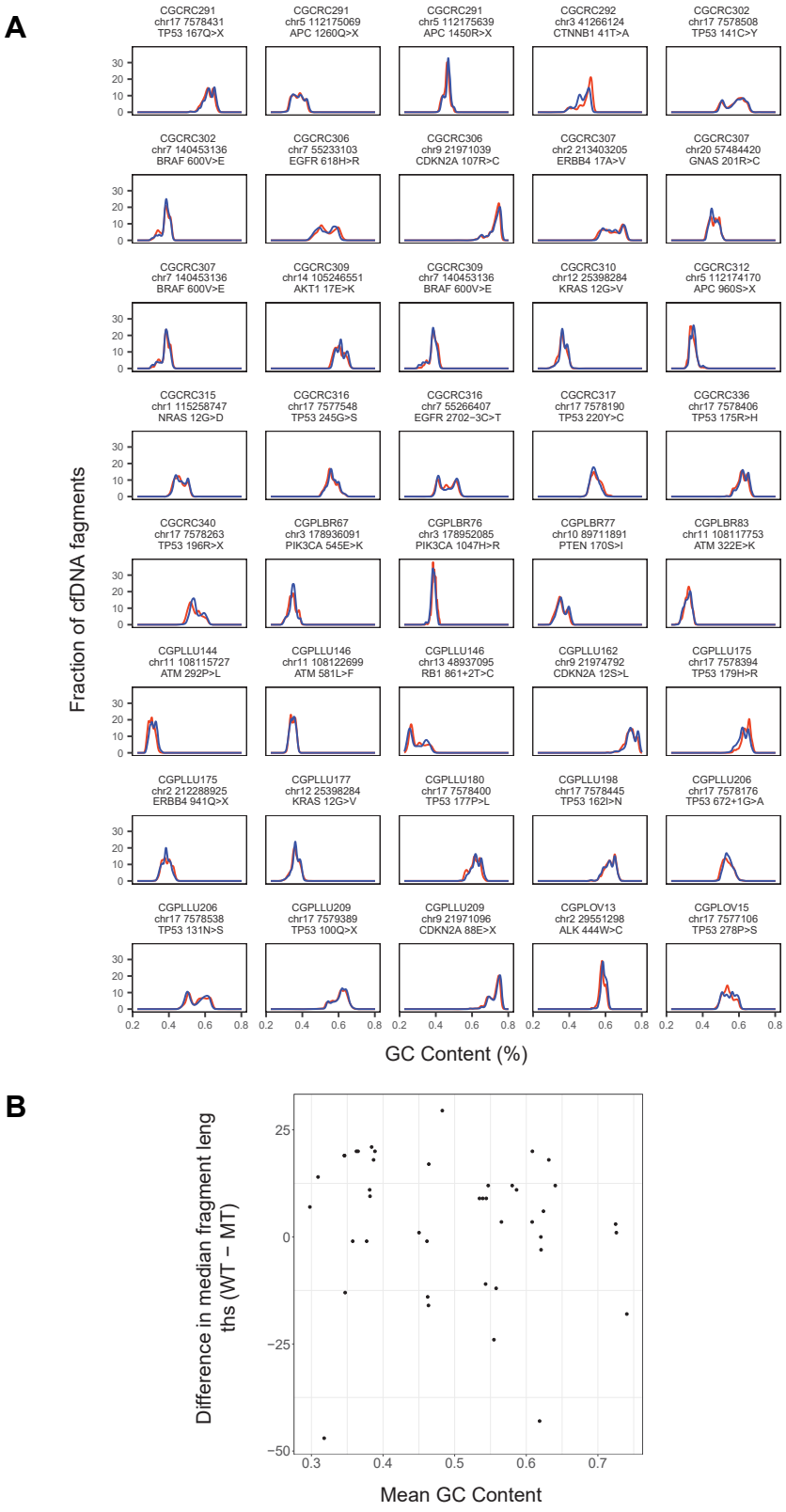


Figure 4.4. Tumor-derived cfDNA GC content and fragment length. A) GC content was similar for mutated and non-mutated fragments. B) GC content was not correlated to fragment length.

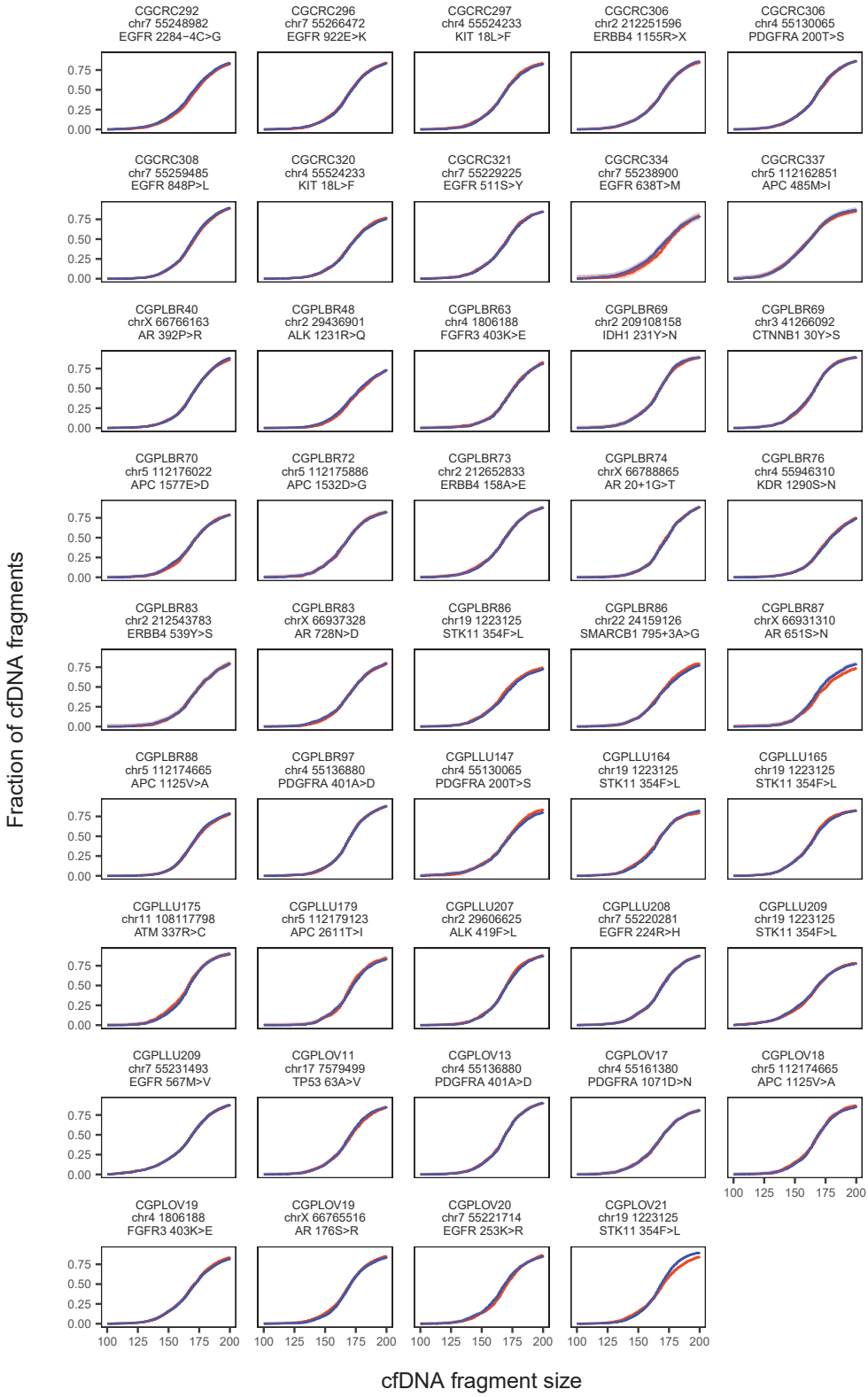


Figure 4.5. Germline cfDNA fragment distributions. Cumulative density functions of fragment lengths at 44 loci containing germline alterations (non-tumor derived) from 38 patients with breast, colorectal, lung, or ovarian cancer are shown with 95% confidence bands. Fragments with germline mutations (red) were comparable in length to wild-type cfDNA fragment lengths (blue).

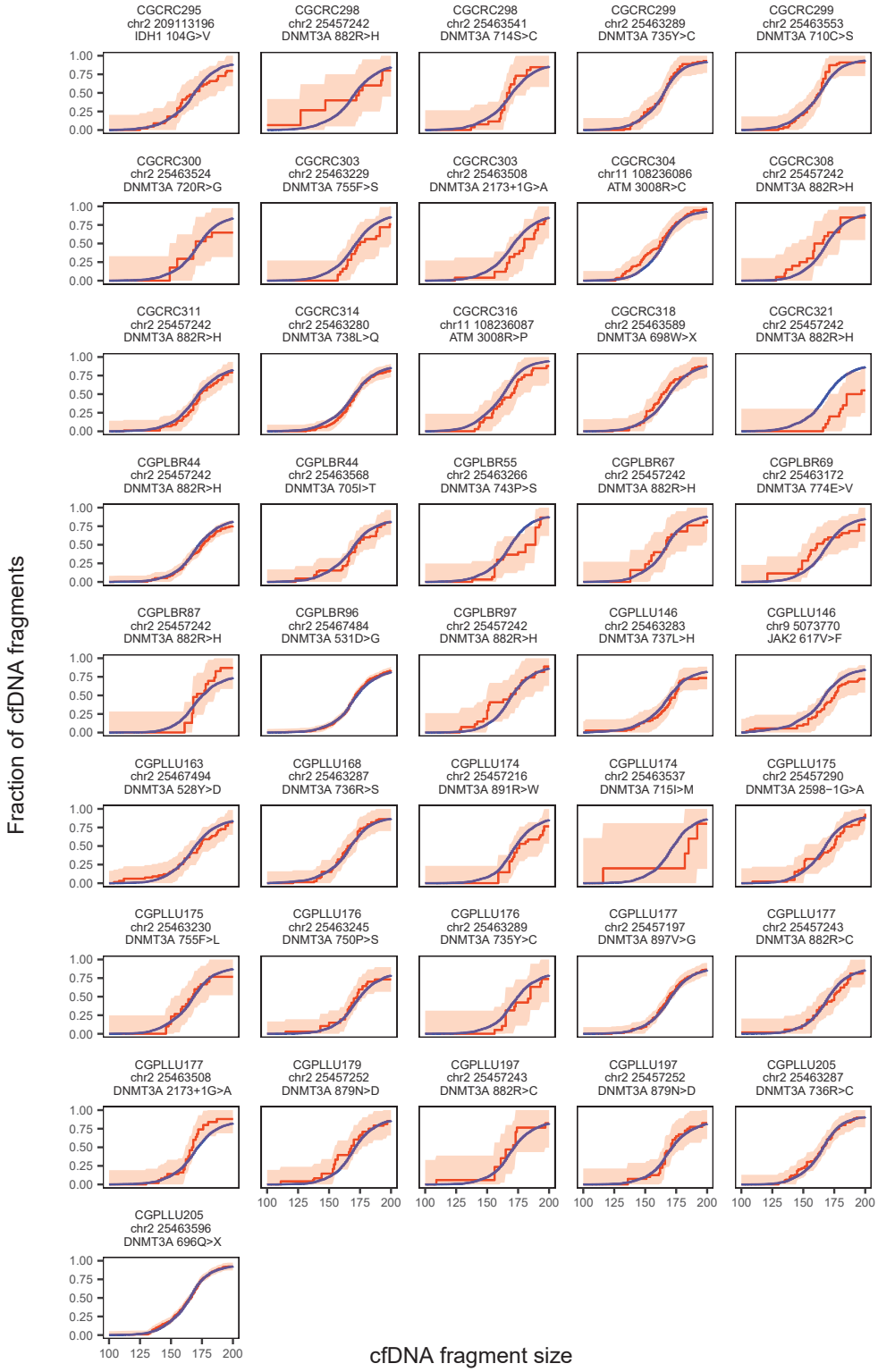


Figure 4.6. Hematopoietic cfDNA fragment distributions. Cumulative density functions of fragment lengths at 41 loci containing hematopoietic alterations (non-tumor derived) from 28 patients with breast, colorectal, lung, or ovarian cancer are shown with 95% confidence bands. After correction for multiple testing, there were no significant differences (α=0.05) in the size distributions of mutated hematopoietic cfDNA fragments (orange) and wild-type cfDNA fragments (blue).

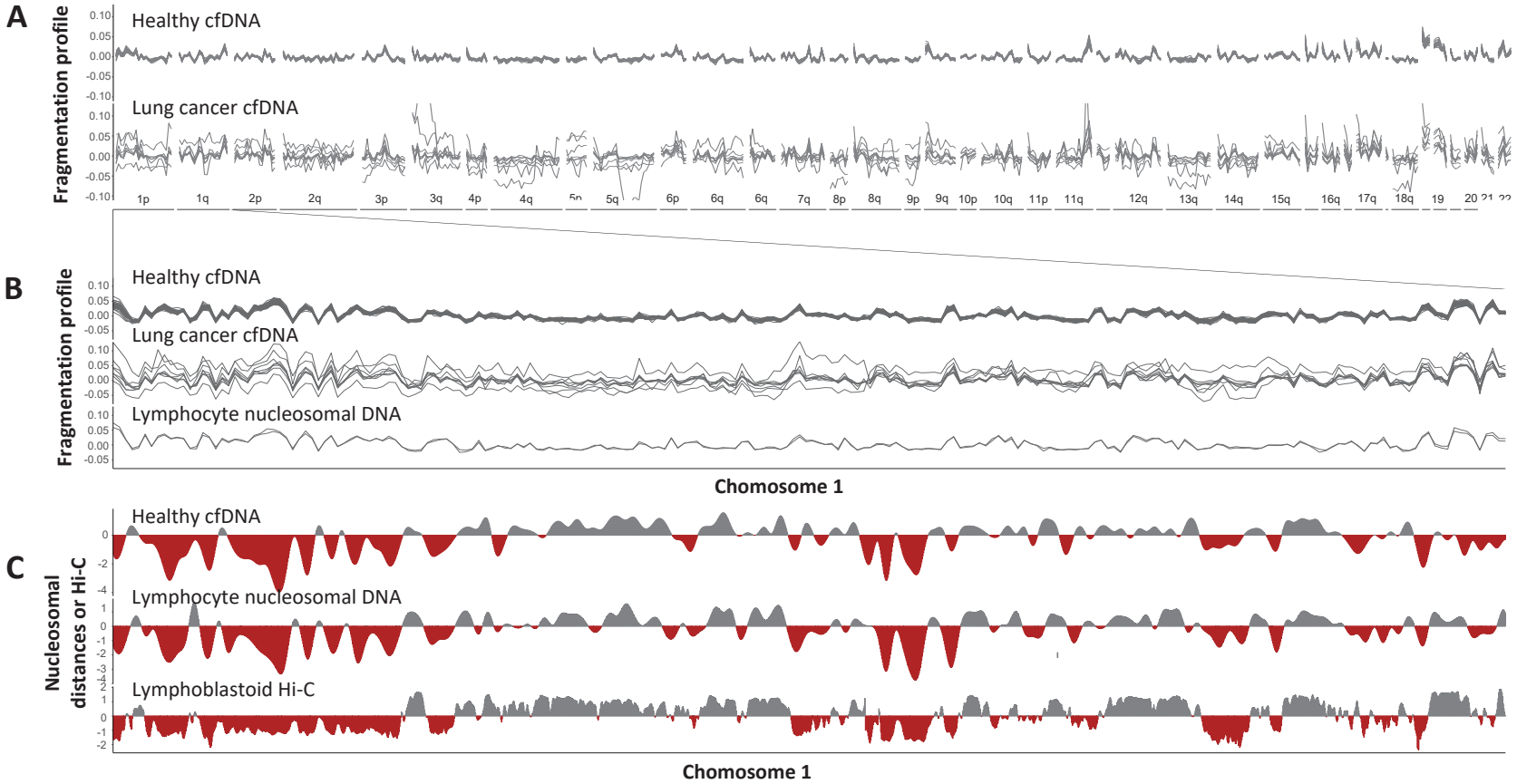


Figure 4.7. cfDNA fragmentation profiles in healthy individuals and patients with cancer. A) Genome-wide cfDNA fragmentation profiles (defined as the ratio of short to long fragments) from ~9x whole genome sequencing are shown in 5 Mb bins for 30 healthy individuals (top) and 8 lung cancer patients (bottom). B) An analysis of healthy cfDNA (top), lung cancer cfDNA (middle), and healthy lymphocyte (bottom) fragmentation profiles and lymphocyte profiles from chromosome 1 at 1 Mb resolution. The healthy lymphocyte profiles were scaled with a standard deviation equal to that of the median healthy cfDNA profiles. Healthy cfDNA patterns closely mirrored those in healthy lymphocytes while lung cancer cfDNA profiles were more varied and differed from both healthy and lymphocyte profiles. C) Smoothed median distances between adjacent nucleosome centered at zero using 100 kb bins from healthy cfDNA (top) and nuclease-digested healthy lymphocytes (middle) are depicted together with the first eigenvector for the genome contact matrix obtained through previously reported Hi-C analyses of lymphoblastoid cells (84) (bottom). Healthy cfDNA nucleosome distances closely mirrored those in nuclease-digested lymphocytes as well as those from lymphoblastoid Hi-C analyses.

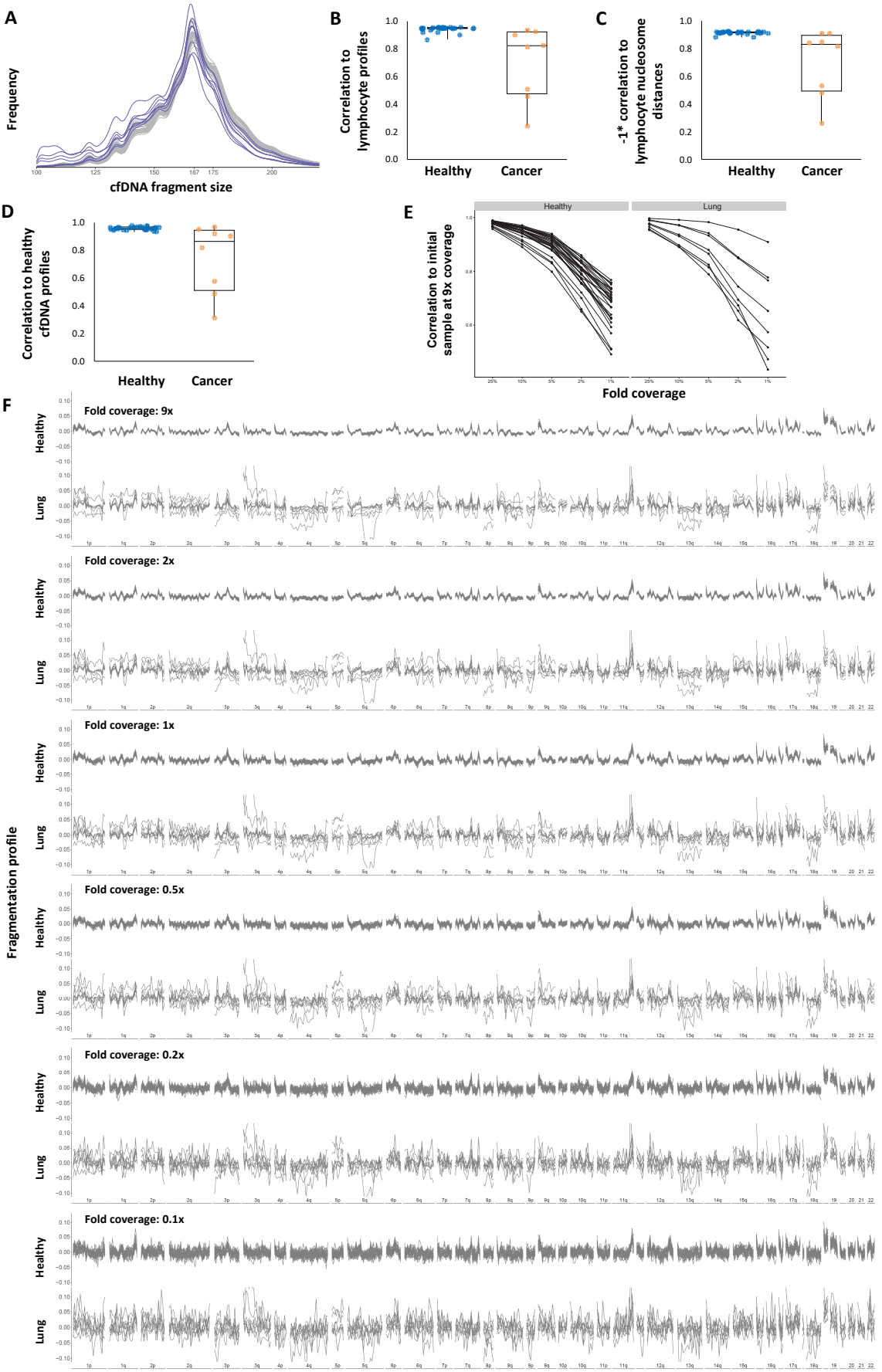

A
Frequency
100
125
150
167
175
200
cfDNA fragment size
B
Correlation to lymphocyte profiles
1.0
0.8
0.6
0.4
0.2
0.0
Healthy
Cancer
C
-1* correlation to lymphocyte nucleosome distances
1.0
0.8
0.6
0.4
0.2
0.0
Healthy
Cancer
D
Correlation to healthy cfDNA profiles
1.0
0.8
0.6
0.4
0.2
0.0
Healthy
Cancer
E
Healthy
Lung
Correlation to initial sample at 9x coverage
1.0
0.8
0.6
25%
10%
5%
2%
1%
Fold coverage
F
Fragmentation profile
Fold coverage: 9x
Fold coverage: 2x
Fold coverage: 1x
Fold coverage: 0.5x
Fold coverage: 0.2x
Fold coverage: 0.1x
Healthy
Lung
0.10
0.05
0.00
−0.05
−0.10
1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12q
13q
14q
15q
16q
17q
18q
19
20
21
22

Figure 4.8. cfDNA fragmentation in healthy individuals and patients with lung cancer. A) cfDNA fragments lengths are shown for healthy individuals (n=30, gray) and patients with lung cancer (n=8, blue). B-D) cfDNA fragmentation profiles from healthy individuals (n=30) had high correlations while patients with lung cancer (n=8) had lower correlations to median fragmentation profiles of B, lymphocytes, C, lymphocyte nucleosome distances, and, D, healthy cfDNA. Pearson correlations are shown with box plots depicting minimum, 25th percentile, median, 75th percentile, and maximum values. E) High coverage (9x) whole-genome sequencing data were subsampled to 2x, 1x, 0.5x, 0.2x, and 0.1x fold coverage. Mean centered genome-wide fragmentation profiles in 5 Mb bins for 30 healthy individuals and 8 patients with lung cancer are depicted for each subsampled fold coverage with median profiles shown in blue. F) Pearson Correlation of subsampled profiles to initial profile at 9x coverage for healthy individuals and patients with lung cancer.

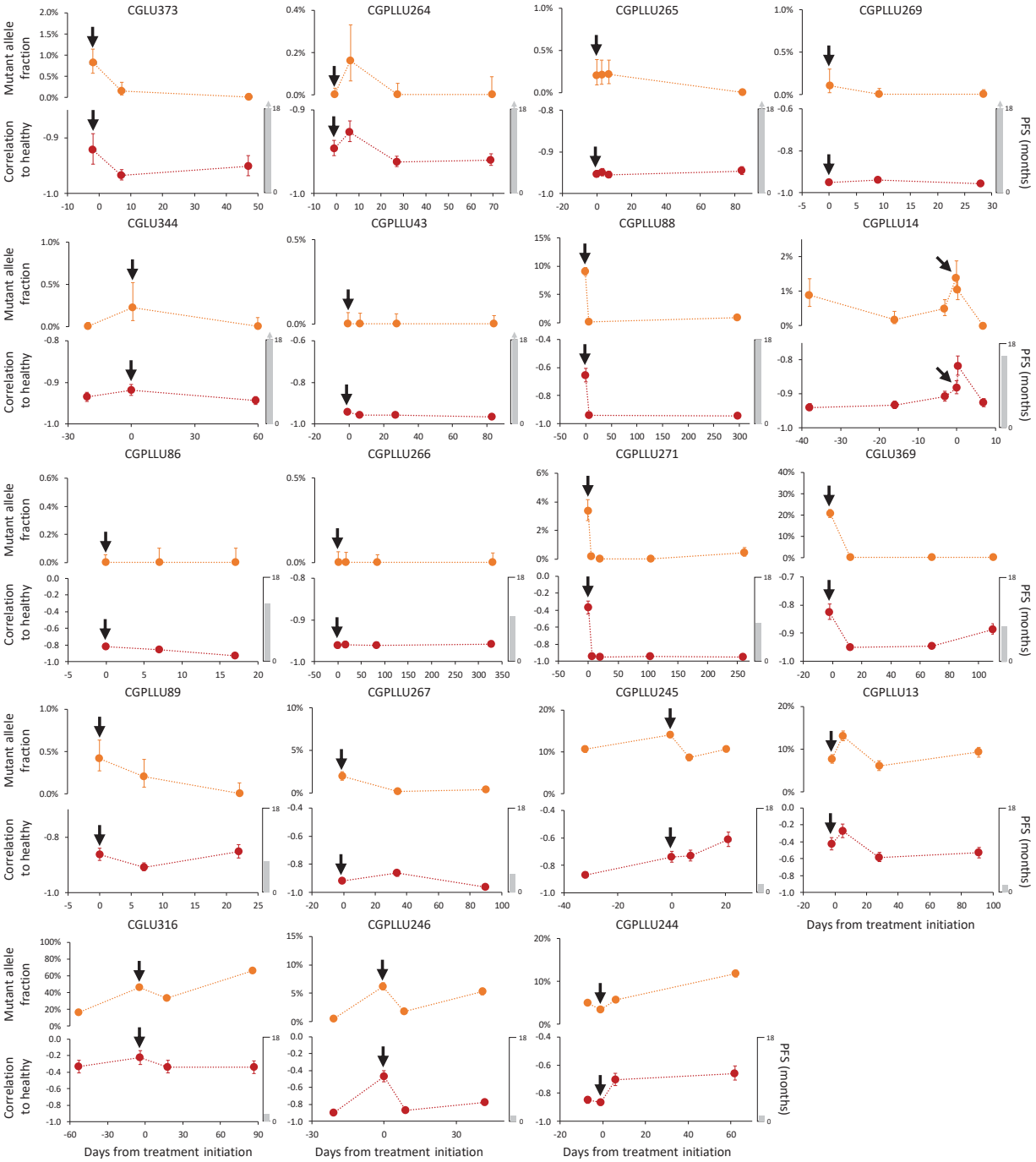


Figure 4.9. cfDNA fragmentation profiles and sequence alterations during therapy. Detection and monitoring of cancer in serial blood draws from NSCLC patients (n=19) undergoing treatment with targeted tyrosine kinase inhibitors (black arrows) was performed using targeted sequencing (top) as previously reported and genome-wide fragmentation profiles (bottom). For each case, the vertical axis of the lower panel displays -1 times the Pearson correlation of each sample to the median healthy cfDNA fragmentation profile. Error bars depict confidence intervals from binomial tests for mutant allele fractions and confidence intervals calculated using Fisher transformation for genome-wide fragmentation profiles. Although the approaches analyze different aspects of cfDNA (whole genome compared to specific alterations) the targeted sequencing and fragmentation profiles were similar for patients responding to therapy as well as those with stable or progressive disease. As fragmentation profiles reflect both genomic and epigenomic alterations, while mutant allele fractions only reflect individual mutations, mutant allele fractions alone may not reflect the absolute level of correlation of fragmentation profiles to healthy individuals.

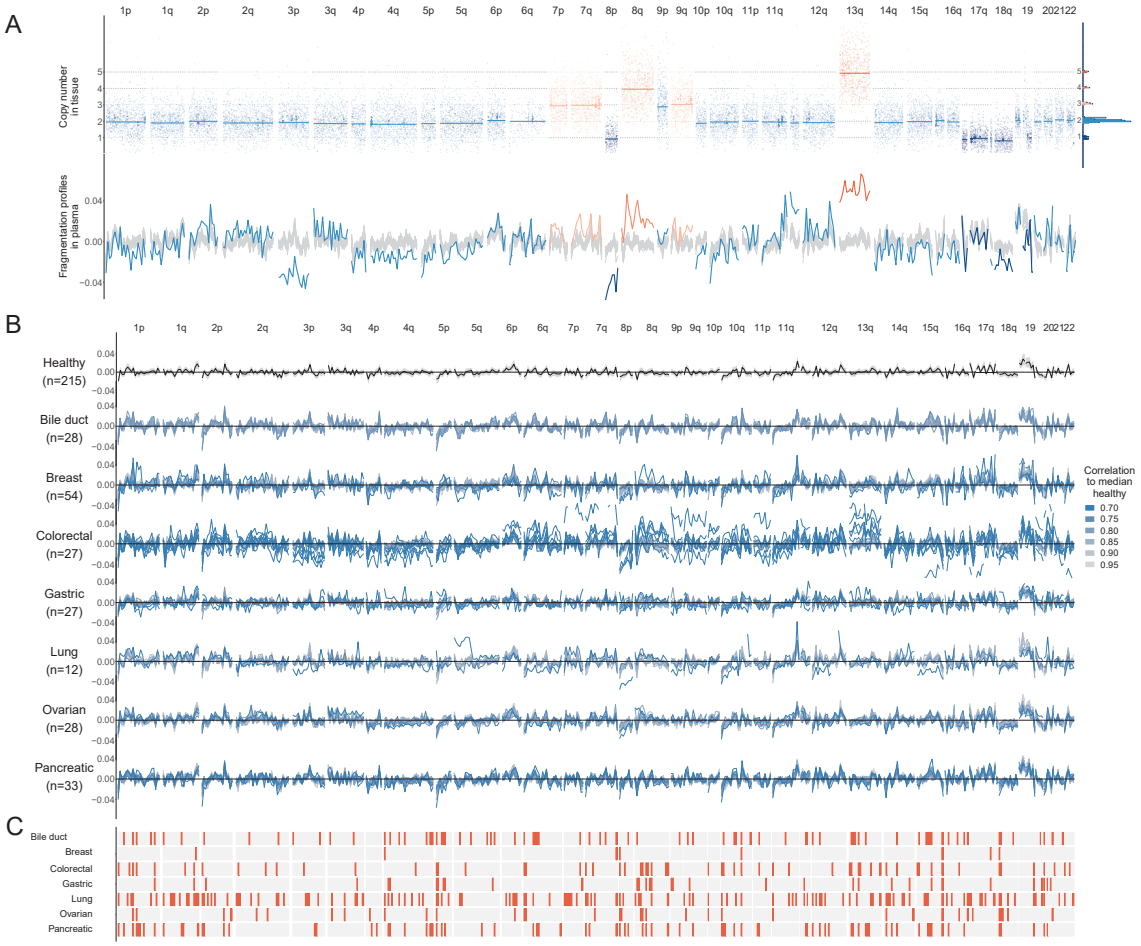


Figure 4.10. cfDNA fragmentation profiles in patients with cancer. cfDNA fragmentation profiles in patients with cancer. A) Fragmentation profiles (bottom) in the context of known copy number changes (top) in a colorectal cancer patient where parallel analyses of tumor tissue were performed. The distribution of segment means corresponding to the inferred integer copy numbers are shown at top right in the indicated colors. Altered fragmentation profiles were present in regions of the genome that were copy neutral and were further affected in regions with copy number changes. B) GC adjusted fragmentation profiles from 1-2x whole genome sequencing for healthy individuals and patients with cancer are depicted per cancer type using 5 Mb windows. The median healthy profile is indicated in black and the 98% confidence band is shown in gray. For patients with cancer, individual profiles are colored based on their Pearson correlation to the healthy median. C) Windows are indicated in orange if more than 10% of the cancer samples had a fragment ratio more than three standard deviations from the median healthy fragment ratio. These analyses highlight the multitude of position dependent alterations across the genome in cfDNA of individuals with cancer.

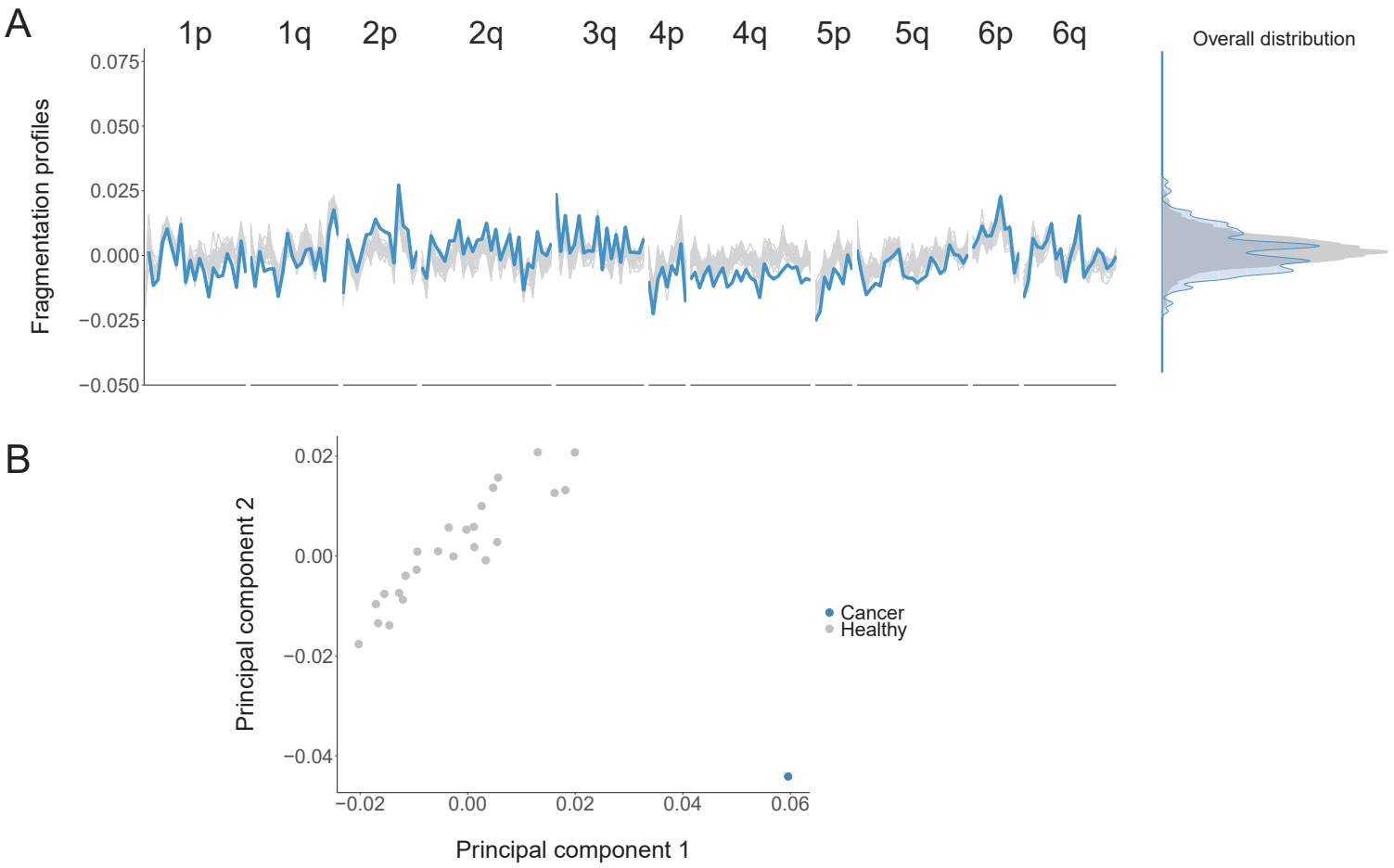


Figure 4.11. Profiles of cfDNA fragment lengths in copy neutral regions in healthy individuals and one patient with colorectal cancer. A) The fragmentation profile in 211 copy neutral windows in chromosomes 1-6 for 25 randomly selected healthy individuals (gray). For a patient with colorectal cancer (CGCRC291) with an estimated mutant allele fraction of 20%, we diluted the cancer fragment length profile to an approximate 10% tumor contribution (blue). A-B) While the marginal densities of the fragment profiles for the healthy samples and cancer patient show substantial overlap (a, right), the fragmentation profiles are different as can be seen visualization of the fragmentation profiles (A, left) and by the separation of the colorectal cancer patient from the healthy samples (n=25) in a principal component analysis (B).

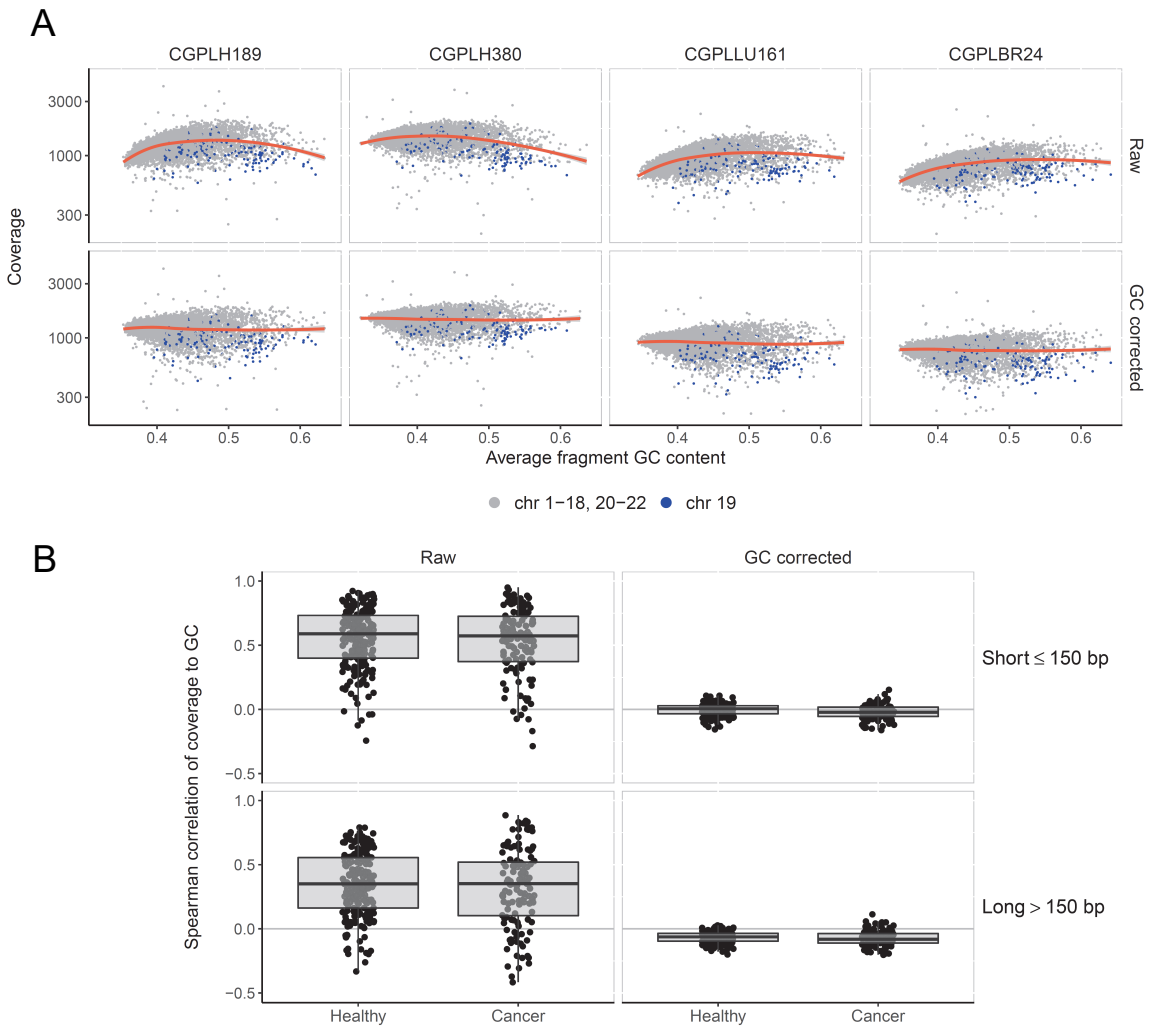


Figure 4.12. Genome-wide GC correction of cfDNA fragments. To estimate and control for the effects of GC content on sequencing coverage, we calculated coverage in non-overlapping 100kb genomic windows across the autosomes. For each window, we calculated the average GC of the aligned fragments. A) Loess smoothing of raw coverage (top row) for two randomly selected healthy subjects (CGPLH189 and CGPLH380) and two cancer patients (CGPLLU161 and CGPLBR24) with undetectable aneuploidy (PA score < 2.35). After subtracting the average coverage predicted by the loess model, the residuals were rescaled to the median autosomal coverage (bottom row). As fragment length may also result in coverage biases, we performed this GC correction procedure separately for short (≤ 150 bp) and long (> 150 bp) fragments. While the 100 kb bins on chromosome 19 (blue points) consistently have less coverage than predicted by the loess model, we did not implement a chromosome-specific correction as such an approach would remove the effects of chromosomal copy number on coverage. B) Overall, we found a limited correlation between short or long fragment coverage and GC content after correction among healthy subjects (n=211, inter-quartile range: -0.03-0.03) and cancer patients (n=128, inter-quartile range: -0.06-0.02) with a PA score <3. Box plots depict minimum, 25th percentile, median, 75th percentile, and maximum values.

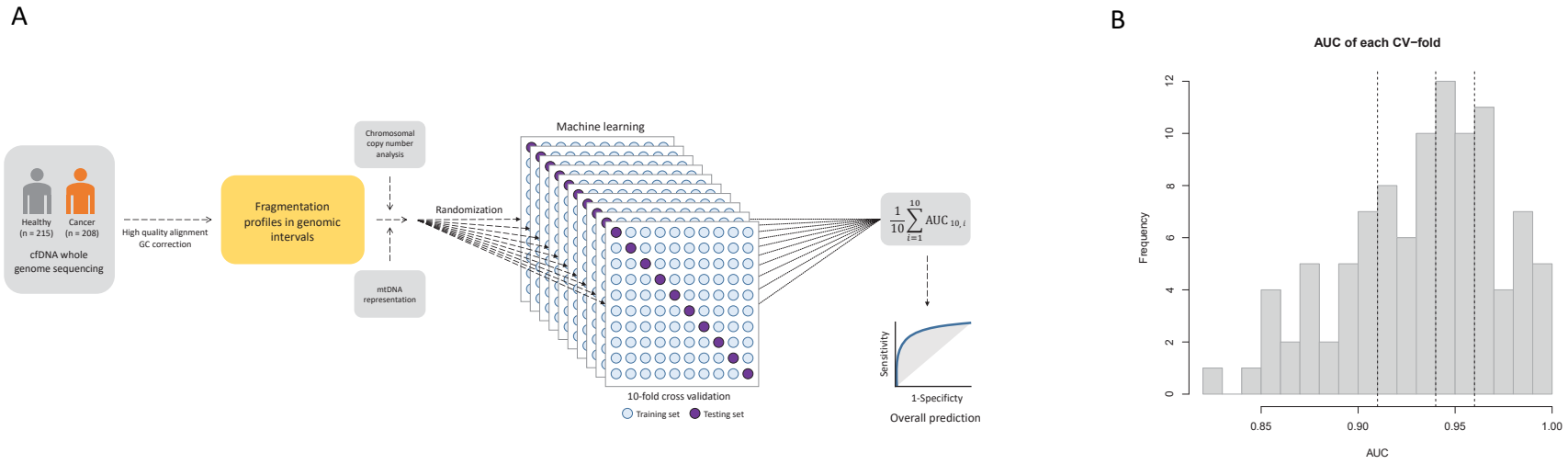


Figure 4.13. Machine learning model. A) We used gradient tree boosting machine learning to examine whether cfDNA can be categorized as having characteristics of a cancer patient or healthy individual. The machine learning model included fragmentation size and coverage characteristics in windows throughout the genome, as well as chromosomal arm and mitochondrial DNA copy numbers. We employed a 10-fold cross-validation approach in which each sample is randomly assigned to a fold and 9 of the folds (90% of the data) are used for training and one-fold (10% of the data) is used for testing. The prediction accuracy from a single cross-validation is an average over the 10 possible combinations of test and training sets. As this prediction accuracy can reflect bias from the initial randomization of patients, we repeat the entire procedure, including the randomization of patients to folds, 10 times. For all cases, feature selection and model estimation were performed on training data and were validated on test data and the test data were never used for feature selection. Ultimately, we obtained a DELFI score that could be used to classify individuals as likely healthy or having cancer. B) Distribution of AUCs across the repeated 10-fold cross-validation. The 25th, 50th, and 75th percentiles of the 100 AUCs for the cohort of 215 healthy individuals and 208 patients with cancer are indicated dashed lines.

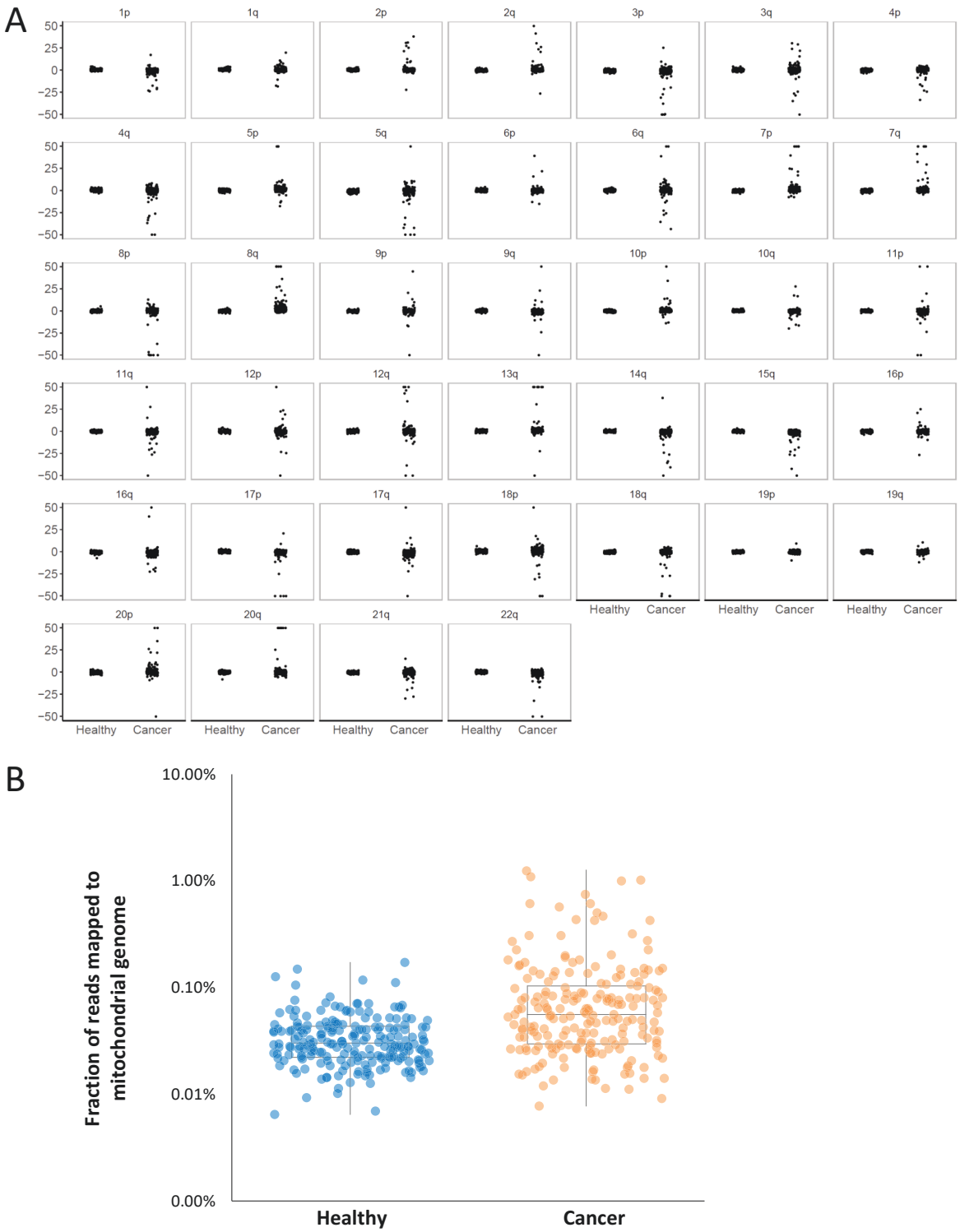


Figure 4.14. Whole-genome analyses of chromosomal arm copy number changes and mitochondrial genome representation. A) Z scores for each autosome arm are depicted for healthy individuals (n=215) and patients with cancer (n=208). The vertical axis depicts normal copy at zero with positive and negative values indicating arm gains and losses, respectively. Z scores greater than 50 or less than -50 are thresholded at the indicated values. B) The fraction of reads mapping to the mitochondrial genome is depicted for healthy individuals (n=215) and patients with cancer (n=208). Box plots depict the minimum, 25th percentile, median, 75th percentile, and maximum values.

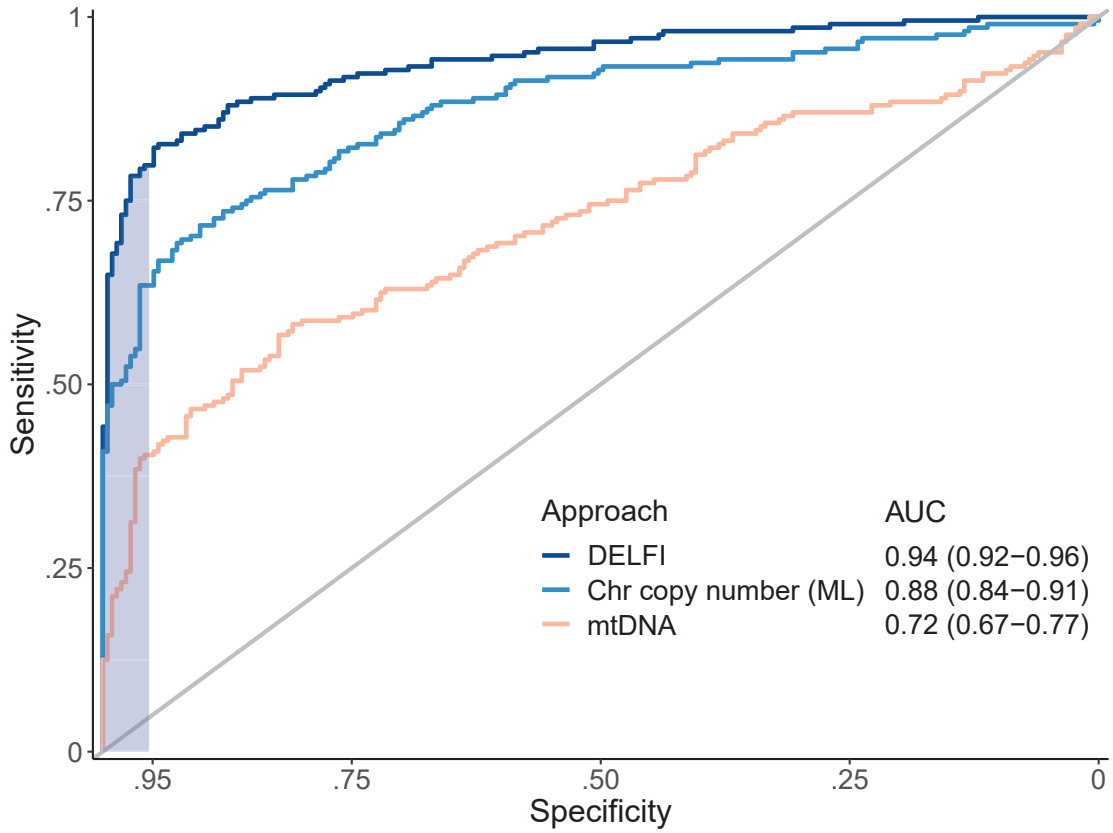


Figure 4.15. Detection of cancer using DELFI. Receiver operator characteristics for detection of cancer using cfDNA fragmentation profiles and other genome-wide features in a machine learning approach are depicted for a cohort of 215 healthy individuals and 208 patients with cancer (DELFI, AUC = 0.94), with ≥ 95% specificity shaded in blue. Machine learning analyses of chromosomal arm copy number (Chr copy number (ML)), and mitochondrial genome copy number analyses (mtDNA), are shown in the indicated colors.

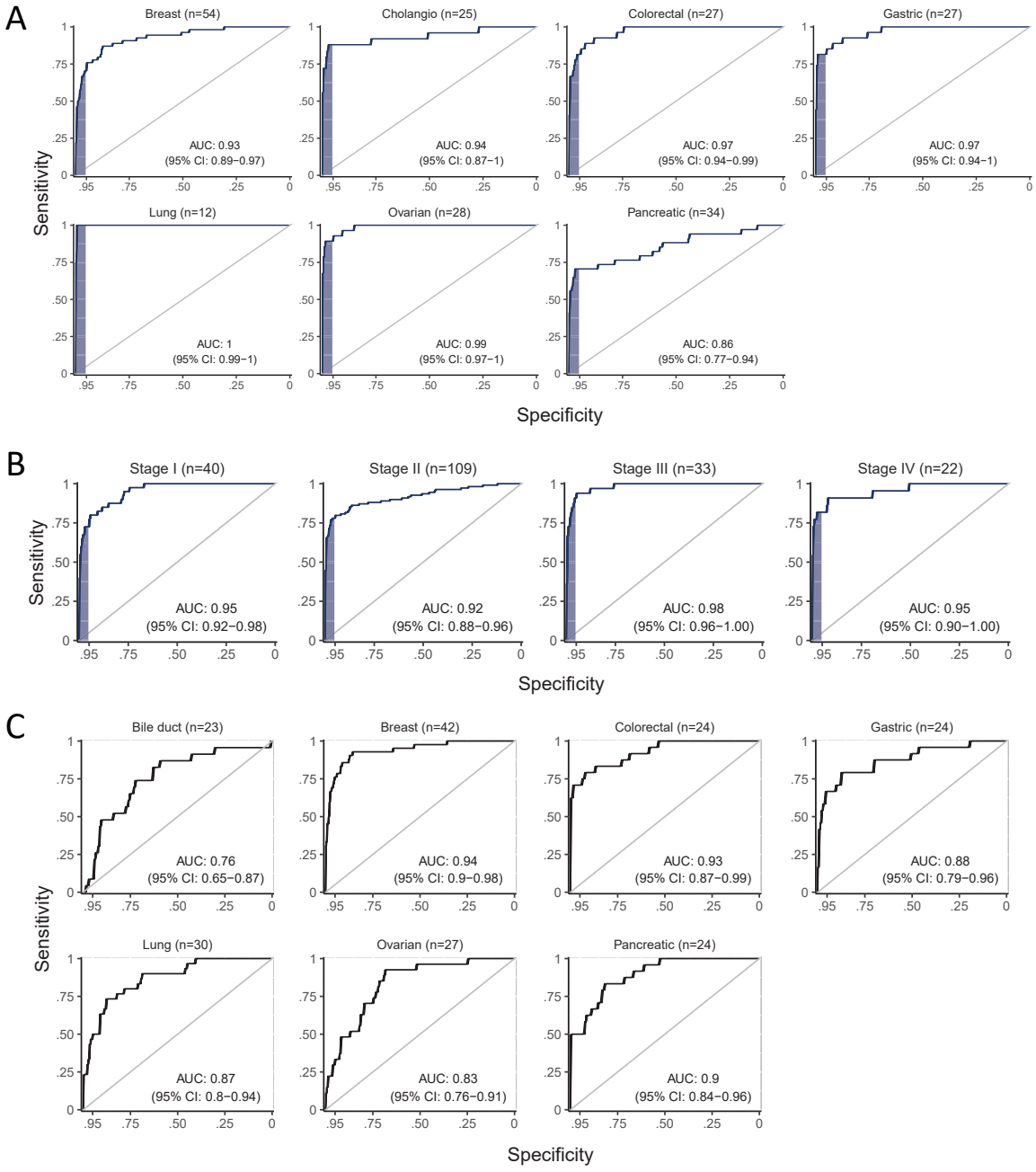


Figure 4.16. DELFI detection of cancer and tissue of origin prediction. DELFI detection of cancer and tissue of origin prediction. A) Analyses of individual cancer types using the DELFI-combined approach had AUCs ranging from 0.86 to >0.99. B) Receiver operatorcharacteristics for detection of cancer using cfDNA fragmentation profiles and other genome-wide features in a machine learning approach are depicted for a cohort of 215 healthy individuals and each stage of 208 patients with cancer with ≥ 95% specificity shaded in blue. C) Receiver operator characteristics for DELFI tissue prediction of bile duct, breast, colorectal, gastric, lung, ovarian, or pancreatic cancer are depicted. In order to increase sample sizes within cancer type classes, we included cases detected with a 90% specificity, and the lung cancer cohort was supplemented with the addition of baseline cfDNA data from 18 lung cancer patients with prior treatment. D) DELFI tissue of origin prediction.

Detection approach*		Patients analyzed	Patients detected	Fraction of patients detected	95% CI
DELFI		126	103	82%	74%-88%
Mutations		126	83	66%	57%-74%
DELFI and Mutations		126	115	91%	85%-96%
Stage	I	32	27	84%	67%-95%
	II	52	48	92%	81%-98%
	III	25	23	92%	74%-99%
	IV	16	16	100%	79%-100%

*Cancer detection using DELFI, sequence mutations, and the combination of DELFI and mutations was performed at specificities of 98%, >99%, and 98%, respectively. Per stage sensitivities are included for all cases except for one patient with stage X.

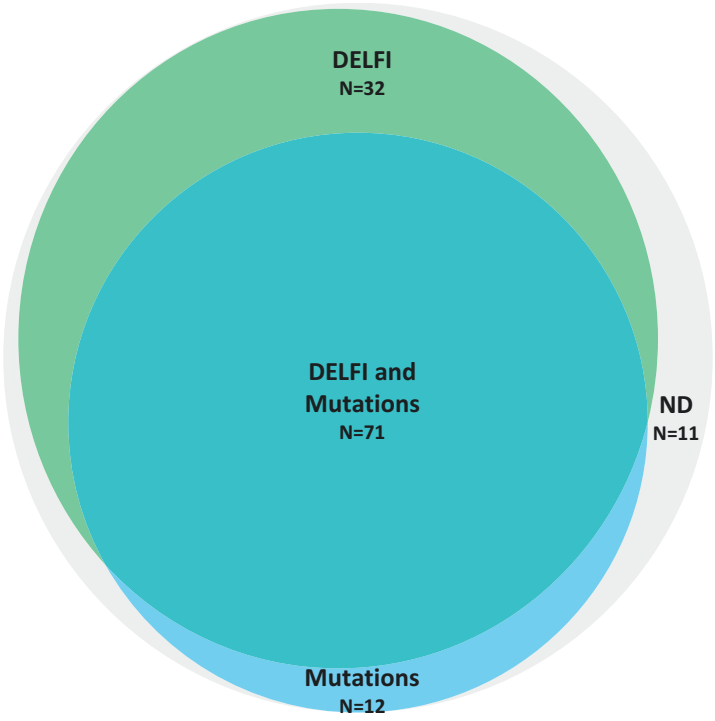


Figure 4.17. Detection of cancer using DELFI and mutation-based cfDNA approaches. Detection of cancer using DELFI and mutation-based cfDNA approaches. DELFI (green) and targeted sequencing10 for mutation identification (blue) were performed independently in a cohort of 126 patients with breast, bile duct, colorectal, gastric, lung, or ovarian cancer. The number of individuals detected by each approach and in combination are indicated for DELFI detection with a specificity of 98%, targeted sequencing specificity at >99%, and a combined specificity of 98%. ND indicates not detected.

Table 4.1. Summary of patients and samples analyzed.

Patient	Patient Type	Sample Type	Age at Diagnosis	Sex	Stage	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)
CGPLPA114	Bile Duct Cancer	cfDNA	NA	F	II	Intra Pancreatic Bile Duct	Intra Pancreatic Bile Duct	NA	None	4.8	26.43	26.43
CGPLPA115	Bile Duct Cancer	cfDNA	NA	M	IV	Intra Hepatic Bile Duct	Intra Hepatic Bile Duct	NA	NA	5.0	31.41	31.41
CGPLPA117	Bile Duct Cancer	cfDNA	NA	M	II	Intra Pancreatic Bile Duct	Intra Pancreatic Bile Duct	NA	None	3.4	2.29	2.29
CGPLPA118	Bile Duct Cancer	cfDNA	68	F	I	Bile Duct	Intra-Ampullary Bile Duct	NA	None	3.8	9.93	9.93
CGPLPA122	Bile Duct Cancer	cfDNA	62	F	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	3.8	66.54	32.89
CGPLPA124	Bile Duct Cancer	cfDNA	83	F	II	Bile Duct	Intra-Ampullary Bile Duct	moderate	None	4.6	29.24	27.17
CGPLPA125	Bile Duct Cancer	cfDNA	58	M	II	Bile Duct	Intra-Pancreatic Bile Duct	poor	None	2.7	8.31	8.31
CGPLPA126	Bile Duct Cancer	cfDNA	60	M	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.3	80.56	29.07
CGPLPA127	Bile Duct Cancer	cfDNA	71	F	IV	Bile Duct	Extra-Pancreatic Bile Duct	NA	NA	3.0	20.60	20.60
CGPLPA128	Bile Duct Cancer	cfDNA	67	M	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	3.9	5.91	5.91
CGPLPA129	Bile Duct Cancer	cfDNA	56	F	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.6	27.07	27.07
CGPLPA130	Bile Duct Cancer	cfDNA	82	F	II	Bile Duct	Intra-Ampullary Bile Duct	well	None	4.0	4.34	4.34
CGPLPA131	Bile Duct Cancer	cfDNA	71	M	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	3.9	68.95	32.05
CGPLPA134	Bile Duct Cancer	cfDNA	68	M	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.1	58.08	30.49
CGPLPA135	Bile Duct Cancer	cfDNA	67	F	I	Bile Duct	Intra-Pancreatic Bile Duct	NA	NA	3.9	4.22	4.22
CGPLPA136	Bile Duct Cancer	cfDNA	69	F	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.1	20.23	20.23
CGPLPA137	Bile Duct Cancer	cfDNA	NA	M	II	Bile Duct	Bile Duct	NA	NA	4.0	5.75	5.75
CGPLPA139	Bile Duct Cancer	cfDNA	NA	M	IV	Bile Duct	Bile Duct	NA	NA	4.0	14.89	14.89
CGPLPA140	Bile Duct Cancer	cfDNA	52	M	II	Extra Hepatic Bile Duct	Intra-Pancreatic Bile Duct	Poor	None	4.7	29.34	26.60
CGPLPA141	Bile Duct Cancer	cfDNA	68	F	II	Extra Hepatic Bile Duct	Intra-Pancreatic Bile Duct	Moderate	None	2.8	53.67	44.64

CGPLPA155	Bile Duct Cancer	cfDNA	NA	F	II	Bile Duct	Bile Duct	NA	NA	4.0	25.72	25.72
CGPLPA165	Bile Duct Cancer	cfDNA	42	M	I	Bile Duct	Intra-Pancreatic Bile Duct with Medullary Features	well	None	3.9	10.48	10.48
CGPLPA168	Bile Duct Cancer	cfDNA	58	M	II	Bile Duct	Extra-Pancreatic Bile Duct	NA	NA	3.6	139.12	34.72
CGPLPA184	Bile Duct Cancer	cfDNA	75	F	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	NA	NA	NA
CGPLPA187	Bile Duct Cancer	cfDNA	67	F	II	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	NA	NA	NA
CGPLBR100	Breast Cancer	cfDNA	44	F	III	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.0	4.25	4.25
CGPLBR101	Breast Cancer	cfDNA	46	F	II	Left Breast	Infiltrating Lobular Carcinoma	Moderate	None	4.0	37.88	37.88
CGPLBR102	Breast Cancer	cfDNA	47	F	II	Right Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.6	13.67	13.67
CGPLBR103	Breast Cancer	cfDNA	48	F	II	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.6	7.11	7.11
CGPLBR104	Breast Cancer	cfDNA	68	F	II	Right Breast	Infiltrating Lobular Carcinoma	Moderate	None	4.7	19.89	19.89
CGPLBR12	Breast Cancer	cfDNA	NA	F	III	Breast	Ductal Carcinoma insitu with Microinvasion	NA	NA	4.3	4.21	4.21
CGPLBR18	Breast Cancer	cfDNA	NA	F	III	Breast	Infiltrating Lobular Carcinoma	NA	NA	4.1	40.39	30.49
CGPLBR23	Breast Cancer	cfDNA	53	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.7	20.09	20.09
CGPLBR24	Breast Cancer	cfDNA	53	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	3.6	58.33	34.72
CGPLBR28	Breast Cancer	cfDNA	59	F	III	Breast	Infiltrating Ductal Carcinoma	NA	None	4.2	12.86	12.86
CGPLBR30	Breast Cancer	cfDNA	61	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.1	59.73	30.49
CGPLBR31	Breast Cancer	cfDNA	54	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	3.4	23.94	23.94
CGPLBR32	Breast Cancer	cfDNA	NA	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.4	71.23	28.41
CGPLBR33	Breast Cancer	cfDNA	47	F	II	Breast	Infiltrating Lobular Carcinoma	NA	None	4.4	11.00	11.00

CGPLBR34	Breast Cancer	cfDNA	60	F	II	Breast	Infiltrating Lobular Carcinoma	NA	None	4.4	23.61	23.61
CGPLBR35	Breast Cancer	cfDNA	43	F	II	Breast	Ductal Carcinoma insitu with Microinvasion	NA	None	4.5	22.58	22.58
CGPLBR36	Breast Cancer	cfDNA	36	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.4	17.73	17.73
CGPLBR37	Breast Cancer	cfDNA	58	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.4	9.39	9.39
CGPLBR38	Breast Cancer	cfDNA	54	F	I	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.0	5.77	5.77
CGPLBR40	Breast Cancer	cfDNA	66	F	III	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	4.6	15.69	15.69
CGPLBR41	Breast Cancer	cfDNA	51	F	III	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.5	11.56	11.56
CGPLBR45	Breast Cancer	cfDNA	57	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	20.36	20.36
CGPLBR46	Breast Cancer	cfDNA	54	F	III	Breast	Infiltrating Ductal Carcinoma	NA	None	3.5	20.17	20.17
CGPLBR47	Breast Cancer	cfDNA	54	F	I	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	13.89	13.89
CGPLBR48	Breast Cancer	cfDNA	47	F	II	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	3.9	7.07	7.07
CGPLBR49	Breast Cancer	cfDNA	37	F	II	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	4.0	5.74	5.74
CGPLBR50	Breast Cancer	cfDNA	51	F	I	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	45.58	27.78
CGPLBR51	Breast Cancer	cfDNA	53	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.0	8.83	8.83
CGPLBR52	Breast Cancer	cfDNA	68	F	III	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	80.71	27.78
CGPLBR55	Breast Cancer	cfDNA	53	F	III	Right Breast	Infiltrating Ductal Carcinoma	Poor	None	4.3	4.57	4.57
CGPLBR56	Breast Cancer	cfDNA	56	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	22.16	22.16
CGPLBR57	Breast Cancer	cfDNA	54	F	III	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.3	4.02	4.02
CGPLBR59	Breast Cancer	cfDNA	42	F	I	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.1	8.24	8.24
CGPLBR60	Breast Cancer	cfDNA	61	F	II	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	11.09	11.09
CGPLBR61	Breast Cancer	cfDNA	67	F	II	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.1	13.25	13.25
CGPLBR63	Breast Cancer	cfDNA	48	F	II	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.0	6.19	6.19

CGPLBR65	Breast Cancer	cfDNA	50	F	II	Left Breast	Infiltrating Ductal Carcinoma	NA	None	3.5	41.75	35.71
CGPLBR68	Breast Cancer	cfDNA	64	F	III	Breast	Infiltrating Ductal Carcinoma	Poor	None	3.4	10.41	10.41
CGPLBR69	Breast Cancer	cfDNA	43	F	II	Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.4	4.07	4.07
CGPLBR70	Breast Cancer	cfDNA	60	F	II	Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.4	11.94	11.94
CGPLBR71	Breast Cancer	cfDNA	65	F	II	Breast	Infiltrating Ductal Carcinoma	Poor	None	3.1	7.64	7.64
CGPLBR72	Breast Cancer	cfDNA	67	F	II	Breast	Infiltrating Ductal Carcinoma	Well	None	3.9	4.43	4.43
CGPLBR73	Breast Cancer	cfDNA	60	F	II	Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.3	14.69	14.69
CGPLBR76	Breast Cancer	cfDNA	53	F	II	Right Breast	Infiltrating Ductal Carcinoma	Well	None	4.9	8.71	8.71
CGPLBR81	Breast Cancer	cfDNA	54	F	II	Breast	Infiltrating Ductal Carcinoma	NA	None	2.5	83.14	50.00
CGPLBR82	Breast Cancer	cfDNA	70	F	I	Right Breast	Infiltrating Lobular Carcinoma	Moderate	None	4.8	23.39	23.39
CGPLBR83	Breast Cancer	cfDNA	53	F	II	Right Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.7	100.17	100.17
CGPLBR84	Breast Cancer	cfDNA	NA	F	III	Breast	Infiltrating Ductal Carcinoma	NA	NA	3.6	16.95	16.95
CGPLBR87	Breast Cancer	cfDNA	80	F	II	Right Breast	Papillary Carcinoma	Well	None	3.6	277.39	69.44
CGPLBR88	Breast Cancer	cfDNA	48	F	II	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	3.6	49.75	49.75
CGPLBR90	Breast Cancer	cfDNA	51	F	II	Right Breast	Infiltrating Ductal Carcinoma	NA	None	3.0	14.24	14.24
CGPLBR91	Breast Cancer	cfDNA	62	F	III	Breast	Infiltrating Lobular Carcinoma	Poor	None	3.2	22.41	22.41
CGPLBR92	Breast Cancer	cfDNA	58	F	II	Breast	Infiltrating Medullary Carcinoma	Poor	None	3.1	81.00	81.00
CGPLBR93	Breast Cancer	cfDNA	59	F	II	Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.3	27.94	27.94
CGCRC291	Colorectal Cancer	cfDNA	69	F	IV	Coecum	Adenocarcinoma	Moderate	Synchronous Liver	7.9	7.80	7.80
CGCRC292	Colorectal Cancer	cfDNA	51	M	IV	Sigmoid Colon	Adenocarcinoma	Moderate	Synchronous Liver, Lung	7.9	6.73	6.73
CGCRC293	Colorectal Cancer	cfDNA	55	M	IV	Rectum	Adenocarcinoma	Moderate	Synchronous Liver	7.2	3.83	3.83
CGCRC294	Colorectal Cancer	cfDNA	67	F	II	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.4	18.87	18.87

CGCRC296	Colorectal Cancer	cfDNA	76	F	II	Coecum	Adenocarcinoma	Poor	None	4.3	31.24	31.24
CGCRC299	Colorectal Cancer	cfDNA	71	M	I	Rectum	Adenocarcinoma	Moderate	None	8.8	10.18	10.18
CGCRC300	Colorectal Cancer	cfDNA	65	M	I	Rectum	Adenocarcinoma	Moderate	None	4.3	10.48	10.48
CGCRC301	Colorectal Cancer	cfDNA	76	F	I	Rectum	Adenocarcinoma	Moderate	None	4.1	6.51	6.51
CGCRC302	Colorectal Cancer	cfDNA	73	M	II	Transverse Colon	Adenocarcinoma	Moderate	None	4.3	52.13	52.13
CGCRC304	Colorectal Cancer	cfDNA	86	F	II	Rectum	Adenocarcinoma	Moderate	None	4.1	30.19	30.19
CGCRC305	Colorectal Cancer	cfDNA	83	F	II	Transverse Colon	Adenocarcinoma	Moderate	None	8.6	9.10	9.10
CGCRC306	Colorectal Cancer	cfDNA	80	F	II	Ascending Colon	Adenocarcinoma	Moderate	None	4.5	24.31	24.31
CGCRC307	Colorectal Cancer	cfDNA	78	F	II	Ascending Colon	Adenocarcinoma	Moderate	None	8.5	14.26	14.26
CGCRC308	Colorectal Cancer	cfDNA	72	F	III	Ascending Colon	Adenocarcinoma	Moderate	None	4.3	46.87	46.87
CGCRC311	Colorectal Cancer	cfDNA	59	M	I	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.5	3.91	3.91
CGCRC315	Colorectal Cancer	cfDNA	74	M	III	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.6	9.67	9.67
CGCRC316	Colorectal Cancer	cfDNA	80	M	III	Transverse Colon	Adenocarcinoma	Moderate	None	4.9	52.16	52.16
CGCRC317	Colorectal Cancer	cfDNA	74	M	III	Descending Colon	Adenocarcinoma	Moderate	None	8.8	16.08	16.08
CGCRC318	Colorectal Cancer	cfDNA	81	M	I	Coecum	Adenocarcinoma	Moderate	None	9.8	18.24	18.24
CGCRC319	Colorectal Cancer	cfDNA	80	F	III	Descending Colon	Adenocarcinoma	Moderate	None	4.2	53.54	53.54
CGCRC320	Colorectal Cancer	cfDNA	73	F	I	Ascending Colon	Adenocarcinoma	Moderate	None	4.5	30.37	30.37
CGCRC321	Colorectal Cancer	cfDNA	68	M	I	Rectum	Adenocarcinoma	Moderate	None	9.3	4.25	4.25
CGCRC333	Colorectal Cancer	cfDNA	NA	F	IV	Colon/Rectum	Adenocarcinoma	NA	Liver	4.0	113.88	113.88
CGCRC336	Colorectal Cancer	cfDNA	NA	M	IV	Colon/Rectum	Adenocarcinoma	NA	Liver	4.4	211.74	211.74
CGCRC338	Colorectal Cancer	cfDNA	NA	F	IV	Colon/Rectum	Adenocarcinoma	NA	Liver	2.3	109.76	109.76
CGCRC341	Colorectal Cancer	cfDNA	NA	F	IV	Colon/Rectum	Adenocarcinoma	NA	Liver	4.6	156.62	156.62
CGCRC342	Colorectal Cancer	cfDNA	NA	M	IV	Colon/Rectum	Adenocarcinoma	NA	Liver	3.9	56.09	56.09
CGPLPA113	Duodenal Cancer	cfDNA	71	M	I	Intra Pancreatic Bile Duct	Intra Pancreatic Bile Duct	NA	None	4.8	8.24	8.24
CGST102	Gastric cancer	cfDNA	76	F	II	Stomach	Tubular Adenocarcinoma	Moderate	None	4.1	8.03	8.03
CGST11	Gastric cancer	cfDNA	49	M	IV	Stomach	Mixed Carcinoma	Moderate	None	3.8	3.57	3.57

CGST110	Gastric cancer	cfDNA	77	M	III	Stomach	Tubular Adenocarcinoma	Moderate	None	3.8	5.00	5.00
CGST114	Gastric cancer	cfDNA	65	M	III	Stomach	Tubular Adenocarcinoma	Poor	None	4.4	10.35	10.35
CGST13	Gastric cancer	cfDNA	72	F	II	Stomach	Signet Ring Cell Carcinoma	Poor	None	4.4	24.33	24.33
CGST131	Gastric cancer	cfDNA	63	M	III	Stomach	Signet ring cell carcinoma	Poor	None	4.0	4.28	4.28
CGST141	Gastric cancer	cfDNA	33	F	III	Stomach	Signet Ring Cell Carcinoma	Poor	None	4.4	10.84	10.84
CGST16	Gastric cancer	cfDNA	78	M	III	Stomach	Tubular Adenocarcinoma	Poor	None	4.0	40.69	40.69
CGST18	Gastric cancer	cfDNA	56	M	II	Stomach	Mucinous Adenocarcinoma	Well	None	4.3	9.78	9.78
CGST21	Gastric cancer	cfDNA	39	M	II	Stomach	Papillary Adenocarcinoma	Moderate	None	4.0	0.83	0.83
CGST26	Gastric cancer	cfDNA	51	M	IV	Stomach	Signet ring cell carcinoma	Poor	None	3.5	5.56	5.56
CGST28	Gastric cancer	cfDNA	55	M	X	Stomach	Undifferentiated Carcinoma	Poor	None	4.0	5.86	5.86
CGST30	Gastric cancer	cfDNA	64	F	III	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.0	4.22	4.22
CGST32	Gastric cancer	cfDNA	67	M	II	Stomach	Tubular Adenocarcinoma	Moderate	None	4.0	11.49	11.49
CGST33	Gastric cancer	cfDNA	61	M	I	Stomach	Tubular Adenocarcinoma	Moderate	None	3.5	5.71	5.71
CGST38	Gastric cancer	cfDNA	71	F	X	Stomach	Mucinous adenocarcinoma	NA	None	4.0	NA	NA
CGST39	Gastric cancer	cfDNA	51	M	IV	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	20.69	20.69
CGST41	Gastric cancer	cfDNA	66	F	IV	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	7.83	7.83
CGST45	Gastric cancer	cfDNA	41	F	II	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.8	7.14	7.14
CGST47	Gastric cancer	cfDNA	74	F	I	Stomach	Tubular Adenocarcinoma	Moderate	None	4.0	4.55	4.55
CGST48	Gastric cancer	cfDNA	62	M	IV	Stomach	Tubular Adenocarcinoma	Poor	None	4.5	8.79	8.79
CGST53	Gastric cancer	cfDNA	70	M	X	Stomach	Stomach	NA	None	3.8	15.82	15.82
CGST58	Gastric cancer	cfDNA	58	M	III	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.8	19.81	19.81
CGST67	Gastric cancer	cfDNA	69	M	I	Stomach	Tubular adenocarcinoma	Moderate	None	3.0	23.01	23.01
CGST77	Gastric cancer	cfDNA	70	M	IV	Stomach	Tubular adenocarcinoma	Moderate	None	4.5	15.09	15.09

CGST80	Gastric cancer	cfDNA	58	M	III	Stomach	Mucinous Adenocarcinoma	Poor	None	4.5	8.56	8.56
CGST81	Gastric cancer	cfDNA	64	F	I	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	37.32	37.32
CGH14	Healthy	Human adult elutriated lymphocytes	NA	M	NA	NA	NA	NA	NA	NA	NA	NA
CGH15	Healthy	Human adult elutriated lymphocytes	NA	F	NA	NA	NA	NA	NA	NA	NA	NA
CGPLH189	Healthy	cfDNA	74	M	NA	NA	NA	NA	NA	5.0	5.84	5.84
CGPLH190	Healthy	cfDNA	67	M	NA	NA	NA	NA	NA	4.7	18.07	18.07
CGPLH192	Healthy	cfDNA	74	M	NA	NA	NA	NA	NA	4.7	12.19	12.19
CGPLH193	Healthy	cfDNA	72	F	NA	NA	NA	NA	NA	5.0	5.47	5.47
CGPLH194	Healthy	cfDNA	75	F	NA	NA	NA	NA	NA	5.0	9.98	9.98
CGPLH196	Healthy	cfDNA	64	M	NA	NA	NA	NA	NA	5.0	11.69	11.69
CGPLH197	Healthy	cfDNA	74	M	NA	NA	NA	NA	NA	5.0	5.69	5.69
CGPLH198	Healthy	cfDNA	66	M	NA	NA	NA	NA	NA	5.0	4.36	4.36
CGPLH199	Healthy	cfDNA	75	F	NA	NA	NA	NA	NA	5.0	9.77	9.77
CGPLH200	Healthy	cfDNA	51	M	NA	NA	NA	NA	NA	5.0	5.60	5.60
CGPLH201	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	5.0	8.82	8.82
CGPLH202	Healthy	cfDNA	73	M	NA	NA	NA	NA	NA	5.0	5.54	5.54
CGPLH203	Healthy	cfDNA	59	M	NA	NA	NA	NA	NA	5.0	9.03	9.03
CGPLH205	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	5.0	4.74	4.74
CGPLH208	Healthy	cfDNA	75	F	NA	NA	NA	NA	NA	5.0	4.67	4.67
CGPLH209	Healthy	cfDNA	74	M	NA	NA	NA	NA	NA	5.0	5.15	5.15
CGPLH210	Healthy	cfDNA	75	M	NA	NA	NA	NA	NA	5.0	5.41	5.41
CGPLH211	Healthy	cfDNA	75	F	NA	NA	NA	NA	NA	5.0	6.24	6.24
CGPLH300	Healthy	cfDNA	72	F	NA	NA	NA	NA	NA	4.4	6.75	6.75
CGPLH307	Healthy	cfDNA	53	M	NA	NA	NA	NA	NA	4.5	3.50	3.50

CGPLH308	Healthy	cfDNA	60	M	NA	NA	NA	NA	NA	4.5	6.01	6.01
CGPLH309	Healthy	cfDNA	61	F	NA	NA	NA	NA	NA	4.5	5.21	5.21
CGPLH310	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.5	15.25	15.25
CGPLH311	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.5	4.47	4.47
CGPLH314	Healthy	cfDNA	59	M	NA	NA	NA	NA	NA	4.5	9.62	9.62
CGPLH314	Healthy	cfDNA, technical replicate	59	M	NA	NA	NA	NA	NA	4.4	16.24	16.24
CGPLH315	Healthy	cfDNA	59	F	NA	NA	NA	NA	NA	4.2	11.55	11.55
CGPLH316	Healthy	cfDNA	64	M	NA	NA	NA	NA	NA	4.5	28.92	27.78
CGPLH317	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.5	7.62	7.62
CGPLH319	Healthy	cfDNA	60	F	NA	NA	NA	NA	NA	4.2	4.41	4.41
CGPLH320	Healthy	cfDNA	75	F	NA	NA	NA	NA	NA	4.5	6.93	6.93
CGPLH322	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.2	8.17	8.17
CGPLH324	Healthy	cfDNA	59	F	NA	NA	NA	NA	NA	5.0	6.63	6.63
CGPLH325	Healthy	cfDNA	54	M	NA	NA	NA	NA	NA	4.6	4.15	4.15
CGPLH326	Healthy	cfDNA	67	F	NA	NA	NA	NA	NA	4.5	6.06	6.06
CGPLH327	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.8	1.24	1.24
CGPLH328	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.4	3.42	3.42
CGPLH328	Healthy	cfDNA, technical replicate	68	F	NA	NA	NA	NA	NA	4.9	5.47	5.47
CGPLH329	Healthy	cfDNA	59	M	NA	NA	NA	NA	NA	4.5	5.27	5.27
CGPLH330	Healthy	cfDNA	75	M	NA	NA	NA	NA	NA	4.3	10.21	10.21
CGPLH331	Healthy	cfDNA	55	M	NA	NA	NA	NA	NA	4.6	2.63	2.63
CGPLH331	Healthy	cfDNA, technical replicate	55	M	NA	NA	NA	NA	NA	4.3	4.15	4.15
CGPLH333	Healthy	cfDNA	60	M	NA	NA	NA	NA	NA	4.7	4.06	4.06
CGPLH335	Healthy	cfDNA	74	M	NA	NA	NA	NA	NA	4.4	9.39	9.39
CGPLH336	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.6	6.64	6.64
CGPLH337	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.2	4.48	4.48

CGPLH338	Healthy	cfDNA	75	M	NA	NA	NA	NA	NA	4.5	59.44	27.78
CGPLH339	Healthy	cfDNA	70	M	NA	NA	NA	NA	NA	4.5	12.27	12.27
CGPLH340	Healthy	cfDNA	62	M	NA	NA	NA	NA	NA	4.5	4.86	4.86
CGPLH341	Healthy	cfDNA	61	F	NA	NA	NA	NA	NA	4.1	7.62	7.62
CGPLH342	Healthy	cfDNA	49	F	NA	NA	NA	NA	NA	4.2	18.29	18.29
CGPLH343	Healthy	cfDNA	58	M	NA	NA	NA	NA	NA	4.5	3.49	3.49
CGPLH344	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.2	8.41	8.41
CGPLH345	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.5	9.73	9.73
CGPLH346	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	7.86	7.86
CGPLH35	Healthy	cfDNA	48	F	NA	NA	NA	NA	NA	4.0	13.15	13.15
CGPLH350	Healthy	cfDNA	65	M	NA	NA	NA	NA	NA	3.5	6.09	6.09
CGPLH351	Healthy	cfDNA	71	M	NA	NA	NA	NA	NA	4.0	15.91	15.91
CGPLH352	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.2	6.47	6.47
CGPLH353	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.2	4.47	4.47
CGPLH354	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.2	17.49	17.49
CGPLH355	Healthy	cfDNA	70	M	NA	NA	NA	NA	NA	4.2	11.58	11.58
CGPLH356	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	3.94	3.94
CGPLH357	Healthy	cfDNA	52	F	NA	NA	NA	NA	NA	4.2	11.79	11.79
CGPLH358	Healthy	cfDNA	55	M	NA	NA	NA	NA	NA	4.2	21.06	21.06
CGPLH36	Healthy	cfDNA	36	F	NA	NA	NA	NA	NA	4.0	13.00	13.00
CGPLH360	Healthy	cfDNA	60	M	NA	NA	NA	NA	NA	4.2	3.48	3.48
CGPLH361	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.3	6.98	6.98
CGPLH362	Healthy	cfDNA	72	F	NA	NA	NA	NA	NA	4.4	8.49	8.49
CGPLH363	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.5	4.44	4.44
CGPLH364	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	17.31	17.31
CGPLH365	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.5	0.55	0.55
CGPLH366	Healthy	cfDNA	61	M	NA	NA	NA	NA	NA	4.5	4.88	4.88
CGPLH367	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	6.48	6.48

CGPLH368	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.3	2.63	2.63
CGPLH369	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.3	10.18	10.18
CGPLH369	Healthy	cfDNA, technical replicate	55	F	NA	NA	NA	NA	NA	4.4	10.71	10.71
CGPLH37	Healthy	cfDNA	39	F	NA	NA	NA	NA	NA	4.0	9.73	9.73
CGPLH370	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	7.22	7.22
CGPLH371	Healthy	cfDNA	57	F	NA	NA	NA	NA	NA	4.6	5.62	5.62
CGPLH380	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.2	6.61	6.61
CGPLH381	Healthy	cfDNA	56	F	NA	NA	NA	NA	NA	4.2	27.38	27.38
CGPLH382	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.5	11.58	11.58
CGPLH383	Healthy	cfDNA	62	F	NA	NA	NA	NA	NA	4.5	25.50	25.50
CGPLH384	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.5	15.66	15.66
CGPLH385	Healthy	cfDNA	69	M	NA	NA	NA	NA	NA	4.5	19.35	19.35
CGPLH386	Healthy	cfDNA	62	M	NA	NA	NA	NA	NA	4.5	6.46	6.46
CGPLH386	Healthy	cfDNA, technical replicate	62	M	NA	NA	NA	NA	NA	4.6	6.54	6.54
CGPLH387	Healthy	cfDNA	71	F	NA	NA	NA	NA	NA	4.5	6.19	6.19
CGPLH388	Healthy	cfDNA	57	F	NA	NA	NA	NA	NA	4.5	6.62	6.62
CGPLH389	Healthy	cfDNA	73	F	NA	NA	NA	NA	NA	4.6	14.78	14.78
CGPLH390	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	12.14	12.14
CGPLH391	Healthy	cfDNA	58	M	NA	NA	NA	NA	NA	4.5	8.88	8.88
CGPLH391	Healthy	cfDNA, technical replicate	58	M	NA	NA	NA	NA	NA	4.5	8.37	8.37
CGPLH392	Healthy	cfDNA	57	F	NA	NA	NA	NA	NA	4.5	8.39	8.39
CGPLH393	Healthy	cfDNA	54	M	NA	NA	NA	NA	NA	4.5	5.27	5.27
CGPLH394	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.4	3.79	3.79
CGPLH395	Healthy	cfDNA	56	F	NA	NA	NA	NA	NA	4.4	9.56	9.56
CGPLH395	Healthy	cfDNA, technical replicate	56	F	NA	NA	NA	NA	NA	4.4	5.40	5.40

CGPLH396	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.4	20.31	20.31
CGPLH398	Healthy	cfDNA	68	M	NA	NA	NA	NA	NA	4.3	13.01	13.01
CGPLH399	Healthy	cfDNA	62	F	NA	NA	NA	NA	NA	4.4	4.79	4.79
CGPLH400	Healthy	cfDNA	64	M	NA	NA	NA	NA	NA	4.4	7.70	7.70
CGPLH400	Healthy	cfDNA, technical replicate	64	M	NA	NA	NA	NA	NA	4.4	6.26	6.26
CGPLH401	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.3	13.01	13.01
CGPLH401	Healthy	cfDNA, technical replicate	50	M	NA	NA	NA	NA	NA	4.4	11.13	11.13
CGPLH402	Healthy	cfDNA	57	F	NA	NA	NA	NA	NA	4.5	2.89	2.89
CGPLH403	Healthy	cfDNA	64	M	NA	NA	NA	NA	NA	4.3	4.41	4.41
CGPLH404	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.2	6.38	6.38
CGPLH405	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	7.28	7.28
CGPLH406	Healthy	cfDNA	57	M	NA	NA	NA	NA	NA	4.2	5.40	5.40
CGPLH407	Healthy	cfDNA	75	F	NA	NA	NA	NA	NA	4.0	13.30	13.30
CGPLH408	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.2	5.18	5.18
CGPLH409	Healthy	cfDNA	53	M	NA	NA	NA	NA	NA	3.7	3.98	3.98
CGPLH410	Healthy	cfDNA	52	M	NA	NA	NA	NA	NA	4.1	6.91	6.91
CGPLH411	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.1	3.30	3.30
CGPLH412	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.1	5.55	5.55
CGPLH413	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.5	8.18	8.18
CGPLH414	Healthy	cfDNA	56	M	NA	NA	NA	NA	NA	3.8	5.85	5.85
CGPLH415	Healthy	cfDNA	59	M	NA	NA	NA	NA	NA	4.7	10.20	10.20
CGPLH416	Healthy	cfDNA	58	F	NA	NA	NA	NA	NA	4.5	11.73	11.73
CGPLH417	Healthy	cfDNA	70	M	NA	NA	NA	NA	NA	4.2	10.98	10.98
CGPLH418	Healthy	cfDNA	70	F	NA	NA	NA	NA	NA	4.5	10.96	10.96
CGPLH419	Healthy	cfDNA	65	F	NA	NA	NA	NA	NA	4.5	10.17	10.17
CGPLH42	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.0	14.30	14.30
CGPLH420	Healthy	cfDNA	51	M	NA	NA	NA	NA	NA	4.2	12.32	12.32

CGPLH422	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.6	5.42	5.42
CGPLH423	Healthy	cfDNA	54	M	NA	NA	NA	NA	NA	4.2	2.85	2.85
CGPLH424	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.7	1.66	1.66
CGPLH425	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.4	5.98	5.98
CGPLH426	Healthy	cfDNA	68	M	NA	NA	NA	NA	NA	4.4	2.84	2.84
CGPLH427	Healthy	cfDNA	68	M	NA	NA	NA	NA	NA	4.4	10.86	10.86
CGPLH428	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	6.27	6.27
CGPLH429	Healthy	cfDNA	63	F	NA	NA	NA	NA	NA	4.5	3.89	3.89
CGPLH43	Healthy	cfDNA	49	F	NA	NA	NA	NA	NA	4.0	8.50	8.50
CGPLH430	Healthy	cfDNA	69	F	NA	NA	NA	NA	NA	4.2	10.33	10.33
CGPLH431	Healthy	cfDNA	59	F	NA	NA	NA	NA	NA	4.8	12.81	12.81
CGPLH432	Healthy	cfDNA	59	F	NA	NA	NA	NA	NA	4.8	2.42	2.42
CGPLH434	Healthy	cfDNA	59	M	NA	NA	NA	NA	NA	4.6	8.83	8.83
CGPLH435	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.5	8.95	8.95
CGPLH436	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	4.29	4.29
CGPLH437	Healthy	cfDNA	56	M	NA	NA	NA	NA	NA	4.6	18.07	18.07
CGPLH438	Healthy	cfDNA	69	M	NA	NA	NA	NA	NA	4.8	16.62	16.62
CGPLH439	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.7	4.38	4.38
CGPLH440	Healthy	cfDNA	72	M	NA	NA	NA	NA	NA	4.7	4.32	4.32
CGPLH441	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.7	7.80	7.80
CGPLH442	Healthy	cfDNA	59	F	NA	NA	NA	NA	NA	4.5	6.15	6.15
CGPLH443	Healthy	cfDNA	52	F	NA	NA	NA	NA	NA	4.4	3.44	3.44
CGPLH444	Healthy	cfDNA	60	F	NA	NA	NA	NA	NA	4.4	4.12	4.12
CGPLH445	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.4	4.38	4.38
CGPLH446	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.4	2.92	2.92
CGPLH447	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.6	3.87	3.87
CGPLH448	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.4	5.29	5.29
CGPLH449	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.5	3.77	3.77

CGPLH45	Healthy	cfDNA	58	F	NA	NA	NA	NA	NA	4.0	10.85	10.85
CGPLH450	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	5.62	5.62
CGPLH451	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.6	7.24	7.24
CGPLH452	Healthy	cfDNA	69	M	NA	NA	NA	NA	NA	4.4	2.54	2.54
CGPLH453	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.6	9.11	9.11
CGPLH455	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.4	2.64	2.64
CGPLH455	Healthy	cfDNA, technical replicate	55	F	NA	NA	NA	NA	NA	4.5	2.42	2.42
CGPLH456	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.5	3.11	3.11
CGPLH457	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.4	5.92	5.92
CGPLH458	Healthy	cfDNA	52	F	NA	NA	NA	NA	NA	4.5	16.04	16.04
CGPLH459	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	6.52	6.52
CGPLH46	Healthy	cfDNA	35	F	NA	NA	NA	NA	NA	4.0	8.25	8.25
CGPLH460	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.6	5.24	5.24
CGPLH463	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.5	22.77	22.77
CGPLH464	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	2.90	2.90
CGPLH465	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	4.76	4.76
CGPLH466	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.6	5.68	5.68
CGPLH466	Healthy	cfDNA, technical replicate	50	F	NA	NA	NA	NA	NA	4.5	6.75	6.75
CGPLH467	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	4.59	4.59
CGPLH468	Healthy	cfDNA	53	M	NA	NA	NA	NA	NA	4.5	11.19	11.19
CGPLH469	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	3.25	3.25
CGPLH47	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.0	7.43	7.43
CGPLH470	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.5	13.64	13.64
CGPLH471	Healthy	cfDNA	70	F	NA	NA	NA	NA	NA	4.3	13.00	13.00
CGPLH472	Healthy	cfDNA	69	F	NA	NA	NA	NA	NA	4.2	10.17	10.17
CGPLH473	Healthy	cfDNA	62	M	NA	NA	NA	NA	NA	4.3	2.98	2.98
CGPLH474	Healthy	cfDNA	63	M	NA	NA	NA	NA	NA	4.3	29.15	29.15

CGPLH475	Healthy	cfDNA	67	F	NA	NA	NA	NA	NA	4.0	7.26	7.26
CGPLH476	Healthy	cfDNA	65	F	NA	NA	NA	NA	NA	4.3	6.16	6.16
CGPLH477	Healthy	cfDNA	61	F	NA	NA	NA	NA	NA	4.3	15.21	15.21
CGPLH478	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.4	7.29	7.29
CGPLH479	Healthy	cfDNA	52	M	NA	NA	NA	NA	NA	4.5	8.73	8.73
CGPLH48	Healthy	cfDNA	38	F	NA	NA	NA	NA	NA	4.0	6.38	6.38
CGPLH480	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	10.62	10.62
CGPLH481	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.3	6.75	6.75
CGPLH482	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.3	23.58	23.58
CGPLH483	Healthy	cfDNA	66	M	NA	NA	NA	NA	NA	4.4	14.44	14.44
CGPLH484	Healthy	cfDNA	72	M	NA	NA	NA	NA	NA	4.2	14.32	14.32
CGPLH485	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.3	9.64	9.64
CGPLH486	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.3	10.16	10.16
CGPLH487	Healthy	cfDNA	50	M	NA	NA	NA	NA	NA	4.4	6.11	6.11
CGPLH488	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	7.88	7.88
CGPLH49	Healthy	cfDNA	39	F	NA	NA	NA	NA	NA	4.0	6.60	6.60
CGPLH490	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	4.18	4.18
CGPLH491	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	13.16	13.16
CGPLH492	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.5	3.83	3.83
CGPLH493	Healthy	cfDNA	64	M	NA	NA	NA	NA	NA	4.5	25.06	25.06
CGPLH494	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.4	5.24	5.24
CGPLH495	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	5.03	5.03
CGPLH496	Healthy	cfDNA	74	M	NA	NA	NA	NA	NA	4.5	34.01	27.78
CGPLH497	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.5	8.24	8.24
CGPLH497	Healthy	cfDNA, technical replicate	68	F	NA	NA	NA	NA	NA	4.4	5.88	5.88
CGPLH498	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.4	5.33	5.33
CGPLH499	Healthy	cfDNA	52	F	NA	NA	NA	NA	NA	4.5	7.85	7.85

CGPLH50	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.0	7.05	7.05
CGPLH500	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.5	3.49	3.49
CGPLH501	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.3	6.29	6.29
CGPLH502	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.5	2.24	2.24
CGPLH503	Healthy	cfDNA	67	M	NA	NA	NA	NA	NA	4.5	11.01	11.01
CGPLH504	Healthy	cfDNA	57	F	NA	NA	NA	NA	NA	4.3	6.60	6.60
CGPLH504	Healthy	cfDNA, technical replicate	57	F	NA	NA	NA	NA	NA	4.2	10.02	10.02
CGPLH505	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.1	5.23	5.23
CGPLH506	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.5	12.23	12.23
CGPLH507	Healthy	cfDNA	56	M	NA	NA	NA	NA	NA	4.1	9.89	9.89
CGPLH508	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.5	8.68	8.68
CGPLH508	Healthy	cfDNA, technical replicate	54	F	NA	NA	NA	NA	NA	4.4	9.55	9.55
CGPLH509	Healthy	cfDNA	60	M	NA	NA	NA	NA	NA	4.0	9.79	9.79
CGPLH51	Healthy	cfDNA	48	F	NA	NA	NA	NA	NA	4.0	7.85	7.85
CGPLH510	Healthy	cfDNA	67	M	NA	NA	NA	NA	NA	4.2	14.20	14.20
CGPLH511	Healthy	cfDNA	75	M	NA	NA	NA	NA	NA	4.5	12.94	12.94
CGPLH512	Healthy	cfDNA	52	M	NA	NA	NA	NA	NA	4.3	8.60	8.60
CGPLH513	Healthy	cfDNA	57	M	NA	NA	NA	NA	NA	4.3	6.54	6.54
CGPLH514	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.4	10.94	10.94
CGPLH515	Healthy	cfDNA	68	F	NA	NA	NA	NA	NA	4.5	8.71	8.71
CGPLH516	Healthy	cfDNA	65	F	NA	NA	NA	NA	NA	4.5	7.32	7.32
CGPLH517	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.6	5.16	5.16
CGPLH517	Healthy	cfDNA, technical replicate	54	F	NA	NA	NA	NA	NA	4.5	9.74	9.74
CGPLH518	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	5.92	5.92
CGPLH519	Healthy	cfDNA	54	M	NA	NA	NA	NA	NA	4.4	6.96	6.96
CGPLH52	Healthy	cfDNA	40	F	NA	NA	NA	NA	NA	4.0	9.90	9.90

CGPLH520	Healthy	cfDNA	51	F	NA	NA	NA	NA	NA	4.3	8.27	8.27
CGPLH54	Healthy	cfDNA	47	F	NA	NA	NA	NA	NA	4.0	14.18	14.18
CGPLH55	Healthy	cfDNA	46	F	NA	NA	NA	NA	NA	4.0	7.35	7.35
CGPLH56	Healthy	cfDNA	42	F	NA	NA	NA	NA	NA	4.0	5.20	5.20
CGPLH57	Healthy	cfDNA	39	F	NA	NA	NA	NA	NA	4.0	7.15	7.15
CGPLH59	Healthy	cfDNA	34	F	NA	NA	NA	NA	NA	4.0	6.03	6.03
CGPLH625	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.0	11.12	11.12
CGPLH625	Healthy	cfDNA, technical replicate	50	F	NA	NA	NA	NA	NA	4.0	11.12	11.12
CGPLH626	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.5	2.69	2.69
CGPLH63	Healthy	cfDNA	47	F	NA	NA	NA	NA	NA	4.0	10.10	10.10
CGPLH639	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	2.00	2.00
CGPLH64	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.0	8.03	8.03
CGPLH640	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.5	9.36	9.36
CGPLH642	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.5	4.99	4.99
CGPLH643	Healthy	cfDNA	55	F	NA	NA	NA	NA	NA	4.4	7.12	7.12
CGPLH644	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	5.06	5.06
CGPLH646	Healthy	cfDNA	50	F	NA	NA	NA	NA	NA	4.4	6.75	6.75
CGPLH75	Healthy	cfDNA	46	F	NA	NA	NA	NA	NA	4.0	3.87	3.87
CGPLH76	Healthy	cfDNA	53	F	NA	NA	NA	NA	NA	4.0	4.03	4.03
CGPLH77	Healthy	cfDNA	46	F	NA	NA	NA	NA	NA	4.0	5.89	5.89
CGPLH78	Healthy	cfDNA	34	F	NA	NA	NA	NA	NA	4.0	2.51	2.51
CGPLH79	Healthy	cfDNA	37	F	NA	NA	NA	NA	NA	4.0	3.68	3.68
CGPLH80	Healthy	cfDNA	37	F	NA	NA	NA	NA	NA	4.0	1.94	1.94
CGPLH81	Healthy	cfDNA	54	F	NA	NA	NA	NA	NA	4.0	5.16	5.16
CGPLH82	Healthy	cfDNA	38	F	NA	NA	NA	NA	NA	4.0	3.30	3.30
CGPLH83	Healthy	cfDNA	60	F	NA	NA	NA	NA	NA	4.0	5.04	5.04
CGPLH84	Healthy	cfDNA	45	F	NA	NA	NA	NA	NA	4.0	3.33	3.33

CGLU316	Lung Cancer	cfDNA	50	F	IV	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	5.0	0.87	1.07
CGLU316	Lung Cancer	cfDNA	50	F	IV	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	2.0	8.74	8.75
CGLU316	Lung Cancer	cfDNA	50	F	IV	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	5.0	2.11	2.11
CGLU316	Lung Cancer	cfDNA	50	F	IV	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	5.0	2.38	2.38
CGLU344	Lung Cancer	cfDNA	65	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	9.22	9.22
CGLU344	Lung Cancer	cfDNA	65	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	5.31	5.32
CGLU344	Lung Cancer	cfDNA	65	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	15.63	15.64
CGLU344	Lung Cancer	cfDNA	65	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	34.77	25.00
CGLU369	Lung Cancer	cfDNA	48	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	5.0	8.41	8.42
CGLU369	Lung Cancer	cfDNA	48	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	5.0	10.09	10.09
CGLU369	Lung Cancer	cfDNA	48	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	5.0	6.69	6.70
CGLU369	Lung Cancer	cfDNA	48	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	2.0	11.28	11.28
CGLU373	Lung Cancer	cfDNA	56	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	6.28	6.28
CGLU373	Lung Cancer	cfDNA	56	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	3.5	5.55	5.55
CGLU373	Lung Cancer	cfDNA	56	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	3.82	3.82
CGLU373	Lung Cancer	cfDNA	56	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	6.35	6.35
CGPLLU13	Lung Cancer	cfDNA	72	F	IV	Right Lung	Adenocarcinoma	NA	Bone	3.2	8.66	8.66
CGPLLU13	Lung Cancer	cfDNA	72	F	IV	Right Lung	Adenocarcinoma	NA	Bone	4.5	8.39	8.39
CGPLLU13	Lung Cancer	cfDNA	72	F	IV	Right Lung	Adenocarcinoma	NA	Bone	5.0	5.97	5.97
CGPLLU13	Lung Cancer	cfDNA	72	F	IV	Right Lung	Adenocarcinoma	NA	Bone	5.0	7.67	7.67
CGPLLU14	Lung Cancer	cfDNA	55	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55
CGPLLU14	Lung Cancer	cfDNA	55	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55

CGPLLU14	Lung Cancer	cfDNA	55	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55
CGPLLU14	Lung Cancer	cfDNA	55	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55
CGPLLU14	Lung Cancer	cfDNA	55	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55
CGPLLU14	Lung Cancer	cfDNA	55	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55
CGPLLU144	Lung Cancer	cfDNA	52	M	II	Lung	Adenocarcinoma	Poor	None	3.5	31.51	31.51
CGPLLU147	Lung Cancer	cfDNA	60	M	III	Lung	Adenosquamous Carcinoma	Poor	None	3.8	6.72	6.72
CGPLLU161	Lung Cancer	cfDNA	41	F	II	Lung	Adenocarcinoma	Well	None	4.0	83.04	83.04
CGPLLU162	Lung Cancer	cfDNA	38	M	II	Right Lung	Adenocarcinoma	Moderate	None	3.1	40.32	40.32
CGPLLU163	Lung Cancer	cfDNA	66	M	II	Left Lung	Adenocarcinoma	Poor	None	5.0	54.03	54.03
CGPLLU165	Lung Cancer	cfDNA	68	F	II	Right Lung	Adenocarcinoma	Well	None	4.5	20.13	20.13
CGPLLU168	Lung Cancer	cfDNA	70	F	I	Lung	Adenocarcinoma	Poor	None	4.3	19.38	19.38
CGPLLU169	Lung Cancer	cfDNA	64	M	I	Lung	Squamous Cell Carcinoma	Moderate	None	4.2	13.70	13.70
CGPLLU175	Lung Cancer	cfDNA	47	M	I	Lung	Squamous Cell Carcinoma	Moderate	None	4.4	16.84	16.84
CGPLLU176	Lung Cancer	cfDNA	58	M	I	Lung	Adenosquamous Carcinoma	Moderate	None	3.2	7.86	7.86
CGPLLU177	Lung Cancer	cfDNA	45	M	II	Right Lung	Adenocarcinoma	NA	None	3.9	19.07	19.07
CGPLLU180	Lung Cancer	cfDNA	57	M	I	Right Lung	Large Cell Carcinoma	Poor	None	3.2	19.31	19.31
CGPLLU198	Lung Cancer	cfDNA	49	F	I	Left Lung	Adenocarcinoma	Moderate	None	4.2	14.09	14.09
CGPLLU202	Lung Cancer	cfDNA	68	M	I	Right Lung	Adenocarcinoma	NA	None	4.4	24.72	24.72
CGPLLU203	Lung Cancer	cfDNA	66	M	II	Right Lung	Squamous Cell Carcinoma	Well	None	4.2	26.24	26.24
CGPLLU205	Lung Cancer	cfDNA	65	M	II	Left Lung	Adenocarcinoma	Poor	None	4.0	18.56	18.56
CGPLLU206	Lung Cancer	cfDNA	55	M	III	Right Lung	Squamous Cell Carcinoma	Poor	None	3.5	18.24	18.24
CGPLLU207	Lung Cancer	cfDNA	60	F	II	Lung	Adenocarcinoma	Well	None	4.0	17.29	17.29
CGPLLU208	Lung Cancer	cfDNA	56	F	II	Lung	Adenocarcinoma	Moderate	None	3.0	24.34	24.34
CGPLLU209	Lung Cancer	cfDNA	65	M	II	Lung	Large Cell Carcinoma	Poor	None	5.5	53.95	53.95
CGPLLU244	Lung Cancer	cfDNA	66	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84

CGPLLU244	Lung Cancer	cfDNA	66	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84
CGPLLU244	Lung Cancer	cfDNA	66	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84
CGPLLU244	Lung Cancer	cfDNA	66	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84
CGPLLU245	Lung Cancer	cfDNA	49	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42
CGPLLU245	Lung Cancer	cfDNA	49	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42
CGPLLU245	Lung Cancer	cfDNA	49	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42
CGPLLU245	Lung Cancer	cfDNA	49	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42
CGPLLU246	Lung Cancer	cfDNA	65	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51
CGPLLU246	Lung Cancer	cfDNA	65	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51
CGPLLU246	Lung Cancer	cfDNA	65	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51
CGPLLU246	Lung Cancer	cfDNA	65	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51
CGPLLU264	Lung Cancer	cfDNA	84	M	IV	Left Middle Lung	Adenocarcinoma	NA	Lung	3.0	7.15	7.15
CGPLLU264	Lung Cancer	cfDNA	84	M	IV	Left Middle Lung	Adenocarcinoma	NA	Lung	4.5	10.53	10.53
CGPLLU264	Lung Cancer	cfDNA	84	M	IV	Left Middle Lung	Adenocarcinoma	NA	Lung	4.0	9.60	9.60
CGPLLU264	Lung Cancer	cfDNA	84	M	IV	Left Middle Lung	Adenocarcinoma	NA	Lung	4.0	22.97	22.97
CGPLLU265	Lung Cancer	cfDNA	71	F	IV	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	4.0	8.11	8.11
CGPLLU265	Lung Cancer	cfDNA	71	F	IV	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	4.2	7.53	7.53
CGPLLU265	Lung Cancer	cfDNA	71	F	IV	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	5.0	16.17	16.17
CGPLLU265	Lung Cancer	cfDNA	71	F	IV	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	4.2	7.16	7.16
CGPLLU266	Lung Cancer	cfDNA	78	M	IV	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	3.5	6.31	6.31
CGPLLU266	Lung Cancer	cfDNA	78	M	IV	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	14.39	14.39
CGPLLU266	Lung Cancer	cfDNA	78	M	IV	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	7.64	7.64
CGPLLU266	Lung Cancer	cfDNA	78	M	IV	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	5.32	5.32

CGPLLU267	Lung Cancer	cfDNA	55	F	IV	Right Upper Lobe of Lung	Squamous Cell Carcinoma	Poor	Lung	4.5	3.34	3.34
CGPLLU267	Lung Cancer	cfDNA	55	F	IV	Right Upper Lobe of Lung	Squamous Cell Carcinoma	Poor	Lung	3.5	3.00	3.00
CGPLLU267	Lung Cancer	cfDNA	55	F	IV	Right Upper Lobe of Lung	Squamous Cell Carcinoma	Poor	Lung	4.5	2.87	2.87
CGPLLU269	Lung Cancer	cfDNA	52	F	IV	Right Paratracheal Lesion	Adenocarcinoma	NA	Brain, Liver, Bone, Pleura	3.5	17.79	17.79
CGPLLU269	Lung Cancer	cfDNA	52	F	IV	Right Paratracheal Lesion	Adenocarcinoma	NA	Brain, Liver, Bone, Pleura	5.0	8.35	8.35
CGPLLU269	Lung Cancer	cfDNA	52	F	IV	Right Paratracheal Lesion	Adenocarcinoma	NA	Brain, Liver, Bone, Pleura	5.0	11.40	11.40
CGPLLU271	Lung Cancer	cfDNA	73	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	4.0	13.77	13.77
CGPLLU271	Lung Cancer	cfDNA	73	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	3.5	13.46	13.46
CGPLLU271	Lung Cancer	cfDNA	73	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	4.0	4.70	4.70
CGPLLU271	Lung Cancer	cfDNA	73	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	4.5	13.84	13.84
CGPLLU271	Lung Cancer	cfDNA	73	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	5.0	18.86	18.86
CGPLLU43	Lung Cancer	cfDNA	57	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	4.0	4.12	4.12
CGPLLU43	Lung Cancer	cfDNA	57	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	3.7	3.26	3.26
CGPLLU43	Lung Cancer	cfDNA	57	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	3.7	8.20	8.20
CGPLLU43	Lung Cancer	cfDNA	57	F	IV	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	4.9	2.17	2.17
CGPLLU86	Lung Cancer	cfDNA	55	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90
CGPLLU86	Lung Cancer	cfDNA	55	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90
CGPLLU86	Lung Cancer	cfDNA	55	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90
CGPLLU86	Lung Cancer	cfDNA	55	M	IV	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90
CGPLLU88	Lung Cancer	cfDNA	59	M	IV	Right Middle Lobe of Lung	Adenocarcinoma	NA	None	4.0	3.04	3.04
CGPLLU88	Lung Cancer	cfDNA	59	M	IV	Right Middle Lobe of Lung	Adenocarcinoma	NA	None	5.0	6.49	6.49

CGPLLU88	Lung Cancer	cfDNA	59	M	IV	Right Middle Lobe of Lung	Adenocarcinoma	NA	None	5.0	27.66	27.66
CGPLLU89	Lung Cancer	cfDNA	54	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain, Bone, Lung	8.0	8.43	8.43
CGPLLU89	Lung Cancer	cfDNA	54	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain, Bone, Lung	8.0	8.43	8.43
CGPLLU89	Lung Cancer	cfDNA	54	F	IV	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain, Bone, Lung	8.0	8.43	8.43
CGPLOV11	Ovarian Cancer	cfDNA	51	F	IV	Right Ovary	Endometrioid Adenoarcinoma	Moderate	Omentum	3.4	17.35	17.35
CGPLOV12	Ovarian Cancer	cfDNA	45	F	I	Ovary	Endometrioid Adenoarcinoma	NA	None	3.2	12.44	12.44
CGPLOV13	Ovarian Cancer	cfDNA	62	F	IV	Right Ovary	Endometrioid Adenoarcinoma	Poor	Omentum	3.8	27.00	27.00
CGPLOV15	Ovarian Cancer	cfDNA	54	F	III	Ovary	Adenocarcinoma	Poor	None	5.0	4.77	4.77
CGPLOV16	Ovarian Cancer	cfDNA	40	F	III	Ovary	Serous Adenocarcinoma	Moderate	None	4.5	27.28	27.28
CGPLOV19	Ovarian Cancer	cfDNA	52	F	II	Ovary	Endometrioid Adenoarcinoma	Moderate	None	5.0	23.46	23.46
CGPLOV20	Ovarian Cancer	cfDNA	52	F	II	Left Ovary	Endometrioid Adenoarcinoma	Poor	None	4.2	5.67	5.67
CGPLOV21	Ovarian Cancer	cfDNA	51	M	IV	Ovary	Serous Adenocarcinoma	Poor	Omentum, Appendix	4.3	56.32	56.32
CGPLOV22	Ovarian Cancer	cfDNA	64	F	III	Left Ovary	Serous Adenocarcinoma	Well	None	4.6	17.42	17.42
CGPLOV23	Ovarian Cancer	cfDNA	47	F	I	Ovary	Serous Adenocarcinoma	Poor	None	5.0	26.73	26.73
CGPLOV24	Ovarian Cancer	cfDNA	14	F	I	Ovary	Germ Cell Tumor	Poor	None	4.2	10.71	10.71
CGPLOV25	Ovarian Cancer	cfDNA	18	F	I	Ovary	Germ Cell Tumor	Poor	None	4.8	6.78	6.78
CGPLOV26	Ovarian Cancer	cfDNA	35	F	I	Ovary	Germ Cell Tumor	Poor	None	4.5	27.90	27.90
CGPLOV28	Ovarian Cancer	cfDNA	63	F	I	Right Ovary	Serous Carcinoma	NA	None	3.2	10.74	10.74
CGPLOV31	Ovarian Cancer	cfDNA	45	F	III	Right Ovary	Clear Cell adenocarcinoma	NA	None	4.0	14.45	14.45
CGPLOV32	Ovarian Cancer	cfDNA	53	F	I	Left Ovary	Mucinous Cystadenoma	NA	None	3.2	27.36	27.36
CGPLOV37	Ovarian Cancer	cfDNA	40	F	I	Ovary	Serous Carcinoma	NA	None	3.2	46.88	46.88
CGPLOV38	Ovarian Cancer	cfDNA	46	F	I	Ovary	Serous Carcinoma	NA	None	2.4	34.29	34.29
CGPLOV40	Ovarian Cancer	cfDNA	53	F	IV	Ovary	Serous Carcinoma	NA	Omentum, Uterus, Appendix	1.6	193.60	156.25
CGPLOV41	Ovarian Cancer	cfDNA	57	F	IV	Ovary	Serous Carcinoma	NA	Omentum, Uterus, Cervix	4.4	10.03	10.03

CGPLOV42	Ovarian Cancer	cfDNA	52	F	I	Ovary	Serous Carcinoma	NA	None	4.2	49.51	49.51
CGPLOV43	Ovarian Cancer	cfDNA	30	F	I	Ovary	Mucinous Cystadenocarcinoma	NA	None	4.4	9.09	9.09
CGPLOV44	Ovarian Cancer	cfDNA	69	F	I	Ovary	Mucinous Adenocarcinoma	NA	None	4.5	8.79	8.79
CGPLOV46	Ovarian Cancer	cfDNA	58	F	I	Ovary	Serous Carcinoma	NA	None	4.1	8.97	8.97
CGPLOV47	Ovarian Cancer	cfDNA	41	F	I	Ovary	Serous Cystadenoma	NA	None	4.5	19.35	19.35
CGPLOV48	Ovarian Cancer	cfDNA	52	F	I	Ovary	Serous Carcinoma	NA	None	3.5	22.80	22.80
CGPLOV49	Ovarian Cancer	cfDNA	68	F	III	Ovary	Serous Carcinoma	NA	None	4.2	16.48	16.48
CGPLOV50	Ovarian Cancer	cfDNA	30	F	III	Ovary	Serous Carcinoma	NA	None	4.5	8.89	8.89
CGPLPA112	Pancreatic Cancer	cfDNA	58	M	II	Intra Pancreatic Bile Duct	Intra Pancreatic Bile Duct	NA	None	3.5	18.52	18.52
CGPLPA14	Pancreatic Cancer	cfDNA	68	M	II	Pancreas	Ductal Adenocarcinoma	Poor	None	4.0	1.30	1.30
CGPLPA15	Pancreatic Cancer	cfDNA	70	F	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	1.92	1.92
CGPLPA156	Pancreatic Cancer	cfDNA	73	F	II	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	4.5	7.54	7.54
CGPLPA17	Pancreatic Cancer	cfDNA	65	M	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	13.08	13.08
CGPLPA23	Pancreatic Cancer	cfDNA	58	F	II	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	4.0	16.62	16.62
CGPLPA25	Pancreatic Cancer	cfDNA	69	F	II	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	4.0	8.71	8.71
CGPLPA26	Pancreatic Cancer	cfDNA	64	M	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	6.97	6.97
CGPLPA28	Pancreatic Cancer	cfDNA	79	F	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	18.13	18.13
CGPLPA33	Pancreatic Cancer	cfDNA	67	F	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	1.80	1.80
CGPLPA34	Pancreatic Cancer	cfDNA	73	M	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	3.36	3.36
CGPLPA37	Pancreatic Cancer	cfDNA	67	F	II	Pancreas	Ductal Adenocarcinoma	NA	Lymph Node	4.0	21.83	21.83
CGPLPA38	Pancreatic Cancer	cfDNA	65	M	II	Pancreas	Ductal Adenocarcinoma	Moderate	None	4.0	5.29	5.29
CGPLPA39	Pancreatic Cancer	cfDNA	67	F	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	11.73	11.73
CGPLPA40	Pancreatic Cancer	cfDNA	64	M	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	4.78	4.78

CGPLPA42	Pancreatic Cancer	cfDNA	73	M	II	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	4.0	3.41	3.41
CGPLPA46	Pancreatic Cancer	cfDNA	59	F	II	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	4.0	0.74	0.74
CGPLPA47	Pancreatic Cancer	cfDNA	67	M	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	6.01	6.01
CGPLPA48	Pancreatic Cancer	cfDNA	72	F	I	Pancreas	Ductal Adenocarcinoma	Well	None	NA	NA	NA
CGPLPA52	Pancreatic Cancer	cfDNA	63	M	II	Pancreas	Ductal Adenocarcinoma	Moderate	None	2.5	9.86	9.86
CGPLPA53	Pancreatic Cancer	cfDNA	46	M	I	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	3.0	14.48	14.48
CGPLPA58	Pancreatic Cancer	cfDNA	74	F	II	Pancreas	Ductal Adenocarcinoma	NA	None	3.0	6.87	6.87
CGPLPA59	Pancreatic Cancer	cfDNA	59	F	II	Pancreas	Ductal Adenocarcinoma or Adenoma	Well	Lymph Node	NA	NA	NA
CGPLPA67	Pancreatic Cancer	cfDNA	55	M	III	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	3.2	9.72	9.72
CGPLPA69	Pancreatic Cancer	cfDNA	70	M	I	Pancreas	Ductal Adenocarcinoma	Well	None	2.0	1.72	1.72
CGPLPA71	Pancreatic Cancer	cfDNA	64	M	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	2.2	39.07	39.07
CGPLPA74	Pancreatic Cancer	cfDNA	71	F	II	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	2.5	4.99	4.99
CGPLPA76	Pancreatic Cancer	cfDNA	69	M	II	Pancreas	Ductal Adenocarcinoma	Poor	None	2.5	23.19	23.19
CGPLPA85	Pancreatic Cancer	cfDNA	77	F	II	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	3.0	152.46	41.67
CGPLPA86	Pancreatic Cancer	cfDNA	66	M	II	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	2.5	11.02	11.02
CGPLPA92	Pancreatic Cancer	cfDNA	72	M	II	Pancreas	Ductal Adenocarcinoma	NA	Lymph Node	2.0	5.34	5.34
CGPLPA93	Pancreatic Cancer	cfDNA	48	M	II	Pancreas	Ductal Adenocarcinoma	Poor	None	3.0	96.28	41.67
CGPLPA94	Pancreatic Cancer	cfDNA	72	F	II	Pancreas	Ductal Adenocarcinoma	NA	Lymph Node	3.0	29.66	29.66
CGPLPA95	Pancreatic Cancer	cfDNA	64	F	II	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	NA	NA	NA

*NA denotes data not available or not applicable for healthy individuals.

Table 4.2. Summary of targeted cfDNA analyses.

Patient	Patient Type	Timepoint	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGCRC291	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7501485600	3771359756	50%	44345	10359
CGCRC292	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6736035200	3098886973	46%	36448	8603
CGCRC293	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6300244000	2818734206	45%	33117	5953
CGCRC294	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7786872600	3911796709	50%	46016	12071
CGCRC295	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8240660200	3478059753	42%	40787	5826
CGCRC296	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	5718556500	2898549356	51%	33912	10180
CGCRC297	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7550826100	3717222432	49%	43545	5870
CGCRC298	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	12501036400	6096393764	49%	71196	9617
CGCRC299	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7812602900	4121569690	53%	48098	10338
CGCRC300	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8648090300	3962285136	46%	46364	5756
CGCRC301	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7538758100	3695480348	49%	43024	6618
CGCRC302	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8573658300	4349420574	51%	51006	13799
CGCRC303	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	5224046400	2505714343	48%	29365	8372
CGCRC304	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	5762112600	2942170530	51%	34462	10208
CGCRC305	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7213384100	3726953480	52%	43516	8589
CGCRC306	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7075579700	3552441899	50%	41507	7372
CGCRC307	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7572687100	3492191519	46%	40793	9680
CGCRC308	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7945738000	3895908986	49%	45224	11809
CGCRC309	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8487455800	3921079811	46%	45736	10739
CGCRC310	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	9003580500	4678812441	52%	54713	11139
CGCRC311	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6528162700	3276653864	50%	38324	6044
CGCRC312	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7683294300	3316719187	43%	38652	4622
CGCRC313	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	5874099200	2896148722	49%	33821	6506
CGCRC314	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6883148500	3382767492	49%	39414	6664
CGCRC315	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7497252500	3775556051	50%	44034	8666

CGCRC316	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	10684720400	5533857153	52%	64693	14289
CGCRC317	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7086877600	3669434216	52%	43538	10944
CGCRC318	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6880041100	3326357413	48%	39077	11571
CGCRC319	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7485342900	3982677483	53%	47327	10502
CGCRC320	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7058703200	3450648135	49%	40888	10198
CGCRC321	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7203625900	3633396892	50%	43065	6499
CGCRC332	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7202969100	3758323705	52%	44580	3243
CGCRC333	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8767144700	4199126827	48%	49781	8336
CGCRC334	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7771869100	3944578280	51%	46518	5014
CGCRC335	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7972524600	4064901201	51%	48308	6151
CGCRC336	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8597346400	4333410573	50%	51390	7551
CGCRC337	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7399611700	3800666199	51%	45083	8092
CGCRC338	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8029493700	4179383804	52%	49380	5831
CGCRC339	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7938963600	4095555110	52%	48397	3808
CGCRC340	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7214889500	3706643098	51%	43805	3014
CGCRC341	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8803159200	3668208527	42%	43106	11957
CGCRC342	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8478811500	3425540889	40%	40328	9592
CGCRC344	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6942167800	3098232737	45%	36823	2300
CGCRC345	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8182868200	2383173431	29%	28233	7973
CGCRC346	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7448272300	3925056341	53%	46679	5582
CGCRC347	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	5804744500	2986809912	51%	35490	4141
CGCRC349	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6943451600	3533145275	51%	41908	5762
CGCRC350	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7434818400	3848923016	52%	45678	4652
CGCRC351	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7306546400	3636910409	50%	43162	5205
CGCRC352	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7864655000	3336939252	42%	39587	4502
CGCRC353	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7501674800	3642919375	49%	43379	4666
CGCRC354	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7938270200	2379068977	30%	28256	4858
CGCRC356	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6013175900	3046754994	51%	36127	3425

CGCRC357	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6013454600	3022035300	50%	35813	4259
CGCRC358	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7227212400	3188723303	44%	37992	5286
CGCRC359	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7818567700	425110101	5%	5040	2566
CGCRC367	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6582043200	3363063597	51%	39844	5839
CGCRC368	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	8042242400	4101646000	51%	48636	11471
CGCRC370	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6940330100	3198954121	46%	38153	4826
CGCRC373	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6587201700	3120088035	47%	37234	5190
CGCRC376	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6727983100	3162416807	47%	37735	3445
CGCRC377	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6716339200	3131415570	47%	37160	4524
CGCRC378	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6523969900	2411096720	37%	28728	3239
CGCRC379	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6996252100	3371081103	48%	39999	2891
CGCRC380	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7097496300	2710244446	38%	32020	3261
CGCRC381	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6961936100	3287050681	47%	38749	9357
CGCRC382	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6959048700	2552325859	37%	30040	5148
CGCRC384	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7012798900	3293884583	47%	39158	3653
CGCRC385	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7542017900	3356570505	45%	39884	3686
CGCRC386	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6876059600	3064412286	45%	36431	2787
CGCRC387	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7399564700	3047254560	41%	36141	6675
CGCRC388	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6592692900	3137284885	48%	37285	5114
CGCRC389	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6651206300	3102100941	47%	36764	6123
CGCRC390	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	7260616800	3376667585	47%	40048	4368
CGCRC391	Colorectal Cancer	Preoperative, Treatment naïve	100	80930	6883624500	3202877881	47%	37978	5029
CGLU316	Lung Cancer	Pre-treatment, Day -53	100	80930	7864415100	1991331171	25%	23601	3565
CGLU316	Lung Cancer	Pre-treatment, Day -53	100	80930	7502591600	3730963390	50%	44262	3966
CGLU316	Lung Cancer	Pre-treatment, Day -53	100	80930	6582515900	3187059470	48%	37813	3539
CGLU316	Lung Cancer	Pre-treatment, Day -53	100	80930	6587281800	1947630979	30%	23094	4439
CGLU344	Lung Cancer	Pre-treatment, Day -21	100	80930	6151628500	2748983603	45%	32462	8063
CGLU344	Lung Cancer	Pre-treatment, Day -21	100	80930	7842910900	1147703178	15%	13565	4303

CGLU344	Lung Cancer	Pre-treatment, Day -21	100	80930	5838083100	2291108925	39%	27067	4287
CGLU344	Lung Cancer	Pre-treatment, Day -21	100	80930	7685989200	3722274529	48%	43945	3471
CGLU369	Lung Cancer	Pre-treatment, Day -2	100	80930	7080245300	1271457982	18%	15109	2364
CGLU369	Lung Cancer	Pre-treatment, Day -2	100	80930	7078131900	1482448715	21%	17583	4275
CGLU369	Lung Cancer	Pre-treatment, Day -2	100	80930	6904701700	2124660124	31%	25230	5278
CGLU369	Lung Cancer	Pre-treatment, Day -2	100	80930	7003452200	3162195578	45%	37509	6062
CGLU373	Lung Cancer	Pre-treatment, Day -2	100	80930	6346267200	3053520676	48%	36137	6251
CGLU373	Lung Cancer	Pre-treatment, Day -2	100	80930	6517189900	3192984468	49%	38066	8040
CGLU373	Lung Cancer	Pre-treatment, Day -2	100	80930	7767146300	3572598842	46%	42378	5306
CGLU373	Lung Cancer	Pre-treatment, Day -2	100	80930	7190999100	3273648804	46%	38784	4454
CGPLBR100	Breast Cancer	Preoperative, Treatment naïve	100	80930	7299964400	3750278051	51%	44794	3249
CGPLBR101	Breast Cancer	Preoperative, Treatment naïve	100	80930	7420822800	3810365416	51%	45565	9784
CGPLBR102	Breast Cancer	Preoperative, Treatment naïve	100	80930	6679304900	3269688319	49%	38679	7613
CGPLBR103	Breast Cancer	Preoperative, Treatment naïve	100	80930	7040304400	3495542468	50%	41786	6748
CGPLBR104	Breast Cancer	Preoperative, Treatment naïve	100	80930	7188389200	3716096781	52%	44316	9448
CGPLBR38	Breast Cancer	Preoperative, Treatment naïve	100	80930	7810293900	4057576306	52%	48098	9868
CGPLBR39	Breast Cancer	Preoperative, Treatment naïve	100	80930	7745701500	3805623239	49%	45084	11065
CGPLBR40	Breast Cancer	Preoperative, Treatment naïve	100	80930	7558990500	3652442341	48%	43333	12948
CGPLBR41	Breast Cancer	Preoperative, Treatment naïve	100	80930	7900994600	3836600101	49%	45535	10847
CGPLBR44	Breast Cancer	Preoperative, Treatment naïve	100	80930	7017744200	3269110569	47%	38672	8344
CGPLBR48	Breast Cancer	Preoperative, Treatment naïve	100	80930	5629044200	2611554623	46%	30860	8652
CGPLBR49	Breast Cancer	Preoperative, Treatment naïve	100	80930	5784711600	2673457893	46%	31274	10429
CGPLBR55	Breast Cancer	Preoperative, Treatment naïve	100	80930	8309154900	4306956261	52%	51143	8328
CGPLBR57	Breast Cancer	Preoperative, Treatment naïve	100	80930	8636181000	4391502618	51%	52108	5857
CGPLBR59	Breast Cancer	Preoperative, Treatment naïve	100	80930	8799457700	4152328555	47%	49281	5855
CGPLBR61	Breast Cancer	Preoperative, Treatment naïve	100	80930	8163706700	3952010628	48%	46755	8522
CGPLBR63	Breast Cancer	Preoperative, Treatment naïve	100	80930	7020533100	3542447304	50%	41956	4773
CGPLBR67	Breast Cancer	Preoperative, Treatment naïve	100	80930	8264353900	3686093696	45%	43516	7752

CGPLBR68	Breast Cancer	Preoperative, Treatment naïve	100	80930	7629312300	4078969547	53%	48389	7402
CGPLBR69	Breast Cancer	Preoperative, Treatment naïve	100	80930	7571501500	3857354512	51%	45322	7047
CGPLBR70	Breast Cancer	Preoperative, Treatment naïve	100	80930	7251760700	3641333708	50%	43203	8884
CGPLBR71	Breast Cancer	Preoperative, Treatment naïve	100	80930	8515402600	4496696391	53%	53340	6805
CGPLBR72	Breast Cancer	Preoperative, Treatment naïve	100	80930	8556946900	4389761697	51%	52081	5632
CGPLBR73	Breast Cancer	Preoperative, Treatment naïve	100	80930	7959392300	4006933338	50%	47555	8791
CGPLBR74	Breast Cancer	Preoperative, Treatment naïve	100	80930	8524536400	4063900599	48%	48252	7013
CGPLBR75	Breast Cancer	Preoperative, Treatment naïve	100	80930	8260379100	3960599885	48%	46955	6319
CGPLBR76	Breast Cancer	Preoperative, Treatment naïve	100	80930	7774235200	3893622420	50%	46192	9628
CGPLBR77	Breast Cancer	Preoperative, Treatment naïve	100	80930	7572797600	3255963429	43%	38568	8263
CGPLBR80	Breast Cancer	Preoperative, Treatment naïve	100	80930	6845325800	3147476693	46%	37201	5595
CGPLBR82	Breast Cancer	Preoperative, Treatment naïve	100	80930	8236705200	4170465005	51%	49361	12319
CGPLBR83	Breast Cancer	Preoperative, Treatment naïve	100	80930	7434568100	3676855019	49%	43628	5458
CGPLBR86	Breast Cancer	Preoperative, Treatment naïve	100	80930	7616282500	3644791327	48%	43490	7048
CGPLBR87	Breast Cancer	Preoperative, Treatment naïve	100	80930	6194021300	3004882010	49%	35765	5306
CGPLBR88	Breast Cancer	Preoperative, Treatment naïve	100	80930	6071567200	2847926237	47%	33945	10319
CGPLBR91	Breast Cancer	Preoperative, Treatment naïve	100	80930	7192457700	3480203404	48%	41570	9912
CGPLBR92	Breast Cancer	Preoperative, Treatment naïve	100	80930	7678981800	3600279233	47%	42975	13580
CGPLBR93	Breast Cancer	Preoperative, Treatment naïve	100	80930	7605717800	3998713397	53%	47866	10329
CGPLBR96	Breast Cancer	Preoperative, Treatment naïve	100	80930	6297446700	2463064737	39%	29341	7937
CGPLBR97	Breast Cancer	Preoperative, Treatment naïve	100	80930	7114921600	3557069027	50%	42488	10712
CGPLH35	Healthy	Preoperative, Treatment naïve	100	80930	6919126300	2312758764	33%	25570	1989
CGPLH36	Healthy	Preoperative, Treatment naïve	100	80930	6089923400	2038548115	33%	22719	1478
CGPLH37	Healthy	Preoperative, Treatment naïve	100	80930	5557270200	1935301929	35%	21673	2312
CGPLH42	Healthy	Preoperative, Treatment naïve	100	80930	5792045400	2388036949	41%	27197	2523
CGPLH43	Healthy	Preoperative, Treatment naïve	100	80930	5568321700	2017813329	36%	23228	1650
CGPLH45	Healthy	Preoperative, Treatment naïve	100	80930	8485593200	2770176078	33%	32829	3114
CGPLH46	Healthy	Preoperative, Treatment naïve	100	80930	5083171100	1899395790	37%	21821	1678

CGPLH47	Healthy	Preoperative, Treatment naïve	100	80930	6016388500	2062392156	34%	23459	1431
CGPLH48	Healthy	Preoperative, Treatment naïve	100	80930	4958945900	1809825992	36%	20702	1698
CGPLH49	Healthy	Preoperative, Treatment naïve	100	80930	7953812200	2511365904	32%	27006	1440
CGPLH50	Healthy	Preoperative, Treatment naïve	100	80930	6989407600	2561288100	37%	29177	2591
CGPLH51	Healthy	Preoperative, Treatment naïve	100	80930	7862073200	2525091396	32%	29999	1293
CGPLH52	Healthy	Preoperative, Treatment naïve	100	80930	6939636800	2397922699	35%	27029	2501
CGPLH54	Healthy	Preoperative, Treatment naïve	100	80930	10611934700	2290823134	22%	27175	3306
CGPLH55	Healthy	Preoperative, Treatment naïve	100	80930	9912569200	2521962244	25%	27082	3161
CGPLH56	Healthy	Preoperative, Treatment naïve	100	80930	5777591900	2023874863	35%	22916	1301
CGPLH57	Healthy	Preoperative, Treatment naïve	100	80930	9234904800	1493926244	16%	15843	1655
CGPLH59	Healthy	Preoperative, Treatment naïve	100	80930	9726052100	2987875484	31%	35427	2143
CGPLH63	Healthy	Preoperative, Treatment naïve	100	80930	8696405000	2521574759	29%	26689	1851
CGPLH64	Healthy	Preoperative, Treatment naïve	100	80930	5438852600	996198502	18%	11477	1443
CGPLH75	Healthy	Preoperative, Treatment naïve	100	80930	3446444000	1505718480	44%	17805	3016
CGPLH76	Healthy	Preoperative, Treatment naïve	100	80930	7499116400	3685762725	49%	43682	4643
CGPLH77	Healthy	Preoperative, Treatment naïve	100	80930	6512408400	2537359345	39%	30280	3131
CGPLH78	Healthy	Preoperative, Treatment naïve	100	80930	7642949300	3946069680	52%	46316	5358
CGPLH79	Healthy	Preoperative, Treatment naïve	100	80930	7785475700	3910639227	50%	45280	6714
CGPLH80	Healthy	Preoperative, Treatment naïve	100	80930	7918361500	3558236955	45%	42171	5062
CGPLH81	Healthy	Preoperative, Treatment naïve	100	80930	6646268900	3112369850	47%	37119	3678
CGPLH82	Healthy	Preoperative, Treatment naïve	100	80930	7744065000	3941700596	51%	46820	5723
CGPLH83	Healthy	Preoperative, Treatment naïve	100	80930	6957686000	1447603106	21%	17280	2875
CGPLH84	Healthy	Preoperative, Treatment naïve	100	80930	8326493200	3969908122	48%	47464	3647
CGPLH86	Healthy	Preoperative, Treatment naïve	100	80930	8664194700	4470145091	52%	53398	5094
CGPLH90	Healthy	Preoperative, Treatment naïve	100	80930	7516078800	3841504088	51%	45907	4414
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	100	80930	5659546100	1721618955	30%	20587	6025
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	100	80930	6199049700	2563659840	41%	30728	6514
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	100	80930	5864396500	1194237002	20%	14331	3952

CGPLLU13	Lung Cancer	Pre-treatment, Day -2	100	80930	5080197700	1373550586	27%	16480	5389
CGPLLU14	Lung Cancer	Pre-treatment, Day -38	100	80930	8668655700	3980731089	46%	48628	3148
CGPLLU14	Lung Cancer	Pre-treatment, Day -16	100	80930	8271043600	4105092738	50%	50152	4497
CGPLLU14	Lung Cancer	Pre-treatment, Day -3	100	80930	7149809200	3405754720	48%	40382	6170
CGPLLU14	Lung Cancer	Pre-treatment, Day 0	100	80930	6556332200	3289504484	50%	39004	4081
CGPLLU14	Lung Cancer	Post-treatment, Day 0.33	100	80930	7410378300	3464236558	47%	41108	4259
CGPLLU14	Lung Cancer	Post-treatment, Day 7	100	80930	7530190700	3752054349	50%	45839	2469
CGPLLU144	Lung Cancer	Preoperative, Treatment naïve	100	80930	8716827400	4216576624	48%	49370	10771
CGPLLU146	Lung Cancer	Preoperative, Treatment naïve	100	80930	8506844200	4195033049	49%	49084	6968
CGPLLU147	Lung Cancer	Preoperative, Treatment naïve	100	80930	7416300600	3530746046	48%	41302	4691
CGPLLU161	Lung Cancer	Preoperative, Treatment naïve	100	80930	7789148700	3280139772	42%	38568	12229
CGPLLU162	Lung Cancer	Preoperative, Treatment naïve	100	80930	7625462000	3470147667	46%	40918	10099
CGPLLU163	Lung Cancer	Preoperative, Treatment naïve	100	80930	8019293200	3946533983	49%	46471	12108
CGPLLU164	Lung Cancer	Preoperative, Treatment naïve	100	80930	8110030900	3592748235	44%	42161	6947
CGPLLU165	Lung Cancer	Preoperative, Treatment naïve	100	80930	8389514600	4147501817	49%	48770	8996
CGPLLU168	Lung Cancer	Preoperative, Treatment naïve	100	80930	7690630000	3868237773	50%	45625	9711
CGPLLU169	Lung Cancer	Preoperative, Treatment naïve	100	80930	9378353000	4800407624	51%	56547	10261
CGPLLU174	Lung Cancer	Preoperative, Treatment naïve	100	80930	7481844600	3067532518	41%	36321	6137
CGPLLU175	Lung Cancer	Preoperative, Treatment naïve	100	80930	8532324200	4002541569	47%	47084	7862
CGPLLU176	Lung Cancer	Preoperative, Treatment naïve	100	80930	8143905000	4054098929	50%	47708	5588
CGPLLU177	Lung Cancer	Preoperative, Treatment naïve	100	80930	8421611300	4197108809	50%	49476	8780
CGPLLU178	Lung Cancer	Preoperative, Treatment naïve	100	80930	8483124700	4169577489	49%	48580	6445
CGPLLU179	Lung Cancer	Preoperative, Treatment naïve	100	80930	7774358700	3304915738	43%	38768	6862
CGPLLU180	Lung Cancer	Preoperative, Treatment naïve	100	80930	8192813800	3937552475	48%	46498	6568
CGPLLU197	Lung Cancer	Preoperative, Treatment naïve	100	80930	7996779200	3082397881	39%	36381	5388
CGPLLU198	Lung Cancer	Preoperative, Treatment naïve	100	80930	7175247200	3545719100	49%	42008	6817
CGPLLU202	Lung Cancer	Preoperative, Treatment naïve	100	80930	6840112800	3427820669	50%	40670	7951
CGPLLU203	Lung Cancer	Preoperative, Treatment naïve	100	80930	7468749900	3762726574	50%	44500	9917

CGPLLU204	Lung Cancer	Preoperative, Treatment naïve	100	80930	7445026400	3703545153	50%	44317	6856
CGPLLU205	Lung Cancer	Preoperative, Treatment naïve	100	80930	9205429100	4350573991	47%	51627	9810
CGPLLU206	Lung Cancer	Preoperative, Treatment naïve	100	80930	7397914600	3635210205	49%	43016	7124
CGPLLU207	Lung Cancer	Preoperative, Treatment naïve	100	80930	7133043900	3736258011	52%	44291	8499
CGPLLU208	Lung Cancer	Preoperative, Treatment naïve	100	80930	7346976400	3855814032	52%	45782	8940
CGPLLU209	Lung Cancer	Preoperative, Treatment naïve	100	80930	6723337800	3362944595	50%	39531	11946
CGPLLU244	Lung Cancer	Pre-treatment, Day -7	100	80930	8305560600	4182616104	50%	50851	7569
CGPLLU244	Lung Cancer	Pre-treatment, Day -1	100	80930	7739951100	3788487116	49%	45925	8552
CGPLLU244	Lung Cancer	Post-treatment, Day 6	100	80930	8061928000	4225322272	52%	51279	8646
CGPLLU244	Lung Cancer	Post-treatment, Day 62	100	80930	8894936700	4437962639	50%	53862	7361
CGPLLU245	Lung Cancer	Pre-treatment, Day -32	100	80930	7679235200	3935822054	51%	47768	7266
CGPLLU245	Lung Cancer	Pre-treatment, Day 0	100	80930	8985252500	4824268339	54%	58338	10394
CGPLLU245	Lung Cancer	Post-treatment, Day 7	100	80930	8518229300	4480236927	53%	54083	10125
CGPLLU245	Lung Cancer	Post-treatment, Day 21	100	80930	9031131000	4824738475	53%	58313	10598
CGPLLU246	Lung Cancer	Pre-treatment, Day -21	100	80930	8520360800	3509660305	41%	42349	8086
CGPLLU246	Lung Cancer	Pre-treatment, Day 0	100	80930	5451467800	2828351657	52%	34243	8256
CGPLLU246	Lung Cancer	Post-treatment, Day 9	100	80930	8137616600	4135036174	51%	50121	6466
CGPLLU246	Lung Cancer	Post-treatment, Day 42	100	80930	8385724600	4413323333	53%	53495	7303
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	100	80930	6254777700	3016326208	48%	36164	12138
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	100	80930	6185331000	3087883231	50%	37003	8388
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	100	80930	6274540300	2861143666	46%	34308	6817
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	100	80930	5701274000	1241270938	22%	14886	4273
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	100	80930	6091276800	2922585558	48%	35004	7742
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	100	80930	6430107900	2945953499	46%	35219	8574
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	100	80930	5869510300	2792208995	48%	33423	8423
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	100	80930	5884330900	2588386038	44%	30977	9803
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	100	80930	5807524900	2347651479	40%	28146	5793
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	100	80930	6064269800	2086938782	34%	24994	6221

CGPLLU266	Lung Cancer	Pre-treatment, Day 0	100	80930	6785913900	3458588505	51%	41432	7765
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	100	80930	6513702000	2096370387	32%	25142	6598
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	100	80930	6610761200	2576886619	39%	31095	4485
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	100	80930	6156102000	2586081726	42%	30714	5309
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	100	80930	6180799700	2013434756	33%	23902	3885
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	100	80930	6221168600	1499602843	24%	17799	6098
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	100	80930	5353961600	1698331125	32%	20094	5252
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	100	80930	5831612800	1521114956	26%	18067	6210
CGPLLU271	Lung Cancer	Post-treatment, Day 259	100	80930	6229704000	1481468974	24%	17608	4633
CGPLLU271	Lung Cancer	Post-treatment, Day 259	100	80930	6134366400	1351029627	22%	16170	7024
CGPLLU271	Lung Cancer	Post-treatment, Day 259	100	80930	6491884900	1622578435	25%	19433	5792
CGPLLU271	Lung Cancer	Post-treatment, Day 259	100	80930	5742881200	2349421128	41%	28171	5723
CGPLLU271	Lung Cancer	Post-treatment, Day 259	100	80930	5503999300	1695782705	31%	20320	5907
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	100	80930	6575907000	3002048491	46%	35997	5445
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	100	80930	6204350900	3016077187	49%	36162	5704
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	100	80930	5997724300	2989608757	50%	35873	6228
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	100	80930	6026261500	2881177658	48%	34568	7221
CGPLLU86	Lung Cancer	Pre-treatment, Day 0	100	80930	8222093400	3523035056	43%	41165	3614
CGPLLU86	Lung Cancer	Post-treatment, Day 0.5	100	80930	8305719500	4271264008	51%	49508	6681
CGPLLU86	Lung Cancer	Post-treatment, Day 7	100	80930	6787785300	3443658418	51%	40192	3643
CGPLLU86	Lung Cancer	Post-treatment, Day 17	100	80930	6213229400	3120325926	50%	36413	3560
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	100	80930	7252433900	3621678746	50%	42719	8599
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	100	80930	7679995800	4004738253	52%	46951	6387
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	100	80930	6509178000	3316053733	51%	39274	2661
CGPLLU89	Lung Cancer	Pre-treatment, Day 0	100	80930	7662496600	3781536306	49%	44097	7909
CGPLLU89	Lung Cancer	Post-treatment, Day 7	100	80930	7005599500	3339612564	48%	38977	5034
CGPLLU89	Lung Cancer	Post-treatment, Day 22	100	80930	8325998600	3094796789	37%	36061	2822
CGPLOV10	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7073534200	3402308123	48%	39820	4059

CGPLOV11	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	6924062200	3324593050	48%	38796	7185
CGPLOV12	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	6552080100	3181854993	49%	37340	6114
CGPLOV13	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	6796755500	3264897084	48%	38340	7931
CGPLOV14	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7856573900	3408425065	43%	39997	7712
CGPLOV15	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7239201500	3322285607	46%	38953	6644
CGPLOV16	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8570755900	4344288233	51%	51009	11947
CGPLOV17	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	6910310400	2805243492	41%	32828	4307
CGPLOV18	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8173037600	4064432407	50%	47714	5182
CGPLOV19	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7732198900	3672564399	47%	43020	11127
CGPLOV20	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7559602000	3678700179	49%	43230	4872
CGPLOV21	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8949032900	4616255499	52%	54012	12777
CGPLOV22	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8680136500	4049934586	47%	46912	9715
CGPLOV23	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	6660696600	3422631774	51%	40810	9460
CGPLOV24	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8634287200	4272258165	49%	50736	8689
CGPLOV25	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	6978295000	3390206388	49%	40188	5856
CGPLOV26	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7041038300	3728879661	53%	44341	8950
CGPLOV28	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7429236900	3753051715	51%	45430	4155
CGPLOV31	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8981384000	4621838729	51%	55429	5458
CGPLOV32	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	9344536800	4737698323	51%	57234	6165
CGPLOV37	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8158083200	4184432898	51%	50648	6934
CGPLOV38	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8654435400	4492987085	52%	53789	6124
CGPLOV40	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	9868640700	4934400809	50%	59049	7721
CGPLOV41	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7689013600	3861448829	50%	46292	4469
CGPLOV42	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	9836516300	4864154366	49%	58302	7632
CGPLOV43	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8756507100	4515479918	52%	54661	4310
CGPLOV44	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7576310800	4120933922	54%	49903	4969
CGPLOV46	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	9346036300	5037820346	54%	61204	3927
CGPLOV47	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	10880620200	5491357828	50%	66363	6895

CGPLOV48	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	7658787800	3335991337	44%	40332	4066
CGPLOV49	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	10076208000	5519656698	55%	67117	5097
CGPLOV50	Ovarian Cancer	Preoperative, Treatment naïve	100	80930	8239290400	4472380276	54%	54150	3836
CGPLPA118	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	9094827600	4828332902	53%	57021	4802
CGPLPA122	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7303323100	3990160379	55%	47240	7875
CGPLPA124	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7573482800	3965807442	52%	46388	8658
CGPLPA126	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7904953600	4061463168	51%	47812	10498
CGPLPA128	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7249238300	2244188735	31%	26436	3413
CGPLPA129	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7559858900	4003725804	53%	47182	5733
CGPLPA130	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	6973946500	1247144905	18%	14691	1723
CGPLPA131	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7226237900	3370664342	47%	39661	5054
CGPLPA134	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7268866100	3754945844	52%	44306	7023
CGPLPA136	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7476690700	4073978408	54%	48134	5244
CGPLPA140	Bile Duct Cancer	Preoperative, Treatment naïve	100	80930	7364654600	3771765342	51%	44479	7080
CGST102	Gastric Cancer	Preoperative, Treatment naïve	100	80930	5715504500	2644902854	46%	31309	4503
CGST110	Gastric Cancer	Preoperative, Treatment naïve	100	80930	9179291500	4298269268	47%	51666	3873
CGST114	Gastric Cancer	Preoperative, Treatment naïve	100	80930	7151572200	3254967293	46%	38496	4839
CGST13	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6449701500	3198545984	50%	38515	6731
CGST141	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6781001300	3440927391	51%	40762	5404
CGST16	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6396470600	2931380289	46%	35354	8148
CGST18	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6647324000	3138967777	47%	37401	4992
CGST28	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6288486100	2884997993	46%	34538	2586
CGST30	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6141213100	3109994564	51%	37194	2555
CGST32	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6969139300	3099120469	44%	36726	3935
CGST33	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6560309400	3168371917	48%	37916	4597
CGST39	Gastric Cancer	Preoperative, Treatment naïve	100	80930	7043791400	2992801875	42%	35620	6737
CGST41	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6975053100	3224065662	46%	38300	4016
CGST45	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6130812200	2944524278	48%	35264	4745

CGST47	Gastric Cancer	Preoperative, Treatment naïve	100	80930	5961400000	3083523351	52%	37008	3112
CGST48	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6418652700	1497230327	23%	17782	2410
CGST58	Gastric Cancer	Preoperative, Treatment naïve	100	80930	5818344500	1274708429	22%	15281	2924
CGST80	Gastric Cancer	Preoperative, Treatment naïve	100	80930	6368064600	3298497188	52%	39692	5280
CGST81	Gastric Cancer	Preoperative, Treatment naïve	100	80930	8655691400	1519121452	18%	17988	6419

Table 4.3. Summary of targeted cfDNA fragment analyses in cancer patients.

Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction
CGCRC291	Colorectal Cancer	IV	Tumor-derived	STK11	39R>C	chr19_1207027-1207027_C_T	Substitution	No	No	0.14%
CGCRC291	Colorectal Cancer	IV	Tumor-derived	TP53	272V>M	chr17_7577124-7577124_C_T	Substitution	Yes	No	0.10%
CGCRC291	Colorectal Cancer	IV	Tumor-derived	TP53	167Q>X	chr17_7578431-7578431_G_A	Substitution	Yes	Yes	22.85%
CGCRC291	Colorectal Cancer	IV	Tumor-derived	KRAS	12G>A	chr12_25398284-25398284_C_G	Substitution	Yes	Yes	14.65%
CGCRC291	Colorectal Cancer	IV	Tumor-derived	APC	1260Q>X	chr5_112175069-112175069_C_T	Substitution	No	Yes	11.23%
CGCRC291	Colorectal Cancer	IV	Tumor-derived	APC	1450R>X	chr5_112175639-112175639_C_T	Substitution	Yes	Yes	11.05%
CGCRC291	Colorectal Cancer	IV	Tumor-derived	PIK3CA	542E>K	chr3_178936082-178936082_G_A	Substitution	Yes	Yes	18.11%
CGCRC292	Colorectal Cancer	IV	Tumor-derived	KRAS	146A>V	chr12_25378561-25378561_G_A	Substitution	Yes	No	1.41%
CGCRC292	Colorectal Cancer	IV	Tumor-derived	CTNNB1	41T>A	chr3_41266124-41266124_A_G	Substitution	Yes	Yes	0.13%
CGCRC292	Colorectal Cancer	IV	Germline	EGFR	2284-4C>G	chr7_55248982-55248982_C_G	Substitution	NA	Yes	31.99%
CGCRC293	Colorectal Cancer	IV	Tumor-derived	TP53	176C>S	chr17_7578404-7578404_A_T	Substitution	No	No	0.35%
CGCRC294	Colorectal Cancer	II	Tumor-derived	APC	213R>X	chr5_112116592-112116592_C_T	Substitution	Yes	Yes	0.14%
CGCRC294	Colorectal Cancer	II	Tumor-derived	APC	1367Q>X	chr5_112175390-112175390_C_T	Substitution	Yes	Yes	0.13%
CGCRC295	Colorectal Cancer	IV	Tumor-derived	PDGFRA	49+4C>T	chr4_55124988-55124988_C_T	Substitution	No	No	0.45%
CGCRC295	Colorectal Cancer	IV	Hematopoietic	IDH1	104G>V	chr2_209113196-209113196_C_A	Substitution	No	Yes	0.34%
CGCRC296	Colorectal Cancer	II	Germline	EGFR	922E>K	chr7_55266472-55266472_G_A	Substitution	NA	Yes	30.48%
CGCRC297	Colorectal Cancer	III	Germline	KIT	18L>F	chr4_55524233-55524233_C_T	Substitution	NA	Yes	41.39%
CGCRC298	Colorectal Cancer	II	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.08%
CGCRC298	Colorectal Cancer	II	Hematopoietic	DNMT3A	714S>C	chr2_25463541-25463541_G_C	Substitution	No	No	0.11%
CGCRC298	Colorectal Cancer	II	Tumor-derived	PIK3CA	414G>V	chr3_178927478-178927478_G_T	Substitution	No	No	0.55%
CGCRC299	Colorectal Cancer	I	Hematopoietic	DNMT3A	735Y>C	chr2_25463289-25463289_T_C	Substitution	No	Yes	0.30%
CGCRC299	Colorectal Cancer	I	Hematopoietic	DNMT3A	710C>S	chr2_25463553-25463553_C_G	Substitution	No	Yes	0.12%
CGCRC300	Colorectal Cancer	I	Hematopoietic	DNMT3A	720R>G	chr2_25463524-25463524_G_C	Substitution	No	No	0.15%
CGCRC301	Colorectal Cancer	I	Tumor-derived	ATM	2397Q>X	chr11_108199847-108199847_C_T	Substitution	No	No	0.21%

CGCRC302	Colorectal Cancer	II	Tumor-derived	TP53	141C>Y	chr17_7578508-7578508_C_T	Substitution	Yes	Yes	0.05%
CGCRC302	Colorectal Cancer	II	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.12%
CGCRC303	Colorectal Cancer	III	Tumor-derived	TP53	173V>L	chr17_7578413-7578413_C_A	Substitution	Yes	Yes	0.08%
CGCRC303	Colorectal Cancer	III	Hematopoietic	DNMT3A	755F>S	chr2_25463229-25463229_A_G	Substitution	No	No	0.21%
CGCRC303	Colorectal Cancer	III	Hematopoietic	DNMT3A	2173+1G>A	chr2_25463508-25463508_C_T	Substitution	No	No	0.17%
CGCRC304	Colorectal Cancer	II	Tumor-derived	EGFR	1131T>S	chr7_55273068-55273068_A_T	Substitution	No	No	0.22%
CGCRC304	Colorectal Cancer	II	Tumor-derived	ATM	3077+1G>A	chr11_108142134-108142134_G_A	Substitution	No	No	0.27%
CGCRC304	Colorectal Cancer	II	Hematopoietic	ATM	3008R>C	chr11_108236086-108236086_C_T	Substitution	No	Yes	0.43%
CGCRC305	Colorectal Cancer	II	Tumor-derived	GNA11	213R>Q	chr19_3118954-3118954_G_A	Substitution	No	Yes	0.11%
CGCRC305	Colorectal Cancer	II	Tumor-derived	TP53	273R>H	chr17_7577120-7577120_C_T	Substitution	Yes	No	0.19%
CGCRC306	Colorectal Cancer	II	Tumor-derived	TP53	196R>X	chr17_7578263-7578263_G_A	Substitution	Yes	No	0.12%
CGCRC306	Colorectal Cancer	II	Tumor-derived	CDKN2A	107R>C	chr9_21971039-21971039_G_A	Substitution	No	Yes	8.02%
CGCRC306	Colorectal Cancer	II	Tumor-derived	KRAS	61Q>K	chr12_25380277-25380277_G_T	Substitution	Yes	Yes	7.30%
CGCRC306	Colorectal Cancer	II	Germline	PDGFRA	200T>S	chr4_55130065-55130065_C_G	Substitution	NA	Yes	34.78%
CGCRC306	Colorectal Cancer	II	Tumor-derived	EGFR	618H>R	chr7_55233103-55233103_A_G	Substitution	No	Yes	6.32%
CGCRC306	Colorectal Cancer	II	Tumor-derived	PIK3CA	545E>A	chr3_178936092-178936092_A_C	Substitution	Yes	No	0.96%
CGCRC306	Colorectal Cancer	II	Germline	ERBB4	1155R>X	chr2_212251596-212251596_G_A	Substitution	NA	Yes	38.70%
CGCRC307	Colorectal Cancer	II	Tumor-derived	JAK2	805L>V	chr9_5080662-5080662_C_G	Substitution	No	No	0.56%
CGCRC307	Colorectal Cancer	II	Tumor-derived	SMARCB1	501-2A>G	chr22_24145480-24145480_A_G	Substitution	No	Yes	0.34%
CGCRC307	Colorectal Cancer	II	Tumor-derived	GNAS	201R>C	chr20_57484420-57484420_C_T	Substitution	Yes	Yes#	0.24%
CGCRC307	Colorectal Cancer	II	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.38%
CGCRC307	Colorectal Cancer	II	Tumor-derived	FBXW7	465R>C	chr4_153249385-153249385_G_A	Substitution	Yes	Yes	0.31%
CGCRC307	Colorectal Cancer	II	Tumor-derived	ERBB4	17A>V	chr2_213403205-213403205_G_A	Substitution	No	No	0.15%
CGCRC308	Colorectal Cancer	III	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.06%
CGCRC308	Colorectal Cancer	III	Germline	EGFR	848P>L	chr7_55259485-55259485_C_T	Substitution	NA	Yes	27.69%
CGCRC308	Colorectal Cancer	III	Tumor-derived	APC	1480Q>X	chr5_112175729-112175729_C_T	Substitution	No	Yes	0.11%
CGCRC309	Colorectal Cancer	III	Tumor-derived	AKT1	17E>K	chr14_105246551-105246551_C_T	Substitution	Yes	Yes	2.70%
CGCRC309	Colorectal Cancer	III	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	3.00%

CGCRC310	Colorectal Cancer	II	Tumor-derived	KRAS	12G>V	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	0.13%
CGCRC310	Colorectal Cancer	II	Tumor-derived	APC	1513E>X	chr5_112175828-112175828_G_T	Substitution	No	Yes	0.11%
CGCRC310	Colorectal Cancer	II	Tumor-derived	APC	1521E>X	chr5_112175852-112175852_G_T	Substitution	No	Yes	0.15%
CGCRC311	Colorectal Cancer	I	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.86%
CGCRC312	Colorectal Cancer	III	Tumor-derived	APC	960S>X	chr5_112174170-112174170_C_G	Substitution	No	Yes	0.59%
CGCRC312	Colorectal Cancer	III	Tumor-derived	NRAS	61Q>K	chr1_115256530-115256530_G_T	Substitution	Yes	Yes	0.47%
CGCRC313	Colorectal Cancer	III	Tumor-derived	KRAS	12G>S	chr12_25398285-25398285_C_T	Substitution	Yes	Yes	0.17%
CGCRC313	Colorectal Cancer	III	Tumor-derived	APC	876R>X	chr5_112173917-112173917_C_T	Substitution	Yes	Yes	0.07%
CGCRC314	Colorectal Cancer	I	Tumor-derived	KRAS	12G>D	chr12_25398284-25398284_C_T	Substitution	Yes	Yes	0.30%
CGCRC314	Colorectal Cancer	I	Hematopoietic	DNMT3A	738L>Q	chr2_25463280-25463280_A_T	Substitution	No	Yes	2.50%
CGCRC314	Colorectal Cancer	I	Tumor-derived	APC	1379E>X	chr5_112175426-112175426_G_T	Substitution	Yes	Yes	0.38%
CGCRC315	Colorectal Cancer	III	Tumor-derived	NRAS	12G>D	chr1_115258747-115258747_C_T	Substitution	Yes	Yes	0.27%
CGCRC315	Colorectal Cancer	III	Tumor-derived	FBXW7	505R>C	chr4_153247289-153247289_G_A	Substitution	Yes	Yes	0.25%
CGCRC316	Colorectal Cancer	III	Tumor-derived	TP53	245G>S	chr17_7577548-7577548_C_T	Substitution	Yes	Yes	6.52%
CGCRC316	Colorectal Cancer	III	Tumor-derived	CDKN2A	1M>R	chr9_21974825-21974825_A_C	Substitution	No	Yes	5.74%
CGCRC316	Colorectal Cancer	III	Tumor-derived	CTNNB1	37S>C	chr3_41266113-41266113_C_G	Substitution	Yes	Yes	5.47%
CGCRC316	Colorectal Cancer	III	Tumor-derived	EGFR	2702-3C>T	chr7_55266407-55266407_C_T	Substitution	No	No	0.11%
CGCRC316	Colorectal Cancer	III	Hematopoietic	ATM	3008R>P	chr11_108236087-108236087_G_C	Substitution	No	Yes	0.13%
CGCRC317	Colorectal Cancer	III	Tumor-derived	TP53	220Y>C	chr17_7578190-7578190_T_C	Substitution	Yes	Yes	0.36%
CGCRC317	Colorectal Cancer	III	Tumor-derived	ATM	1026W>R	chr11_108142132-108142132_T_C	Substitution	No	Yes	0.23%
CGCRC317	Colorectal Cancer	III	Tumor-derived	APC	216R>X	chr5_112128143-112128143_C_T	Substitution	Yes	No	0.29%
CGCRC318	Colorectal Cancer	I	Hematopoietic	DNMT3A	698W>X	chr2_25463589-25463589_C_T	Substitution	No	Yes	0.25%
CGCRC320	Colorectal Cancer	I	Germline	KIT	18L>F	chr4_55524233-55524233_C_T	Substitution	NA	Yes	34.76%
CGCRC320	Colorectal Cancer	I	Tumor-derived	ERBB4	78R>W	chr2_212989479-212989479_G_A	Substitution	No	No	0.12%
CGCRC321	Colorectal Cancer	I	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.20%
CGCRC321	Colorectal Cancer	I	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.08%
CGCRC321	Colorectal Cancer	I	Germline	EGFR	511S>Y	chr7_55229225-55229225_C_A	Substitution	NA	Yes	41.86%
CGCRC332	Colorectal Cancer	IV	Tumor-derived	TP53	125T>R	chr17_7579313-7579313_G_C	Substitution	No	Yes	19.98%

CGCRC333	Colorectal Cancer	IV	Tumor-derived	TP53	673-2A>G	chr17_7577610-7577610_T_C	Substitution	No	Yes	43.03%
CGCRC333	Colorectal Cancer	IV	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	22.26%
CGCRC333	Colorectal Cancer	IV	Tumor-derived	ERBB4	691E>A	chr2_212495194-212495194_T_G	Substitution	No	No	1.00%
CGCRC334	Colorectal Cancer	IV	Tumor-derived	TP53	245G>S	chr17_7577548-7577548_C_T	Substitution	Yes	Yes	13.44%
CGCRC334	Colorectal Cancer	IV	Germline	EGFR	638T>M	chr7_55238900-55238900_C_T	Substitution	NA	Yes	35.28%
CGCRC334	Colorectal Cancer	IV	Tumor-derived	PIK3CA	104P>R	chr3_178916924-178916924_C_G	Substitution	No	No	3.85%
CGCRC335	Colorectal Cancer	IV	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.32%
CGCRC336	Colorectal Cancer	IV	Tumor-derived	TP53	175R>H	chr17_7578406-7578406_C_T	Substitution	Yes	Yes	75.26%
CGCRC336	Colorectal Cancer	IV	Tumor-derived	KRAS	12G>V	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	42.87%
CGCRC336	Colorectal Cancer	IV	Tumor-derived	APC	1286E>X	chr5_112175147-112175147_G_T	Substitution	No	Yes	81.61%
CGCRC337	Colorectal Cancer	IV	Tumor-derived	STK11	734+2T>A	chr19_1220718-1220718_T_A	Substitution	No	No	0.12%
CGCRC337	Colorectal Cancer	IV	Germline	APC	485M>I	chr5_112162851-112162851_G_A	Substitution	NA	Yes	46.26%
CGCRC338	Colorectal Cancer	IV	Tumor-derived	KRAS	12G>D	chr12_25398284-25398284_C_T	Substitution	Yes	Yes	27.03%
CGCRC339	Colorectal Cancer	IV	Tumor-derived	KRAS	13G>D	chr12_25398281-25398281_C_T	Substitution	Yes	Yes	1.94%
CGCRC339	Colorectal Cancer	IV	Tumor-derived	APC	876R>X	chr5_112173917-112173917_C_T	Substitution	Yes	Yes	2.35%
CGCRC339	Colorectal Cancer	IV	Tumor-derived	PIK3CA	407C>F	chr3_178927457-178927457_G_T	Substitution	No	Yes	3.14%
CGCRC339	Colorectal Cancer	IV	Tumor-derived	PIK3CA	1047H>L	chr3_178952085-178952085_A_T	Substitution	Yes	Yes	1.71%
CGCRC340	Colorectal Cancer	IV	Tumor-derived	TP53	196R>X	chr17_7578263-7578263_G_A	Substitution	Yes	Yes	18.26%
CGCRC340	Colorectal Cancer	IV	Tumor-derived	APC	1306E>X	chr5_112175207-112175207_G_T	Substitution	Yes	Yes	22.57%
CGPLBR38	Breast Cancer	I	Tumor-derived	TP53	241S>P	chr17_7577560-7577560_A_G	Substitution	No	Yes	0.53%
CGPLBR40	Breast Cancer	III	Germline	AR	392P>R	chrX_66766163-66766163_C_G	Substitution	NA	Yes	28.99%
CGPLBR44	Breast Cancer	III	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	1.82%
CGPLBR44	Breast Cancer	III	Hematopoietic	DNMT3A	705I>T	chr2_25463568-25463568_A_G	Substitution	No	Yes	0.41%
CGPLBR44	Breast Cancer	III	Tumor-derived	PDGFRA	859V>M	chr4_55153609-55153609_G_A	Substitution	No	Yes	0.13%
CGPLBR48	Breast Cancer	II	Germline	ALK	1231R>Q	chr2_29436901-29436901_C_T	Substitution	NA	Yes	34.61%
CGPLBR48	Breast Cancer	II	Tumor-derived	EGFR	669R>Q	chr7_55240762-55240762_G_A	Substitution	No	No	0.18%
CGPLBR55	Breast Cancer	III	Hematopoietic	DNMT3A	743P>S	chr2_25463266-25463266_G_A	Substitution	No	No	0.18%
CGPLBR55	Breast Cancer	III	Tumor-derived	GNAS	201R>H	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.68%

CGPLBR55	Breast Cancer	III	Tumor-derived	PIK3CA	345N>K	chr3_178921553-178921553_T_A	Substitution	Yes	Yes	0.42%
CGPLBR63	Breast Cancer	II	Germline	FGFR3	403K>E	chr4_1806188-1806188_A_G	Substitution	NA	Yes	34.82%
CGPLBR67	Breast Cancer	III	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.11%
CGPLBR67	Breast Cancer	III	Tumor-derived	PIK3CA	545E>K	chr3_178936091-178936091_G_A	Substitution	Yes	Yes	0.68%
CGPLBR67	Breast Cancer	III	Tumor-derived	ERBB4	1000D>A	chr2_212285302-212285302_T_G	Substitution	No	No	0.28%
CGPLBR69	Breast Cancer	II	Hematopoietic	DNMT3A	774E>V	chr2_25463172-25463172_T_A	Substitution	No	No	0.29%
CGPLBR69	Breast Cancer	II	Germline	CTNNB1	30Y>S	chr3_41266092-41266092_A_C	Substitution	NA	Yes	41.74%
CGPLBR69	Breast Cancer	II	Germline	IDH1	231Y>N	chr2_209108158-209108158_A_T	Substitution	NA	Yes	41.66%
CGPLBR70	Breast Cancer	II	Tumor-derived	ATM	2832R>H	chr11_108216546-108216546_G_A	Substitution	No	No	0.36%
CGPLBR70	Breast Cancer	II	Germline	APC	1577E>D	chr5_112176022-112176022_A_C	Substitution	NA	Yes	40.28%
CGPLBR71	Breast Cancer	II	Tumor-derived	TP53	273R>H	chr17_7577120-7577120_C_T	Substitution	Yes	Yes	0.10%
CGPLBR72	Breast Cancer	II	Germline	APC	1532D>G	chr5_112175886-112175886_A_G	Substitution	NA	Yes	44.03%
CGPLBR73	Breast Cancer	II	Tumor-derived	ALK	708S>P	chr2_29474053-29474053_A_G	Substitution	No	No	0.27%
CGPLBR73	Breast Cancer	II	Germline	ERBB4	158A>E	chr2_212652833-212652833_G_T	Substitution	NA	Yes	35.58%
CGPLBR74	Breast Cancer	II	Germline	AR	20+1G>T	chrX_66788865-66788865_G_T	Substitution	NA	Yes	36.23%
CGPLBR75	Breast Cancer	II	Tumor-derived	PIK3CA	1047H>R	chr3_178952085-178952085_A_G	Substitution	Yes	Yes	0.14%
CGPLBR76	Breast Cancer	II	Germline	KDR	1290S>N	chr4_55946310-55946310_C_T	Substitution	NA	Yes	36.57%
CGPLBR76	Breast Cancer	II	Tumor-derived	PIK3CA	1047H>R	chr3_178952085-178952085_A_G	Substitution	Yes	Yes	0.12%
CGPLBR77	Breast Cancer	III	Tumor-derived	PTEN	170S>I	chr10_89711891-89711891_G_T	Substitution	No	Yes	2.29%
CGPLBR80	Breast Cancer	II	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.54%
CGPLBR83	Breast Cancer	II	Germline	AR	728N>D	chrX_66937328-66937328_A_G	Substitution	NA	Yes	42.66%
CGPLBR83	Breast Cancer	II	Tumor-derived	ATM	322E>K	chr11_108117753-108117753_G_A	Substitution	No	No	0.28%
CGPLBR83	Breast Cancer	II	Germline	ERBB4	539Y>S	chr2_212543783-212543783_T_G	Substitution	NA	Yes	44.91%
CGPLBR86	Breast Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	42.32%
CGPLBR86	Breast Cancer	II	Germline	SMARCB1	795+3A>G	chr22_24159126-24159126_A_G	Substitution	NA	Yes	43.38%
CGPLBR87	Breast Cancer	II	Tumor-derived	JAK2	215R>X	chr9_5054591-5054591_C_T	Substitution	No	No	0.35%
CGPLBR87	Breast Cancer	II	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.31%
CGPLBR87	Breast Cancer	II	Tumor-derived	SMAD4	496R>C	chr18_48604664-48604664_C_T	Substitution	No	No	0.40%

CGPLBR87	Breast Cancer	II	Germline	AR	651S>N	chrX_66931310-66931310_G_A	Substitution	NA	Yes	42.94%
CGPLBR88	Breast Cancer	II	Tumor-derived	CDK6	51E>K	chr7_92462487-92462487_C_T	Substitution	No	No	0.13%
CGPLBR88	Breast Cancer	II	Germline	APC	1125V>A	chr5_112174665-112174665_T_C	Substitution	NA	Yes	31.19%
CGPLBR92	Breast Cancer	II	Tumor-derived	TP53	257L>P	chr17_7577511-7577511_A_G	Substitution	No	Yes	0.20%
CGPLBR96	Breast Cancer	II	Tumor-derived	TP53	213R>X	chr17.fa:7578212-7578212_G_A	Substitution	Yes	No	0.10%
CGPLBR96	Breast Cancer	II	Hematopoietic	DNMT3A	531D>G	chr2_25467484-25467484_T_C	Substitution	No	Yes	5.81%
CGPLBR96	Breast Cancer	II	Tumor-derived	AR	13R>Q	chrX_66765026-66765026_G_A	Substitution	No	No	0.60%
CGPLBR97	Breast Cancer	II	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.11%
CGPLBR97	Breast Cancer	II	Germline	PDGFRA	401A>D	chr4_55136880-55136880_C_A	Substitution	NA	Yes	34.12%
CGPLBR97	Breast Cancer	II	Tumor-derived	GNAS	201R>H	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.13%
CGPLLU144	Lung Cancer	II	Tumor-derived	TP53	241S>F	chr17_7577559-7577559_G_A	Substitution	Yes	Yes	1.95%
CGPLLU144	Lung Cancer	II	Tumor-derived	KRAS	12G>C	chr12_25398285-25398285_C_A	Substitution	Yes	Yes	5.10%
CGPLLU144	Lung Cancer	II	Tumor-derived	EGFR	373P>S	chr7_55224336-55224336_C_T	Substitution	No	Yes	0.16%
CGPLLU144	Lung Cancer	II	Tumor-derived	ATM	292P>L	chr11_108115727-108115727_C_T	Substitution	No	No	0.22%
CGPLLU144	Lung Cancer	II	Tumor-derived	PIK3CA	545E>K	chr3_178936091-178936091_G_A	Substitution	Yes	Yes	2.94%
CGPLLU144	Lung Cancer	II	Tumor-derived	ERBB4	426R>K	chr2_212568841-212568841_C_T	Substitution	No	No	0.18%
CGPLLU146	Lung Cancer	II	Hematopoietic	JAK2	617V>F	chr9_5073770-5073770_G_T	Substitution	Yes	No	0.25%
CGPLLU146	Lung Cancer	II	Tumor-derived	TP53	282R>P	chr17_7577093-7577093_C_G	Substitution	No	Yes	1.30%
CGPLLU146	Lung Cancer	II	Hematopoietic	DNMT3A	737L>H	chr2_25463283-25463283_A_T	Substitution	No	Yes	0.84%
CGPLLU146	Lung Cancer	II	Tumor-derived	RB1	861+2T>C	chr13_48937095-48937095_T_C	Substitution	No	Yes	0.87%
CGPLLU146	Lung Cancer	II	Tumor-derived	ATM	581L>F	chr11_108122699-108122699_A_T	Substitution	No	No	0.20%
CGPLLU147	Lung Cancer	III	Tumor-derived	TP53	248R>Q	chr17_7577538-7577538_C_T	Substitution	Yes	No	0.15%
CGPLLU147	Lung Cancer	III	Tumor-derived	TP53	201L>X	chr17_7578247-7578247_A_T	Substitution	No	Yes	0.55%
CGPLLU147	Lung Cancer	III	Tumor-derived	ALK	1537G>E	chr2_29416343-29416343_C_T	Substitution	No	Yes	0.94%
CGPLLU147	Lung Cancer	III	Germline	PDGFRA	200T>S	chr4_55130065-55130065_C_G	Substitution	NA	Yes	43.47%
CGPLLU162	Lung Cancer	II	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.22%
CGPLLU162	Lung Cancer	II	Tumor-derived	EGFR	858L>R	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.22%
CGPLLU162	Lung Cancer	II	Tumor-derived	BRAF	354R>Q	chr7_140494187-140494187_C_T	Substitution	No	No	0.14%

CGPLLU163	Lung Cancer	II	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.21%
CGPLLU163	Lung Cancer	II	Hematopoietic	DNMT3A	528Y>D	chr2_25467494-25467494_A_C	Substitution	No	Yes	0.15%
CGPLLU164	Lung Cancer	II	Tumor-derived	STK11	216S>Y	chr19_1220629-1220629_C_A	Substitution	No	Yes	1.23%
CGPLLU164	Lung Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	42.52%
CGPLLU164	Lung Cancer	II	Tumor-derived	GNA11	606-3C>T	chr19_3118919-3118919_C_T	Substitution	No	No	0.20%
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	278P>S	chr17_7577106-7577106_G_A	Substitution	Yes	No	0.10%
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	161A>S	chr17_7578449-7578449_C_A	Substitution	No	Yes	1.78%
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	160M>I	chr17_7578450-7578450_C_A	Substitution	No	Yes	1.86%
CGPLLU164	Lung Cancer	II	Tumor-derived	ERBB4	1299P>L	chr2_212248371-212248371_G_A	Substitution	No	Yes	0.96%
CGPLLU164	Lung Cancer	II	Tumor-derived	ERBB4	253N>S	chr2_212587243-212587243_T_C	Substitution	No	No	0.22%
CGPLLU165	Lung Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	36.62%
CGPLLU165	Lung Cancer	II	Tumor-derived	GNAS	201R>H	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.16%
CGPLLU168	Lung Cancer	I	Tumor-derived	TP53	136Q>X	chr17.fa:7578524-7578524_G_A	Substitution	Yes	Yes	0.06%
CGPLLU168	Lung Cancer	I	Hematopoietic	DNMT3A	736R>S	chr2_25463287-25463287_G_T	Substitution	No	No	0.39%
CGPLLU168	Lung Cancer	I	Tumor-derived	EGFR	858L>R	chr7.fa:55259515-55259515_T_G	Substitution	Yes	Yes	0.07%
CGPLLU174	Lung Cancer	I	Tumor-derived	STK11	597+1G>T	chr19_1220505-1220505_G_T	Substitution	No	Yes	0.33%
CGPLLU174	Lung Cancer	I	Tumor-derived	JAK2	160D>Y	chr9_5050695-5050695_G_T	Substitution	No	Yes	0.40%
CGPLLU174	Lung Cancer	I	Tumor-derived	KRAS	12G>C	chr12_25398285-25398285_C_A	Substitution	Yes	Yes	0.16%
CGPLLU174	Lung Cancer	I	Hematopoietic	DNMT3A	891R>W	chr2_25457216-25457216_G_A	Substitution	No	Yes	0.29%
CGPLLU174	Lung Cancer	I	Hematopoietic	DNMT3A	715I>M	chr2_25463537-25463537_G_C	Substitution	No	Yes	0.26%
CGPLLU175	Lung Cancer	I	Tumor-derived	TP53	179H>R	chr17_7578394-7578394_T_C	Substitution	Yes	Yes	8.03%
CGPLLU175	Lung Cancer	I	Hematopoietic	DNMT3A	2598-1G>A	chr2_25457290-25457290_C_T	Substitution	No	No	0.21%
CGPLLU175	Lung Cancer	I	Hematopoietic	DNMT3A	755F>L	chr2_25463230-25463230_A_G	Substitution	No	Yes	0.15%
CGPLLU175	Lung Cancer	I	Germline	ATM	337R>C	chr11_108117798-108117798_C_T	Substitution	NA	Yes	43.84%
CGPLLU175	Lung Cancer	I	Tumor-derived	ERBB4	941Q>X	chr2_212288925-212288925_G_A	Substitution	No	Yes	3.64%
CGPLLU176	Lung Cancer	I	Hematopoietic	DNMT3A	750P>S	chr2_25463245-25463245_G_A	Substitution	No	Yes	0.92%
CGPLLU176	Lung Cancer	I	Hematopoietic	DNMT3A	735Y>C	chr2_25463289-25463289_T_C	Substitution	No	Yes	0.21%
CGPLLU177	Lung Cancer	II	Tumor-derived	KRAS	12G>V	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	2.49%

CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	897V>G	chr2_25457197-25457197_A_C	Substitution	No	Yes	1.53%
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	882R>C	chr2_25457243-25457243_G_A	Substitution	Yes	No	0.29%
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	2173+1G>A	chr2_25463508-25463508_C_T	Substitution	No	No	0.13%
CGPLLU178	Lung Cancer	I	Tumor-derived	CDH1	251T>M	chr16_68844164-68844164_C_T	Substitution	No	No	0.29%
CGPLLU178	Lung Cancer	I	Tumor-derived	PIK3CA	861Q>X	chr3_178947145-178947145_C_T	Substitution	No	No	0.17%
CGPLLU179	Lung Cancer	I	Hematopoietic	DNMT3A	879N>D	chr2_25457252-25457252_T_C	Substitution	No	Yes	0.38%
CGPLLU179	Lung Cancer	I	Germline	APC	2611T>I	chr5_112179123-112179123_C_T	Substitution	NA	Yes	39.91%
CGPLLU180	Lung Cancer	I	Tumor-derived	STK11	237D>Y	chr19_1220691-1220691_G_T	Substitution	No	Yes	2.43%
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	293G>V	chr17_7577060-7577060_C_A	Substitution	No	Yes	2.07%
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	282R>P	chr17_7577093-7577093_C_G	Substitution	No	Yes	1.94%
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	177P>L	chr17.fa:7578400-7578400_G_A	Substitution	Yes	No	0.08%
CGPLLU180	Lung Cancer	I	Tumor-derived	RB1	565S>X	chr13_48955578-48955578_C_G	Substitution	No	Yes	1.01%
CGPLLU197	Lung Cancer	I	Hematopoietic	DNMT3A	882R>C	chr2_25457243-25457243_G_A	Substitution	Yes	No	0.16%
CGPLLU197	Lung Cancer	I	Hematopoietic	DNMT3A	879N>D	chr2_25457252-25457252_T_C	Substitution	No	No	0.38%
CGPLLU198	Lung Cancer	I	Tumor-derived	TP53	162I>N	chr17_7578445-7578445_A_T	Substitution	No	Yes	0.87%
CGPLLU198	Lung Cancer	I	Tumor-derived	EGFR	858L>R	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.52%
CGPLLU202	Lung Cancer	I	Tumor-derived	EGFR	790T>M	chr7.fa:55249071-55249071_C_T	Substitution	Yes	Yes	0.05%
CGPLLU202	Lung Cancer	I	Tumor-derived	EGFR	868E>X	chr7_55259544-55259544_G_T	Substitution	No	No	0.13%
CGPLLU204	Lung Cancer	I	Tumor-derived	KIT	956R>Q	chr4_55604659-55604659_G_A	Substitution	No	No	0.26%
CGPLLU205	Lung Cancer	II	Hematopoietic	DNMT3A	736R>C	chr2_25463287-25463287_G_A	Substitution	No	Yes	0.70%
CGPLLU205	Lung Cancer	II	Hematopoietic	DNMT3A	696Q>X	chr2_25463596-25463596_G_A	Substitution	No	Yes	3.47%
CGPLLU206	Lung Cancer	III	Tumor-derived	TP53	672+1G>A	chr17_7578176-7578176_C_T	Substitution	Yes	Yes	26.13%
CGPLLU206	Lung Cancer	III	Tumor-derived	TP53	131N>S	chr17_7578538-7578538_T_C	Substitution	No	No	0.21%
CGPLLU207	Lung Cancer	II	Tumor-derived	TP53	376-1G>A	chr17_7578555-7578555_C_T	Substitution	Yes	Yes	0.32%
CGPLLU207	Lung Cancer	II	Germline	ALK	419F>L	chr2_29606625-29606625_A_G	Substitution	NA	Yes	34.58%
CGPLLU207	Lung Cancer	II	Tumor-derived	EGFR	790T>M	chr7.fa:55249071-55249071_C_T	Substitution	Yes	No	0.09%
CGPLLU208	Lung Cancer	II	Tumor-derived	TP53	250P>L	chr17_7577532-7577532_G_A	Substitution	Yes	Yes	1.33%
CGPLLU208	Lung Cancer	II	Germline	EGFR	224R>H	chr7_55220281-55220281_G_A	Substitution	NA	Yes	39.34%

CGPLLU208	Lung Cancer	II	Tumor-derived	EGFR	858L>R	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.86%
CGPLLU208	Lung Cancer	II	Tumor-derived	MYC	98R>W	chr8_128750755-128750755_C_T	Substitution	No	No	0.17%
CGPLLU209	Lung Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	26.84%
CGPLLU209	Lung Cancer	II	Tumor-derived	TP53	100Q>X	chr17_7579389-7579389_G_A	Substitution	No	Yes	9.97%
CGPLLU209	Lung Cancer	II	Tumor-derived	CDKN2A	88E>X	chr9_21971096-21971096_C_A	Substitution	Yes	Yes	9.13%
CGPLLU209	Lung Cancer	II	Tumor-derived	PDGFRA	921A>T	chr4_55155052-55155052_G_A	Substitution	No	Yes	9.82%
CGPLLU209	Lung Cancer	II	Germline	EGFR	567M>V	chr7_55231493-55231493_A_G	Substitution	NA	Yes	30.41%
CGPLOV10	Ovarian Cancer	I	Tumor-derived	TP53	342R>X	chr17_7574003-7574003_G_A	Substitution	Yes	Yes	3.14%
CGPLOV11	Ovarian Cancer	IV	Tumor-derived	TP53	248R>Q	chr17_7577538-7577538_C_T	Substitution	Yes	Yes	0.87%
CGPLOV11	Ovarian Cancer	IV	Germline	TP53	63A>V	chr17_7579499-7579499_G_A	Substitution	NA	Yes	37.77%
CGPLOV13	Ovarian Cancer	IV	Tumor-derived	ALK	444W>C	chr2_29551298-29551298_C_A	Substitution	No	Yes	0.12%
CGPLOV13	Ovarian Cancer	IV	Germline	PDGFRA	401A>D	chr4_55136880-55136880_C_A	Substitution	NA	Yes	37.98%
CGPLOV13	Ovarian Cancer	IV	Tumor-derived	KIT	135R>H	chr4_55564516-55564516_G_A	Substitution	No	Yes	0.35%
CGPLOV14	Ovarian Cancer	I	Tumor-derived	HNF1A	230E>K	chr12_121431484-121431484_G_A	Substitution	No	No	0.14%
CGPLOV15	Ovarian Cancer	III	Tumor-derived	TP53	278P>S	chr17_7577106-7577106_G_A	Substitution	Yes	Yes	3.54%
CGPLOV15	Ovarian Cancer	III	Tumor-derived	EGFR	433H>D	chr7_55225445-55225445_C_G	Substitution	No	No	0.19%
CGPLOV17	Ovarian Cancer	I	Tumor-derived	TP53	248R>Q	chr17_7577538-7577538_C_T	Substitution	Yes	Yes	0.32%
CGPLOV17	Ovarian Cancer	I	Germline	PDGFRA	1071D>N	chr4_55161380-55161380_G_A	Substitution	NA	Yes	44.10%
CGPLOV18	Ovarian Cancer	I	Germline	APC	1125V>A	chr5_112174665-112174665_T_C	Substitution	NA	Yes	40.81%
CGPLOV19	Ovarian Cancer	II	Germline	FGFR3	403K>E	chr4_1806188-1806188_A_G	Substitution	NA	Yes	23.80%
CGPLOV19	Ovarian Cancer	II	Tumor-derived	TP53	273R>H	chr17_7577120-7577120_C_T	Substitution	Yes	Yes	36.83%
CGPLOV19	Ovarian Cancer	II	Germline	AR	176S>R	chrX_66765516-66765516_C_A	Substitution	NA	Yes	65.29%
CGPLOV19	Ovarian Cancer	II	Tumor-derived	APC	1378Q>X	chr5_112175423-112175423_C_T	Substitution	Yes	Yes	46.35%
CGPLOV20	Ovarian Cancer	II	Tumor-derived	TP53	195I>T	chr17_7578265-7578265_A_G	Substitution	Yes	Yes	0.21%
CGPLOV20	Ovarian Cancer	II	Germline	EGFR	253K>R	chr7_55221714-55221714_A_G	Substitution	NA	Yes	44.05%
CGPLOV21	Ovarian Cancer	IV	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	7.68%
CGPLOV21	Ovarian Cancer	IV	Tumor-derived	TP53	275C>Y	chr17_7577114-7577114_C_T	Substitution	No	Yes	2.04%
CGPLOV21	Ovarian Cancer	IV	Tumor-derived	ERBB4	602S>T	chr2_212530114-212530114_C_G	Substitution	No	No	14.36%

CGPLOV22	Ovarian Cancer	III	Tumor-derived	TP53	193H>P	chr17_7578271-7578271_T_G	Substitution	No	Yes	0.49%
CGPLOV22	Ovarian Cancer	III	Tumor-derived	CTNNB1	41T>A	chr3_41266124-41266124_A_G	Substitution	Yes	Yes	0.34%

Table 4.3. Summary of targeted cfDNA fragment analyses in cancer patients (cont.)

Patient	Wild-type Fragments							
	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)	Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)
CGCRC291	11688	100	151	167	169	179	188	400
CGCRC291	11779	100	155	171	169	182	185	400
CGCRC291	11026	100	156	166	169	180	183	400
CGCRC291	7632	97	152	169	167	177	182	400
CGCRC291	7218	101	155	167	169	184	185	400
CGCRC291	10757	86	154	166	167	181	182	400
CGCRC291	5429	100	151	171	167	176	180	400
CGCRC292	6120	101	157	167	169	176	183	399
CGCRC292	10693	100	155	169	168	177	182	400
CGCRC292	7587	97	158	166	171	183	188	399
CGCRC293	7672	95	159	168	170	188	186	400
CGCRC294	7339	84	155	166	167	175	179	396
CGCRC294	12054	89	159	167	170	184	185	400
CGCRC295	5602	101	157	164	170	179	185	397
CGCRC295	8330	100	157	166	169	179	182	397
CGCRC296	8375	89	161	166	172	185	188	400
CGCRC297	3580	102	159	164	170	187	188	400
CGCRC298	13032	100	159	168	171	184	187	399
CGCRC298	13475	93	158	169	170	183	185	400
CGCRC298	5815	100	156	168	169	181	182	397
CGCRC299	11995	100	154	164	165	172	175	400
CGCRC299	15363	96	151	166	164	169	174	400

CGCRC300	7487	100	162	170	173	189	187	399
CGCRC301	5881	100	156	169	169	176	183	400
CGCRC302	24784	84	153	165	164	169	175	397
CGCRC302	11763	95	154	165	165	166	173	397
CGCRC303	13967	95	159	169	171	184	186	400
CGCRC303	10167	81	160	169	172	185	186	400
CGCRC303	10845	100	160	169	172	185	187	400
CGCRC304	16168	90	153	167	164	167	175	394
CGCRC304	10502	100	152	165	163	167	173	397
CGCRC304	12987	101	154	165	165	170	175	398
CGCRC305	12507	100	159	169	171	190	189	400
CGCRC305	10301	100	156	168	168	182	182	399
CGCRC306	8594	101	157	165	169	189	187	399
CGCRC306	9437	90	159	167	171	192	193	400
CGCRC306	6090	100	152	163	166	173	179	391
CGCRC306	4585	103	158	167	170	181	185	399
CGCRC306	7395	81	160	166	171	178	184	399
CGCRC306	4885	100	152	170	167	175	179	398
CGCRC306	3700	100	159	168	171	181	186	396
CGCRC307	6860	100	158	170	170	180	183	399
CGCRC307	10065	95	157	168	169	183	184	397
CGCRC307	7520	102	156	167	168	185	184	400
CGCRC307	8623	76	157	169	168	176	180	400
CGCRC307	10606	100	155	167	168	180	184	399
CGCRC307	13189	90	158	168	171	185	187	400
CGCRC308	16287	90	159	168	169	179	182	399
CGCRC308	7729	100	160	164	170	176	184	398
CGCRC308	14067	92	157	170	169	182	182	399

CGCRC309	13036	85	157	170	169	181	182	395
CGCRC309	9084	101	157	166	168	175	180	397
CGCRC310	7393	100	153	165	164	165	172	397
CGCRC310	11689	100	152	166	164	170	173	398
CGCRC310	10273	100	153	166	164	171	173	400
CGCRC311	8456	94	160	171	172	189	189	400
CGCRC312	4719	100	160	165	173	189	189	400
CGCRC312	3391	101	157	172	170	178	184	399
CGCRC313	5013	100	163	166	174	188	189	399
CGCRC313	8150	72	161	171	174	194	192	400
CGCRC314	4684	100	158	165	169	180	183	394
CGCRC314	6902	85	159	165	170	183	185	399
CGCRC314	7229	102	158	167	170	186	186	398
CGCRC315	8739	94	155	167	169	192	195	399
CGCRC315	9623	101	158	166	170	182	184	399
CGCRC316	12880	100	150	166	163	166	172	396
CGCRC316	7479	93	157	164	168	175	180	400
CGCRC316	13682	100	149	165	162	165	172	399
CGCRC316	16716	85	153	166	166	170	177	397
CGCRC316	17060	100	150	166	163	166	173	398
CGCRC317	14587	84	152	166	164	180	178	400
CGCRC317	10483	100	152	164	165	172	177	400
CGCRC317	3497	101	149	166	163	171	174	386
CGCRC318	16436	98	158	170	170	180	183	400
CGCRC320	6521	100	163	170	175	194	199	399
CGCRC320	11633	100	162	174	174	184	188	400
CGCRC321	6918	88	161	167	174	194	198	399
CGCRC321	9559	94	159	171	170	182	184	399

CGCRC321	5545	100	159	172	172	183	186	397
CGCRC332	605	104	164	170	176	202	203	393
CGCRC333	1265	89	159	165	171	195	195	397
CGCRC333	3338	102	153	165	169	185	189	400
CGCRC333	3008	102	153	169	169	185	189	396
CGCRC334	1725	105	160	170	175	203	210	391
CGCRC334	1168	100	159	164	174	188	194	399
CGCRC334	1798	103	159	166	173	193	193	396
CGCRC335	2411	99	155	167	167	172	179	396
CGCRC336	757	104	156	171	170	186	188	387
CGCRC336	1080	102	150	166	167	177	183	392
CGCRC336	391	102	161	165	171	194	200	377
CGCRC337	6497	72	153	169	177	202	259	400
CGCRC337	1686	100	147	170	163	171	178	395
CGCRC338	1408	105	153	164	166	178	182	374
CGCRC339	1256	106	158	168	169	179	184	397
CGCRC339	1639	101	158	165	172	195	194	400
CGCRC339	1143	100	154	170	167	176	179	397
CGCRC339	1584	108	161	171	173	188	191	390
CGCRC340	876	101	162	170	175	205	207	399
CGCRC340	796	105	159	164	174	196	195	397
CGPLBR38	9684	95	156	166	168	186	184	400
CGPLBR40	10277	78	162	168	173	179	186	400
CGPLBR44	10715	99	162	171	173	191	190	400
CGPLBR44	10837	100	159	169	171	191	189	400
CGPLBR44	12640	100	159	168	171	187	189	400
CGPLBR48	5631	100	164	170	179	202	202	400
CGPLBR48	12467	101	167	174	180	196	201	400

CGPLBR55	10527	101	158	169	169	181	182	397
CGPLBR55	6011	101	153	166	167	181	181	400
CGPLBR55	3973	101	153	166	166	176	179	398
CGPLBR63	3405	97	165	170	176	191	192	398
CGPLBR67	10259	87	157	168	168	179	181	399
CGPLBR67	5163	100	151	167	166	171	177	399
CGPLBR67	6250	100	155	166	167	172	179	399
CGPLBR69	7558	100	159	166	170	186	184	398
CGPLBR69	3938	101	154	169	166	176	178	397
CGPLBR69	2387	101	157	166	168	176	178	385
CGPLBR70	6916	100	158	171	169	182	184	400
CGPLBR70	3580	107	160	169	173	194	193	400
CGPLBR71	7930	85	156	166	168	179	180	398
CGPLBR72	2389	100	157	160	170	188	187	400
CGPLBR73	11348	95	161	173	174	189	192	400
CGPLBR73	3422	102	157	168	169	178	184	399
CGPLBR74	3784	101	163	175	174	179	187	391
CGPLBR75	7290	103	162	173	172	183	186	398
CGPLBR76	4342	104	166	171	179	197	201	400
CGPLBR76	11785	100	165	168	177	191	194	400
CGPLBR77	6161	100	158	166	169	183	183	400
CGPLBR80	3643	96	166	166	185	211	230	400
CGPLBR83	3479	106	162	164	174	193	193	400
CGPLBR83	3496	103	165	170	177	197	199	400
CGPLBR83	1748	100	164	173	175	193	195	399
CGPLBR86	4241	98	160	168	175	204	207	400
CGPLBR86	3096	88	160	167	174	196	195	400
CGPLBR87	3680	101	162	168	175	202	203	400

CGPLBR87	6180	101	163	164	175	205	203	400
CGPLBR87	7746	86	160	167	175	195	196	400
CGPLBR87	2266	106	160	166	172	195	192	400
CGPLBR88	17537	89	185	200	223	238	280	400
CGPLBR88	5919	101	162	172	173	197	194	400
CGPLBR92	15530	77	150	164	162	172	173	398
CGPLBR96	9893	100	159	164	171	196	191	399
CGPLBR96	8620	95	162	167	173	189	190	400
CGPLBR96	8036	85	162	169	175	194	195	400
CGPLBR97	14856	93	160	168	170	184	184	400
CGPLBR97	5329	100	161	165	171	179	184	399
CGPLBR97	7010	97	158	169	170	187	185	399
CGPLLU144	11371	100	156	165	167	179	179	395
CGPLLU144	7641	100	155	167	166	172	177	399
CGPLLU144	9996	100	158	168	169	179	183	400
CGPLLU144	4956	101	159	166	169	182	182	397
CGPLLU144	6540	100	153	170	166	172	177	397
CGPLLU144	7648	101	156	164	166	171	177	399
CGPLLU146	5920	100	155	164	168	180	183	399
CGPLLU146	9356	100	155	166	168	184	184	400
CGPLLU146	7284	101	158	165	170	186	187	399
CGPLLU146	4183	103	160	166	170	183	185	400
CGPLLU146	6778	100	157	166	168	182	184	400
CGPLLU147	4807	100	155	166	170	192	191	400
CGPLLU147	5282	100	156	167	171	199	205	400
CGPLLU147	7122	100	158	174	173	191	193	400
CGPLLU147	2825	101	160	165	173	190	191	389
CGPLLU162	9940	95	161	164	174	192	197	400

CGPLLU162	13855	87	160	174	173	183	189	400
CGPLLU162	11251	100	153	167	166	175	178	400
CGPLLU163	10805	85	159	165	173	194	202	400
CGPLLU163	20185	83	158	166	170	184	186	400
CGPLLU164	6795	91	156	161	169	191	190	396
CGPLLU164	4561	92	157	164	169	188	185	394
CGPLLU164	8097	100	158	170	170	186	186	399
CGPLLU164	9241	100	155	165	167	180	180	397
CGPLLU164	10806	100	157	168	169	182	182	400
CGPLLU164	10919	100	157	168	169	182	182	400
CGPLLU164	5412	103	159	175	171	180	182	395
CGPLLU164	5151	101	160	166	169	177	182	400
CGPLLU165	7448	95	155	167	167	185	184	399
CGPLLU165	5822	102	154	166	166	181	179	394
CGPLLU168	15985	97	152	165	166	177	180	400
CGPLLU168	11070	100	156	165	168	179	181	400
CGPLLU168	11063	83	157	166	169	177	182	400
CGPLLU174	5881	88	162	165	174	200	199	399
CGPLLU174	3696	100	162	167	172	184	185	392
CGPLLU174	4941	101	162	167	172	182	184	395
CGPLLU174	7527	100	163	168	173	186	187	399
CGPLLU174	8353	101	162	168	173	186	186	396
CGPLLU175	10214	100	160	166	170	185	183	399
CGPLLU175	9739	100	157	168	168	179	180	400
CGPLLU175	9509	100	157	165	168	181	181	400
CGPLLU175	2710	101	157	165	167	176	179	392
CGPLLU175	6565	100	158	166	168	174	180	399
CGPLLU176	6513	101	164	168	175	197	194	399

CGPLLU176	5962	100	164	174	175	195	194	399
CGPLLU177	7044	102	160	165	170	178	182	395
CGPLLU177	9950	88	160	169	171	183	185	398
CGPLLU177	11233	100	160	168	171	185	184	397
CGPLLU177	10966	75	160	169	172	190	188	395
CGPLLU178	8378	100	162	176	172	186	187	398
CGPLLU178	7235	101	159	167	170	179	184	400
CGPLLU179	8350	103	161	169	171	185	185	394
CGPLLU179	2609	108	162	171	173	189	187	398
CGPLLU180	6085	91	158	165	170	198	200	398
CGPLLU180	8680	92	158	164	169	190	188	400
CGPLLU180	7790	92	158	167	168	184	184	400
CGPLLU180	9036	101	160	169	171	191	189	397
CGPLLU180	4679	100	157	169	168	181	182	398
CGPLLU197	7196	102	162	166	172	191	189	399
CGPLLU197	7147	100	161	166	172	191	189	399
CGPLLU198	9322	97	157	165	168	180	181	399
CGPLLU198	8303	100	160	173	172	181	186	400
CGPLLU202	14197	90	151	165	166	169	179	398
CGPLLU202	9279	51	150	168	167	170	181	398
CGPLLU204	7185	100	157	165	168	175	181	391
CGPLLU205	10739	96	156	165	166	175	177	400
CGPLLU205	12065	100	154	165	165	172	176	400
CGPLLU206	6746	94	148	165	164	179	178	398
CGPLLU206	11225	100	147	167	164	175	178	399
CGPLLU207	11224	100	159	165	170	187	186	400
CGPLLU207	4960	101	160	166	170	181	184	400
CGPLLU207	13216	85	161	165	172	182	187	400

CGPLLU208	9211	101	156	166	168	181	183	400
CGPLLU208	5253	100	159	164	170	179	184	400
CGPLLU208	10233	100	160	170	171	181	186	400
CGPLLU208	11421	100	158	165	171	187	190	397
CGPLLU209	11695	96	153	166	169	190	192	400
CGPLLU209	12771	94	155	163	168	174	182	400
CGPLLU209	16557	92	157	169	170	185	188	400
CGPLLU209	13057	97	158	167	171	182	187	400
CGPLLU209	8521	100	155	167	169	176	183	396
CGPLOV10	4421	101	161	165	172	186	188	399
CGPLOV11	7987	100	157	164	169	186	185	399
CGPLOV11	3782	97	160	166	171	183	185	392
CGPLOV13	12072	88	157	165	169	182	183	399
CGPLOV13	4107	103	159	166	169	177	181	399
CGPLOV13	8427	100	161	165	171	181	184	400
CGPLOV14	11418	92	154	167	171	183	191	400
CGPLOV15	7689	102	157	164	169	187	185	399
CGPLOV15	7617	101	159	167	171	182	188	400
CGPLOV17	4463	96	156	168	169	186	187	397
CGPLOV17	2884	110	157	170	170	188	189	400
CGPLOV18	2945	101	159	164	169	183	183	391
CGPLOV19	9727	95	158	167	172	185	189	395
CGPLOV19	4387	100	158	165	169	184	184	398
CGPLOV19	2775	93	161	171	171	182	187	400
CGPLOV19	3818	102	156	170	170	186	185	400
CGPLOV20	5404	94	159	165	170	193	190	400
CGPLOV20	3744	102	158	166	169	182	185	394
CGPLOV21	21823	81	158	166	169	179	180	400

CGPLOV21	18806	101	159	165	169	175	179	400
CGPLOV21	10801	89	160	166	169	175	180	394
CGPLOV22	11952	100	155	165	167	184	182	400
CGPLOV22	12399	92	150	165	164	172	176	395

Table 4.3. Summary of targeted cfDNA fragment analyses in cancer patients (cont.).

Patient	Mutant Fragments								Difference between Median Mutant and Wild-type cfDNA Fragment Sizes (bp)	Difference between Mean Mutant and Wild-type cfDNA Fragment Sizes (bp)	Adjusted P Value of Difference between Mutant and Wild-type cfDNA Fragment Sizes
	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)	Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)			
CGCRC291	19	100	142	233	165	180	230	305	-4.0	1.54	0.475
CGCRC291	21	132	166	182	176	191	198	309	7.0	8.33	0.250
CGCRC291	5411	92	152	167	169	186	191	399	0.0	5.89	0.000
CGCRC291	1903	100	148	166	166	177	183	383	-1.0	-0.25	0.874
CGCRC291	1344	108	155	167	170	189	191	398	1.0	5.37	0.009
CGCRC291	2108	100	153	166	168	185	187	386	1.0	3.80	0.025
CGCRC291	1951	101	149	175	167	179	182	397	0.0	2.65	0.148
CGCRC292	75	123	162	167	172	182	190	370	3.0	5.31	0.368
CGCRC292	28	101	130	130	139	164	155	345	-29.5	-12.79	0.000
CGCRC292	6863	100	160	168	173	186	189	400	2.0	3.13	0.002
CGCRC293	34	77	154	171	170	177	192	335	-0.5	-11.46	0.571
CGCRC294	9	138	147	176	171	177	176	290	4.0	1.22	0.475
CGCRC294	21	115	145	155	159	176	175	368	-11.0	-7.99	0.052
CGCRC295	30	137	149	181	162	182	181	369	-8.0	3.49	0.061
CGCRC295	44	125	155	155	169	185	194	338	0.0	5.78	0.623
CGCRC296	8167	101	160	166	171	184	187	400	-1.0	-1.27	0.212
CGCRC297	3562	102	158	168	170	185	185	399	0.0	-2.62	0.114
CGCRC298	15	93	137	127	174	173	193	261	3.0	-11.00	0.507
CGCRC298	26	137	163	166	167	179	180	364	-3.0	-4.34	0.430
CGCRC298	35	118	147	176	163	172	176	336	-6.0	-9.35	0.166
CGCRC299	71	133	152	170	165	169	173	301	0.0	-3.57	0.668
CGCRC299	55	130	153	165	164	166	168	325	0.0	-2.15	0.630

CGCRC300	17	149	155	326	170	221	301	387	-3.0	32.43	0.453
CGCRC301	18	156	170	174	174	210	219	372	5.0	33.84	0.368
CGCRC302	51	108	143	268	152	164	178	268	-12.0	-5.12	0.000
CGCRC302	26	118	147	153	156	174	168	327	-9.5	8.37	0.036
CGCRC303	45	116	151	168	163	175	177	346	-8.0	-8.84	0.057
CGCRC303	25	157	165	191	175	207	199	350	3.0	22.93	0.465
CGCRC303	25	124	168	180	180	189	191	338	8.0	4.06	0.154
CGCRC304	86	121	155	169	166	168	175	309	2.0	0.46	0.445
CGCRC304	45	124	143	197	162	166	168	377	-1.0	-0.91	0.482
CGCRC304	108	126	147	162	162	164	174	302	-3.0	-6.74	0.064
CGCRC305	23	131	148	145	166	189	205	333	-5.0	-0.80	0.297
CGCRC305	42	138	155	155	174	177	187	343	5.5	-4.51	0.171
CGCRC306	25	126	153	176	176	188	229	305	7.0	-0.19	0.234
CGCRC306	977	101	149	189	170	182	192	380	-1.0	-9.76	0.000
CGCRC306	525	102	140	168	159	168	176	382	-7.0	-5.57	0.052
CGCRC306	4010	100	158	166	170	181	185	398	0.0	0.37	0.770
CGCRC306	625	100	140	167	162	172	181	380	-9.0	-6.68	0.009
CGCRC306	37	111	143	142	166	172	186	321	-1.0	-2.38	0.572
CGCRC306	3184	102	159	168	172	182	187	400	0.5	0.95	0.564
CGCRC307	47	111	148	144	169	176	183	353	-1.0	-4.83	0.598
CGCRC307	39	111	146	182	162	182	185	337	-7.0	-0.44	0.064
CGCRC307	24	110	146	309	182	208	284	355	14.0	22.31	0.031
CGCRC307	32	117	146	154	157	167	166	298	-11.0	-8.94	0.013
CGCRC307	43	111	143	144	177	187	212	319	9.0	7.22	0.062
CGCRC307	29	109	140	204	159	188	204	387	-12.0	3.32	0.031
CGCRC308	20	128	152	180	163	166	180	219	-6.5	-13.04	0.155
CGCRC308	7515	101	160	170	171	177	185	400	1.0	1.08	0.166
CGCRC308	31	85	146	137	166	167	176	316	-3.0	-14.62	0.469

CGCRC309	428	100	135	138	149	158	166	340	-20.0	-23.47	0.000
CGCRC309	352	97	136	132	147	149	159	326	-21.0	-26.04	0.000
CGCRC310	15	131	137	132	144	163	171	323	-20.0	-1.73	0.000
CGCRC310	25	107	138	159	161	175	190	299	-3.0	4.83	0.384
CGCRC310	27	122	147	161	161	173	171	342	-3.0	2.54	0.354
CGCRC311	91	112	165	168	173	196	192	379	1.0	6.83	0.571
CGCRC312	27	124	144	154	154	167	172	320	-19.0	-22.39	0.000
CGCRC312	24	105	143	132	159	183	190	367	-11.0	4.67	0.054
CGCRC313	8	122	143	122	161	168	195	241	-13.0	-19.21	0.100
CGCRC313	17	144	163	173	173	213	261	372	-1.0	19.22	0.587
CGCRC314	15	132	159	186	166	174	185	265	-3.0	-5.62	0.461
CGCRC314	233	131	162	167	172	190	187	394	2.0	7.27	0.137
CGCRC314	27	136	155	183	163	170	178	262	-7.0	-16.03	0.131
CGCRC315	23	137	144	175	152	190	212	327	-17.0	-1.78	0.018
CGCRC315	29	131	157	177	171	183	179	319	1.0	0.74	0.564
CGCRC316	1616	100	146	164	159	163	170	354	-3.5	-3.57	0.000
CGCRC316	806	96	158	169	169	179	184	366	1.0	3.80	0.054
CGCRC316	1410	102	140	149	154	164	170	398	-8.0	-0.35	0.816
CGCRC316	49	99	153	143	182	206	284	333	16.0	36.25	0.000
CGCRC316	33	140	155	154	170	180	180	296	7.0	14.38	0.104
CGCRC317	73	95	140	140	155	173	178	324	-9.0	-6.66	0.000
CGCRC317	38	115	160	164	167	182	179	329	1.5	10.09	0.479
CGCRC317	6	124	137	170	156	153	168	178	-7.5	-18.98	0.411
CGCRC318	70	124	151	151	164	182	183	385	-6.0	1.71	0.064
CGCRC320	6586	96	162	168	175	193	196	399	0.0	-1.79	0.166
CGCRC320	41	112	172	176	177	195	195	373	3.0	11.02	0.397
CGCRC321	35	149	168	175	175	181	186	312	1.0	-13.40	0.587
CGCRC321	20	166	180	185	191	205	219	357	21.0	23.48	0.013

CGCRC321	5338	102	159	175	171	183	185	394	-1.0	0.03	0.984
CGCRC332	178	101	150	168	171	198	240	357	-5.0	-4.34	0.571
CGCRC333	1350	104	153	163	171	201	258	400	0.0	5.94	0.066
CGCRC333	1257	100	153	168	170	189	202	392	1.0	4.37	0.064
CGCRC333	30	117	163	164	172	175	179	372	3.0	-10.29	0.463
CGCRC334	336	105	153	141	171	200	240	399	-4.0	-3.10	0.571
CGCRC334	741	101	161	169	176	190	194	400	2.0	1.96	0.571
CGCRC334	89	100	145	171	171	197	229	393	-2.0	3.42	0.479
CGCRC335	12	129	143	143	153	163	166	275	-14.0	-8.99	0.084
CGCRC336	3559	91	155	164	173	195	211	398	3.0	8.92	0.001
CGCRC336	873	102	149	163	164	177	181	400	-3.0	-0.39	0.880
CGCRC336	1909	100	158	167	176	202	242	398	5.0	7.98	0.061
CGCRC337	27	122	157	164	179	199	231	350	2.0	-3.82	0.685
CGCRC337	1818	103	147	169	162	173	180	396	-1.0	1.92	0.372
CGCRC338	546	102	151	166	166	180	182	381	0.0	2.87	0.416
CGCRC339	26	132	142	138	171	183	188	351	1.5	3.29	0.572
CGCRC339	53	117	157	166	169	192	198	336	-3.0	-2.86	0.451
CGCRC339	40	124	150	169	166	181	176	309	-1.0	4.53	0.539
CGCRC339	38	107	153	180	174	185	210	326	0.5	-2.59	0.576
CGCRC340	217	102	146	144	163	188	212	360	-12.0	-17.11	0.004
CGCRC340	266	111	147	150	166	188	204	379	-8.0	-7.53	0.208
CGPLBR38	76	123	157	171	169	182	182	346	1.0	-3.64	0.479
CGPLBR40	9832	93	161	166	172	180	186	399	-1.0	1.04	0.155
CGPLBR44	277	104	162	160	176	201	200	384	3.0	9.95	0.061
CGPLBR44	65	123	165	166	172	198	192	371	1.0	7.08	0.560
CGPLBR44	31	136	163	171	167	201	199	387	-4.0	14.14	0.341
CGPLBR48	5286	102	166	168	181	201	203	400	2.0	-0.88	0.587
CGPLBR48	102	138	166	161	179	199	209	372	-1.5	2.90	0.679

CGPLBR55	30	138	158	189	185	191	191	311	16.0	9.25	0.000
CGPLBR55	64	113	158	163	167	179	176	318	0.0	-2.85	0.679
CGPLBR55	27	121	163	200	171	187	190	392	5.0	10.89	0.314
CGPLBR63	2943	100	165	176	176	187	192	398	0.0	-3.83	0.015
CGPLBR67	25	138	153	138	167	181	184	340	-1.0	2.00	0.571
CGPLBR67	60	110	136	147	147	161	159	327	-19.0	-9.77	0.000
CGPLBR67	26	139	147	180	176	176	184	344	9.0	3.52	0.015
CGPLBR69	35	121	149	360	161	197	195	360	-9.0	10.77	0.314
CGPLBR69	4000	103	155	166	167	176	178	397	0.5	0.65	0.610
CGPLBR69	2390	99	157	164	168	178	180	400	0.0	1.78	0.314
CGPLBR70	28	131	160	168	167	177	179	338	-2.0	-5.83	0.463
CGPLBR70	3545	100	161	169	173	194	192	399	0.0	0.40	0.825
CGPLBR71	15	121	146	166	166	172	204	221	-2.0	-7.32	0.564
CGPLBR72	2587	103	158	162	169	189	186	399	-1.0	1.12	0.598
CGPLBR73	86	121	165	183	177	189	193	373	3.0	-0.01	0.293
CGPLBR73	3339	101	157	165	169	177	184	400	0.0	-1.73	0.598
CGPLBR74	3193	101	163	178	173	180	186	389	-1.0	0.22	0.839
CGPLBR75	13	111	153	153	161	171	179	323	-11.0	-12.36	0.061
CGPLBR76	4140	102	166	169	179	197	200	400	0.0	-0.32	0.839
CGPLBR76	16	130	143	143	157	173	173	325	-20.0	-18.40	0.000
CGPLBR77	209	125	154	175	170	196	233	357	1.0	12.55	0.025
CGPLBR80	41	158	176	197	186	215	220	374	1.0	3.72	0.603
CGPLBR83	3445	94	162	175	174	194	194	399	0.0	0.65	0.714
CGPLBR83	23	123	182	248	224	232	260	359	47.0	34.97	0.000
CGPLBR83	1787	100	163	163	176	192	194	400	1.0	-0.85	0.718
CGPLBR86	4100	100	159	164	173	200	202	400	-2.0	-3.65	0.062
CGPLBR86	3096	79	159	161	173	194	191	397	-1.0	-2.45	0.251
CGPLBR87	73	142	178	178	184	237	338	377	9.0	35.30	0.114

CGPLBR87	23	161	168	168	171	189	186	380	-4.0	-16.38	0.435
CGPLBR87	170	125	158	173	173	188	190	400	-2.0	-6.17	0.293
CGPLBR87	2089	101	162	169	176	203	203	400	4.5	8.80	0.000
CGPLBR88	125	84	192	194	207	243	324	400	-16.0	5.51	0.574
CGPLBR88	5715	108	163	164	174	200	196	400	1.0	2.87	0.065
CGPLBR92	109	78	148	149	158	166	173	302	-4.0	-5.94	0.190
CGPLBR96	35	119	161	172	171	191	180	390	0.0	-4.34	0.627
CGPLBR96	826	102	162	166	171	187	187	395	-2.0	-1.94	0.475
CGPLBR96	95	135	160	161	170	182	184	400	-5.0	-11.54	0.155
CGPLBR97	27	128	150	150	169	174	185	319	-1.0	-9.68	0.571
CGPLBR97	4771	103	161	168	171	179	183	400	0.0	0.15	0.880
CGPLBR97	7	147	154	154	167	164	174	177	-3.0	-22.90	0.155
CGPLLU144	330	106	152	166	166	178	178	361	-1.0	-1.35	0.685
CGPLLU144	536	106	151	167	163	172	175	363	-3.0	-0.34	0.880
CGPLLU144	45	138	163	175	172	185	191	380	3.0	6.52	0.368
CGPLLU144	16	138	146	146	155	162	170	224	-14.0	-19.82	0.007
CGPLLU144	293	101	152	169	164	170	174	392	-2.0	-1.37	0.646
CGPLLU144	23	130	152	162	162	163	177	232	-4.0	-7.62	0.252
CGPLLU146	54	104	161	154	176	195	206	383	7.5	14.58	0.064
CGPLLU146	154	96	149	157	163	176	185	347	-5.5	-7.87	0.154
CGPLLU146	79	102	163	177	174	200	203	372	4.0	14.61	0.270
CGPLLU146	44	118	149	163	163	185	188	338	-7.0	1.98	0.039
CGPLLU146	35	136	164	204	181	194	203	369	13.0	11.80	0.039
CGPLLU147	13	138	164	169	169	198	173	333	-1.0	6.05	0.610
CGPLLU147	50	128	155	161	171	216	301	360	0.0	17.02	0.623
CGPLLU147	81	108	150	108	173	198	224	385	0.0	6.48	0.624
CGPLLU147	2597	101	159	165	172	185	187	397	-1.0	-5.17	0.005
CGPLLU162	58	92	173	192	192	202	200	397	18.0	9.79	0.007

CGPLLU162	74	90	147	142	167	176	182	391	-6.5	-6.78	0.061
CGPLLU162	37	144	163	185	172	192	186	375	6.0	17.15	0.005
CGPLLU163	61	93	164	181	181	197	211	370	8.0	3.34	0.169
CGPLLU163	66	104	158	194	174	189	194	379	3.5	4.60	0.270
CGPLLU164	101	126	155	176	176	194	213	331	7.0	2.50	0.718
CGPLLU164	4718	100	156	164	168	190	187	393	-1.0	2.54	0.113
CGPLLU164	30	134	161	175	175	190	208	339	5.0	4.07	0.302
CGPLLU164	34	139	163	165	170	178	175	349	3.0	-1.65	0.407
CGPLLU164	262	101	150	152	165	181	186	393	-4.0	-0.65	0.876
CGPLLU164	277	101	150	147	166	182	185	393	-3.0	0.36	0.926
CGPLLU164	65	121	158	161	167	186	188	338	-4.0	6.15	0.234
CGPLLU164	16	144	172	179	179	187	180	376	10.0	9.98	0.130
CGPLLU165	7186	100	154	167	166	183	181	396	-1.0	-1.73	0.154
CGPLLU165	21	108	164	164	173	196	200	357	7.0	14.95	0.213
CGPLLU168	18	111	127	127	158	189	186	352	-8.0	12.47	0.179
CGPLLU168	72	121	156	173	166	183	179	396	-2.0	4.31	0.427
CGPLLU168	30	106	160	174	174	180	186	282	5.0	3.09	0.252
CGPLLU174	36	131	147	143	177	196	227	298	2.5	-4.24	0.479
CGPLLU174	20	144	173	266	178	199	215	269	6.0	15.13	0.252
CGPLLU174	16	147	156	156	164	177	169	302	-8.0	-4.82	0.119
CGPLLU174	34	159	168	168	176	206	196	365	3.0	20.55	0.415
CGPLLU174	5	116	182	182	185	201	192	329	12.0	14.62	0.263
CGPLLU175	1073	100	142	164	152	157	164	346	-18.0	-27.67	0.000
CGPLLU175	46	109	151	143	175	174	183	325	7.0	-5.22	0.054
CGPLLU175	30	146	154	146	168	186	181	367	-0.5	5.19	0.568
CGPLLU175	2742	102	154	164	166	176	178	387	-1.0	-0.24	0.874
CGPLLU175	298	103	140	148	150	152	162	288	-18.0	-22.25	0.000
CGPLLU176	67	115	164	250	173	187	201	366	-2.0	-9.89	0.425

CGPLLU176	19	156	165	165	185	197	199	361	10.0	2.20	0.154
CGPLLU177	189	105	138	141	150	164	175	348	-20.0	-14.58	0.000
CGPLLU177	227	123	160	168	169	185	184	396	-2.0	1.68	0.706
CGPLLU177	53	78	161	175	175	189	188	392	4.0	3.80	0.241
CGPLLU177	50	130	161	168	168	184	175	377	-4.5	-5.86	0.234
CGPLLU178	28	139	150	173	170	170	173	354	-2.5	-15.88	0.416
CGPLLU178	24	130	153	176	170	193	199	359	0.0	13.13	0.598
CGPLLU179	48	111	154	170	168	173	183	295	-3.0	-11.80	0.270
CGPLLU179	2337	100	163	166	172	187	185	394	-1.0	-1.27	0.564
CGPLLU180	172	83	152	160	166	193	226	396	-4.0	-4.93	0.490
CGPLLU180	215	123	151	159	163	188	196	365	-6.0	-1.72	0.735
CGPLLU180	207	121	151	157	161	181	179	365	-7.0	-3.01	0.571
CGPLLU180	17	143	170	217	214	198	217	294	43.0	7.08	0.000
CGPLLU180	52	122	152	167	164	179	173	372	-4.5	-2.07	0.137
CGPLLU197	17	109	161	173	171	181	174	293	-1.0	-9.24	0.576
CGPLLU197	40	136	164	166	171	185	185	335	-1.0	-5.86	0.571
CGPLLU198	127	88	149	131	162	168	178	311	-6.0	-11.80	0.005
CGPLLU198	68	141	166	175	176	198	207	387	4.0	17.11	0.184
CGPLLU202	10	81	167	167	167	159	176	182	1.0	-10.20	0.589
CGPLLU202	33	107	162	167	167	174	185	322	0.0	4.57	0.636
CGPLLU204	23	112	156	190	164	175	190	349	-4.0	-0.92	0.308
CGPLLU205	109	130	153	169	166	175	178	382	0.0	-0.09	0.987
CGPLLU205	684	105	153	167	166	172	175	385	1.0	0.00	0.999
CGPLLU206	2946	100	138	157	155	172	174	398	-9.0	-7.28	0.000
CGPLLU206	30	121	165	165	176	198	219	325	12.0	22.37	0.007
CGPLLU207	63	140	155	154	167	201	215	372	-3.0	13.70	0.286
CGPLLU207	4754	101	160	170	170	179	181	393	0.0	-1.72	0.154
CGPLLU207	31	131	162	162	174	180	185	352	2.0	-2.26	0.494

CGPLLU208	150	110	144	166	162	176	173	385	-6.0	-5.86	0.314
CGPLLU208	5290	95	159	167	169	179	184	400	-1.0	0.11	0.909
CGPLLU208	140	101	155	175	167	179	180	352	-4.5	-2.77	0.589
CGPLLU208	20	92	141	241	168	178	209	283	-3.0	-9.82	0.479
CGPLLU209	8065	85	156	164	169	190	190	399	0.0	-0.08	0.942
CGPLLU209	2586	101	147	165	165	169	179	386	-3.5	-4.59	0.000
CGPLLU209	2808	100	150	158	167	189	200	399	-3.0	4.17	0.007
CGPLLU209	2227	100	154	162	171	183	190	398	0.0	1.00	0.564
CGPLLU209	8425	100	155	165	169	176	184	400	0.0	0.54	0.568
CGPLOV10	142	112	146	140	159	180	193	352	-13.0	-5.41	0.463
CGPLOV11	104	132	158	159	167	189	180	331	-2.0	3.05	0.657
CGPLOV11	3462	101	160	173	172	184	187	396	1.0	0.82	0.576
CGPLOV13	25	94	140	140	158	159	163	341	-11.0	-23.47	0.027
CGPLOV13	3789	101	159	168	169	176	181	395	0.0	-0.66	0.576
CGPLOV13	57	131	152	170	170	179	184	327	-1.0	-2.41	0.568
CGPLOV14	36	118	154	201	182	187	201	328	11.0	3.60	0.114
CGPLOV15	362	110	152	143	180	207	268	389	11.0	20.70	0.000
CGPLOV15	20	158	163	311	174	198	209	311	3.0	15.25	0.475
CGPLOV17	23	126	151	184	168	185	185	328	-1.0	-1.49	0.571
CGPLOV17	2980	100	158	169	170	187	189	398	0.0	-0.84	0.637
CGPLOV18	2793	91	158	167	170	181	182	389	1.0	-2.30	0.171
CGPLOV19	7357	100	158	175	171	182	187	399	-1.0	-2.37	0.008
CGPLOV19	5186	101	157	165	170	185	186	400	1.0	1.72	0.240
CGPLOV19	15595	64	159	167	170	181	185	397	-1.0	-1.39	0.245
CGPLOV19	6749	101	158	167	170	185	187	400	0.0	-0.52	0.702
CGPLOV20	23	127	148	148	194	222	292	378	24.0	29.58	0.027
CGPLOV20	3901	101	160	167	171	182	185	398	2.0	0.32	0.821
CGPLOV21	4633	100	158	169	170	185	187	400	1.0	6.16	0.000

CGPLOV21	734	101	151	155	165	176	178	366	-4.0	0.48	0.823
CGPLOV21	4022	101	159	167	168	172	178	399	-1.0	-2.84	0.000
CGPLOV22	117	116	156	156	172	199	184	399	5.0	15.08	0.084
CGPLOV22	65	109	145	177	167	181	181	306	3.0	9.11	0.293

Table 4.4. Summary of whole genome cfDNA analyses.

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGCRC291	Preoperative treatment naïve	WGS	Colorectal Cancer	100	7232125000	4695396600	1.86
CGCRC292	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6794092800	4471065400	1.77
CGCRC293	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8373899600	5686176000	2.26
CGCRC294	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8081312000	5347045800	2.12
CGCRC296	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10072029200	6770998200	2.69
CGCRC299	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10971591600	7632723200	3.03
CGCRC300	Preoperative treatment naïve	WGS	Colorectal Cancer	100	9894332600	6699951000	2.66
CGCRC301	Preoperative treatment naïve	WGS	Colorectal Cancer	100	7857346200	5021002000	1.99
CGCRC302	Preoperative treatment naïve	WGS	Colorectal Cancer	100	11671913000	8335275800	3.31
CGCRC304	Preoperative treatment naïve	WGS	Colorectal Cancer	100	19011739200	12957614200	5.14
CGCRC305	Preoperative treatment naïve	WGS	Colorectal Cancer	100	7177341400	4809957200	1.91
CGCRC306	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8302233200	5608043600	2.23
CGCRC307	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8034729400	5342620000	2.12
CGCRC308	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8670084800	5934037200	2.35
CGCRC311	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6947634400	4704601800	1.87
CGCRC315	Preoperative treatment naïve	WGS	Colorectal Cancer	100	5205544000	3419565400	1.36
CGCRC316	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6405388600	4447534800	1.76
CGCRC317	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6060390400	4104616600	1.63
CGCRC318	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6848768600	4439404800	1.76
CGCRC319	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10545294400	7355181600	2.92
CGCRC320	Preoperative treatment naïve	WGS	Colorectal Cancer	100	5961999200	3945054000	1.57
CGCRC321	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8248095400	5614355000	2.23
CGCRC333	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10540267600	6915490600	2.74
CGCRC336	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10675581800	7087691800	2.81
CGCRC338	Preoperative treatment naïve	WGS	Colorectal Cancer	100	13788172600	8970308600	3.56
CGCRC341	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10753467600	7311539200	2.90

CGCRC342	Preoperative treatment naïve	WGS	Colorectal Cancer	100	11836966000	7552793200	3.00
CGH14	Human adult elutriated lymphocytes	WGS	Healthy	100	36525427600	24950300200	9.90
CGH15	Human adult elutriated lymphocytes	WGS	Healthy	100	29930855000	23754049400	9.43
CGLU316	Pre-treatment, Day -53	WGS	Lung Cancer	100	10354123200	6896471400	2.74
CGLU316	Pre-treatment, Day -4	WGS	Lung Cancer	100	7870039200	5254938800	2.09
CGLU316	Post-treatment, Day 18	WGS	Lung Cancer	100	8155322000	5416262400	2.15
CGLU316	Post-treatment, Day 87	WGS	Lung Cancer	100	9442310400	6087893400	2.42
CGLU344	Pre-treatment, Day -21	WGS	Lung Cancer	100	8728318600	5769097200	2.29
CGLU344	Pre-treatment, Day 0	WGS	Lung Cancer	100	11710249400	7826902600	3.11
CGLU344	Post-treatment, Day 0.1875	WGS	Lung Cancer	100	11569683000	7654701600	3.04
CGLU344	Post-treatment, Day 59	WGS	Lung Cancer	100	11042459200	6320138800	2.51
CGLU369	Pre-treatment, Day -2	WGS	Lung Cancer	100	8630932800	5779595800	2.29
CGLU369	Post-treatment, Day 12	WGS	Lung Cancer	100	9227709600	6136755200	2.44
CGLU369	Post-treatment, Day 68	WGS	Lung Cancer	100	7995282600	5239077200	2.08
CGLU369	Post-treatment, Day 110	WGS	Lung Cancer	100	8750541000	5626139000	2.23
CGLU373	Pre-treatment, Day -2	WGS	Lung Cancer	100	11746059600	7547485800	3.00
CGLU373	Post-treatment, Day 0.125	WGS	Lung Cancer	100	13801136800	9255579400	3.67
CGLU373	Post-treatment, Day 7	WGS	Lung Cancer	100	11537896800	7654111200	3.04
CGLU373	Post-treatment, Day 47	WGS	Lung Cancer	100	8046326400	5397702400	2.14
CGPLBR100	Preoperative treatment naïve	WGS	Breast Cancer	100	8440532400	5729474800	2.27
CGPLBR101	Preoperative treatment naïve	WGS	Breast Cancer	100	9786253600	6673495200	2.65
CGPLBR102	Preoperative treatment naïve	WGS	Breast Cancer	100	8664980400	5669781600	2.25
CGPLBR103	Preoperative treatment naïve	WGS	Breast Cancer	100	9846936200	6662883400	2.64
CGPLBR104	Preoperative treatment naïve	WGS	Breast Cancer	100	9443375400	6497061000	2.58
CGPLBR12	Preoperative treatment naïve	WGS	Breast Cancer	100	7017577800	4823327400	1.91
CGPLBR18	Preoperative treatment naïve	WGS	Breast Cancer	100	10309652800	7130386000	2.83
CGPLBR23	Preoperative treatment naïve	WGS	Breast Cancer	100	9034484800	6219625800	2.47
CGPLBR24	Preoperative treatment naïve	WGS	Breast Cancer	100	9891454200	6601857400	2.62

CGPLBR28	Preoperative treatment naïve	WGS	Breast Cancer	100	7997607200	5400803200	2.14
CGPLBR30	Preoperative treatment naïve	WGS	Breast Cancer	100	8502597200	5885822400	2.34
CGPLBR31	Preoperative treatment naïve	WGS	Breast Cancer	100	12660085600	8551995600	3.39
CGPLBR32	Preoperative treatment naïve	WGS	Breast Cancer	100	8773498600	5839034600	2.32
CGPLBR33	Preoperative treatment naïve	WGS	Breast Cancer	100	10931742800	6967030600	2.76
CGPLBR34	Preoperative treatment naïve	WGS	Breast Cancer	100	10861398600	7453225800	2.96
CGPLBR35	Preoperative treatment naïve	WGS	Breast Cancer	100	9180193600	6158440200	2.44
CGPLBR36	Preoperative treatment naïve	WGS	Breast Cancer	100	9159948400	6091817800	2.42
CGPLBR37	Preoperative treatment naïve	WGS	Breast Cancer	100	10307505800	6929530600	2.75
CGPLBR38	Preoperative treatment naïve	WGS	Breast Cancer	100	9983824000	6841725400	2.71
CGPLBR40	Preoperative treatment naïve	WGS	Breast Cancer	100	10148823800	7024345400	2.79
CGPLBR41	Preoperative treatment naïve	WGS	Breast Cancer	100	11168192000	7562945800	3.00
CGPLBR45	Preoperative treatment naïve	WGS	Breast Cancer	100	8793780600	6011109400	2.39
CGPLBR46	Preoperative treatment naïve	WGS	Breast Cancer	100	7228607600	4706130000	1.87
CGPLBR47	Preoperative treatment naïve	WGS	Breast Cancer	100	7906911400	5341655000	2.12
CGPLBR48	Preoperative treatment naïve	WGS	Breast Cancer	100	6992032000	4428636200	1.76
CGPLBR49	Preoperative treatment naïve	WGS	Breast Cancer	100	7311195000	4559460200	1.81
CGPLBR50	Preoperative treatment naïve	WGS	Breast Cancer	100	11107960600	7582776600	3.01
CGPLBR51	Preoperative treatment naïve	WGS	Breast Cancer	100	8393547400	5102069000	2.02
CGPLBR52	Preoperative treatment naïve	WGS	Breast Cancer	100	9491894800	6141729000	2.44
CGPLBR55	Preoperative treatment naïve	WGS	Breast Cancer	100	9380109800	6518855200	2.59
CGPLBR56	Preoperative treatment naïve	WGS	Breast Cancer	100	12191816800	8293011200	3.29
CGPLBR57	Preoperative treatment naïve	WGS	Breast Cancer	100	9847584400	6713638000	2.66
CGPLBR59	Preoperative treatment naïve	WGS	Breast Cancer	100	7476477000	5059878200	2.01
CGPLBR60	Preoperative treatment naïve	WGS	Breast Cancer	100	6531354600	4331253800	1.72
CGPLBR61	Preoperative treatment naïve	WGS	Breast Cancer	100	9311029200	6430920800	2.55
CGPLBR63	Preoperative treatment naïve	WGS	Breast Cancer	100	8971949000	6044009600	2.40
CGPLBR65	Preoperative treatment naïve	WGS	Breast Cancer	100	7197301400	4835015200	1.92

CGPLBR68	Preoperative treatment naïve	WGS	Breast Cancer	100	10003774000	6974918800	2.77
CGPLBR69	Preoperative treatment naïve	WGS	Breast Cancer	100	10080881800	6903459200	2.74
CGPLBR70	Preoperative treatment naïve	WGS	Breast Cancer	100	8824002800	6002533800	2.38
CGPLBR71	Preoperative treatment naïve	WGS	Breast Cancer	100	10164136800	6994668600	2.78
CGPLBR72	Preoperative treatment naïve	WGS	Breast Cancer	100	18416841400	12328783000	4.89
CGPLBR73	Preoperative treatment naïve	WGS	Breast Cancer	100	10281460200	7078613200	2.81
CGPLBR76	Preoperative treatment naïve	WGS	Breast Cancer	100	10105270400	6800705000	2.70
CGPLBR81	Preoperative treatment naïve	WGS	Breast Cancer	100	5087126000	3273367200	1.30
CGPLBR82	Preoperative treatment naïve	WGS	Breast Cancer	100	10576496600	7186662600	2.85
CGPLBR83	Preoperative treatment naïve	WGS	Breast Cancer	100	8977124400	5947525000	2.36
CGPLBR84	Preoperative treatment naïve	WGS	Breast Cancer	100	6272538600	4066870600	1.61
CGPLBR87	Preoperative treatment naïve	WGS	Breast Cancer	100	8460954800	5375710200	2.13
CGPLBR88	Preoperative treatment naïve	WGS	Breast Cancer	100	8665810400	5499898200	2.18
CGPLBR90	Preoperative treatment naïve	WGS	Breast Cancer	100	6663469200	4392442400	1.74
CGPLBR91	Preoperative treatment naïve	WGS	Breast Cancer	100	10933002400	7647842000	3.03
CGPLBR92	Preoperative treatment naïve	WGS	Breast Cancer	100	10392674000	6493598000	2.58
CGPLBR93	Preoperative treatment naïve	WGS	Breast Cancer	100	5659836000	3931106800	1.56
CGPLH189	Preoperative treatment naïve	WGS	Healthy	100	11400610400	7655568800	3.04
CGPLH190	Preoperative treatment naïve	WGS	Healthy	100	11444671600	7581175200	3.01
CGPLH192	Preoperative treatment naïve	WGS	Healthy	100	12199010800	8126804800	3.22
CGPLH193	Preoperative treatment naïve	WGS	Healthy	100	10201897600	6635285400	2.63
CGPLH194	Preoperative treatment naïve	WGS	Healthy	100	11005087400	7081652600	2.81
CGPLH196	Preoperative treatment naïve	WGS	Healthy	100	12891462800	8646881800	3.43
CGPLH197	Preoperative treatment naïve	WGS	Healthy	100	11961841600	8052855200	3.20
CGPLH198	Preoperative treatment naïve	WGS	Healthy	100	13605489000	8885716000	3.53
CGPLH199	Preoperative treatment naïve	WGS	Healthy	100	1818090200	5615316000	2.23
CGPLH200	Preoperative treatment naïve	WGS	Healthy	100	14400027600	9310342000	3.69
CGPLH201	Preoperative treatment naïve	WGS	Healthy	100	6208766800	4171848400	1.66

CGPLH202	Preoperative treatment naïve	WGS	Healthy	100	11282922800	7363530600	2.92
CGPLH203	Preoperative treatment naïve	WGS	Healthy	100	13540689600	9068747600	3.60
CGPLH205	Preoperative treatment naïve	WGS	Healthy	100	10343537800	6696988600	2.66
CGPLH208	Preoperative treatment naïve	WGS	Healthy	100	12796300000	8272073400	3.28
CGPLH209	Preoperative treatment naïve	WGS	Healthy	100	13123035400	8531813600	3.39
CGPLH210	Preoperative treatment naïve	WGS	Healthy	100	10184218800	6832204600	2.71
CGPLH211	Preoperative treatment naïve	WGS	Healthy	100	14655260200	8887067600	3.53
CGPLH300	Preoperative treatment naïve	WGS	Healthy	100	7062083400	4553351200	1.81
CGPLH307	Preoperative treatment naïve	WGS	Healthy	100	7239128200	4547697200	1.80
CGPLH308	Preoperative treatment naïve	WGS	Healthy	100	8512551400	5526653600	2.19
CGPLH309	Preoperative treatment naïve	WGS	Healthy	100	11664474200	7431836600	2.95
CGPLH310	Preoperative treatment naïve	WGS	Healthy	100	11045691000	7451506200	2.96
CGPLH311	Preoperative treatment naïve	WGS	Healthy	100	10406803200	6786479600	2.69
CGPLH314	Preoperative treatment naïve	WGS	Healthy	100	10371343800	6925866600	2.75
CGPLH315	Preoperative treatment naïve	WGS	Healthy	100	9508538400	6208744600	2.46
CGPLH316	Preoperative treatment naïve	WGS	Healthy	100	10131063600	6891181000	2.73
CGPLH317	Preoperative treatment naïve	WGS	Healthy	100	8364314400	5302232600	2.10
CGPLH319	Preoperative treatment naïve	WGS	Healthy	100	8780528200	5585897000	2.22
CGPLH320	Preoperative treatment naïve	WGS	Healthy	100	8956232600	5784619200	2.30
CGPLH322	Preoperative treatment naïve	WGS	Healthy	100	9563837800	6445517800	2.56
CGPLH324	Preoperative treatment naïve	WGS	Healthy	100	6765038600	4469201600	1.77
CGPLH325	Preoperative treatment naïve	WGS	Healthy	100	8008213400	5099262800	2.02
CGPLH326	Preoperative treatment naïve	WGS	Healthy	100	9554226200	6112544800	2.43
CGPLH327	Preoperative treatment naïve	WGS	Healthy	100	8239168800	5351280200	2.12
CGPLH328	Preoperative treatment naïve	WGS	Healthy	100	7197086800	4516894800	1.79
CGPLH329	Preoperative treatment naïve	WGS	Healthy	100	8921554800	5493709800	2.18
CGPLH330	Preoperative treatment naïve	WGS	Healthy	100	10693603400	7077793600	2.81
CGPLH331	Preoperative treatment naïve	WGS	Healthy	100	8982792000	5538096200	2.20

CGPLH333	Preoperative treatment naïve	WGS	Healthy	100	7856985400	5178829600	2.06
CGPLH335	Preoperative treatment naïve	WGS	Healthy	100	9370663400	6035739400	2.40
CGPLH336	Preoperative treatment naïve	WGS	Healthy	100	8002498200	5340331400	2.12
CGPLH337	Preoperative treatment naïve	WGS	Healthy	100	7399022000	4954467600	1.97
CGPLH338	Preoperative treatment naïve	WGS	Healthy	100	8917121600	6170927200	2.45
CGPLH339	Preoperative treatment naïve	WGS	Healthy	100	8591130800	5866411400	2.33
CGPLH340	Preoperative treatment naïve	WGS	Healthy	100	8046351000	5368062000	2.13
CGPLH341	Preoperative treatment naïve	WGS	Healthy	100	7914788600	5200304800	2.06
CGPLH342	Preoperative treatment naïve	WGS	Healthy	100	8633473000	5701972400	2.26
CGPLH343	Preoperative treatment naïve	WGS	Healthy	100	6694769800	4410670800	1.75
CGPLH344	Preoperative treatment naïve	WGS	Healthy	100	7628192400	4961476600	1.97
CGPLH345	Preoperative treatment naïve	WGS	Healthy	100	7121569400	4747223000	1.88
CGPLH346	Preoperative treatment naïve	WGS	Healthy	100	7707924600	4873321600	1.93
CGPLH35	Preoperative treatment naïve	WGS	Healthy	100	47305985200	4774186200	12.63
CGPLH350	Preoperative treatment naïve	WGS	Healthy	100	9745839800	6054055200	2.40
CGPLH351	Preoperative treatment naïve	WGS	Healthy	100	13317435800	8714465000	3.46
CGPLH352	Preoperative treatment naïve	WGS	Healthy	100	7659351600	4752309400	1.89
CGPLH353	Preoperative treatment naïve	WGS	Healthy	100	8435782400	5275098200	2.09
CGPLH354	Preoperative treatment naïve	WGS	Healthy	100	8018644000	4857577600	1.93
CGPLH355	Preoperative treatment naïve	WGS	Healthy	100	8624675800	5709726400	2.27
CGPLH356	Preoperative treatment naïve	WGS	Healthy	100	8817952800	5729595200	2.27
CGPLH357	Preoperative treatment naïve	WGS	Healthy	100	11931696200	7690004400	3.05
CGPLH358	Preoperative treatment naïve	WGS	Healthy	100	12802561200	8451274800	3.35
CGPLH36	Preoperative treatment naïve	WGS	Healthy	100	40173545600	3974810400	10.52
CGPLH360	Preoperative treatment naïve	WGS	Healthy	100	7280078400	4918566200	1.95
CGPLH361	Preoperative treatment naïve	WGS	Healthy	100	7493498400	4966813800	1.97
CGPLH362	Preoperative treatment naïve	WGS	Healthy	100	11345644200	7532133600	2.99
CGPLH363	Preoperative treatment naïve	WGS	Healthy	100	6117382800	3965952400	1.57

CGPLH364	Preoperative treatment naïve	WGS	Healthy	100	10823498400	7195657000	2.86
CGPLH365	Preoperative treatment naïve	WGS	Healthy	100	5938367400	3954556200	1.57
CGPLH366	Preoperative treatment naïve	WGS	Healthy	100	7063168600	4731853000	1.88
CGPLH367	Preoperative treatment naïve	WGS	Healthy	100	7119631800	4627888200	1.84
CGPLH368	Preoperative treatment naïve	WGS	Healthy	100	7726718400	4975233400	1.97
CGPLH369	Preoperative treatment naïve	WGS	Healthy	100	10967584200	7130956800	2.83
CGPLH37	Preoperative treatment naïve	WGS	Healthy	100	45970545400	4591328800	12.15
CGPLH370	Preoperative treatment naïve	WGS	Healthy	100	9237170600	6106373800	2.42
CGPLH371	Preoperative treatment naïve	WGS	Healthy	100	8077798800	5237070600	2.08
CGPLH380	Preoperative treatment naïve	WGS	Healthy	100	14049589200	8614241200	3.42
CGPLH381	Preoperative treatment naïve	WGS	Healthy	100	16743792000	10767882800	4.27
CGPLH382	Preoperative treatment naïve	WGS	Healthy	100	18474025200	12276437200	4.87
CGPLH383	Preoperative treatment naïve	WGS	Healthy	100	13215954000	8430420600	3.35
CGPLH384	Preoperative treatment naïve	WGS	Healthy	100	8481814000	5463636200	2.17
CGPLH385	Preoperative treatment naïve	WGS	Healthy	100	9596118800	6445445600	2.56
CGPLH386	Preoperative treatment naïve	WGS	Healthy	100	7399540400	4915484800	1.95
CGPLH387	Preoperative treatment naïve	WGS	Healthy	100	6860332600	4339724400	1.72
CGPLH388	Preoperative treatment naïve	WGS	Healthy	100	8679705600	5463945400	2.17
CGPLH389	Preoperative treatment naïve	WGS	Healthy	100	7266863600	4702386000	1.87
CGPLH390	Preoperative treatment naïve	WGS	Healthy	100	7509035600	4913901800	1.95
CGPLH391	Preoperative treatment naïve	WGS	Healthy	100	7252286000	4702404800	1.87
CGPLH392	Preoperative treatment naïve	WGS	Healthy	100	7302618200	4722407000	1.87
CGPLH393	Preoperative treatment naïve	WGS	Healthy	100	8879138000	5947871800	2.36
CGPLH394	Preoperative treatment naïve	WGS	Healthy	100	8737031000	5599777400	2.22
CGPLH395	Preoperative treatment naïve	WGS	Healthy	100	7783904800	4907146000	1.95
CGPLH396	Preoperative treatment naïve	WGS	Healthy	100	7585567200	5076638200	2.01
CGPLH398	Preoperative treatment naïve	WGS	Healthy	100	13001418200	8607025000	3.42
CGPLH399	Preoperative treatment naïve	WGS	Healthy	100	9867699200	5526646000	2.19

CGPLH400	Preoperative treatment naïve	WGS	Healthy	100	10573939000	6290438200	2.50
CGPLH401	Preoperative treatment naïve	WGS	Healthy	100	9415150000	6139638000	2.44
CGPLH402	Preoperative treatment naïve	WGS	Healthy	100	5541458000	2972027800	1.18
CGPLH403	Preoperative treatment naïve	WGS	Healthy	100	6470913200	3549772600	1.41
CGPLH404	Preoperative treatment naïve	WGS	Healthy	100	7369651800	4120205000	1.64
CGPLH405	Preoperative treatment naïve	WGS	Healthy	100	7360239000	4293522600	1.70
CGPLH406	Preoperative treatment naïve	WGS	Healthy	100	6026125400	3426007400	1.36
CGPLH407	Preoperative treatment naïve	WGS	Healthy	100	7073375200	4079286800	1.62
CGPLH408	Preoperative treatment naïve	WGS	Healthy	100	8006103200	5121285600	2.03
CGPLH409	Preoperative treatment naïve	WGS	Healthy	100	7343124600	4432335600	1.76
CGPLH410	Preoperative treatment naïve	WGS	Healthy	100	7551842000	4818779600	1.91
CGPLH411	Preoperative treatment naïve	WGS	Healthy	100	6119676400	3636478400	1.44
CGPLH412	Preoperative treatment naïve	WGS	Healthy	100	7960821200	4935752200	1.96
CGPLH413	Preoperative treatment naïve	WGS	Healthy	100	7623405400	4827888400	1.92
CGPLH414	Preoperative treatment naïve	WGS	Healthy	100	7381312400	4743337200	1.88
CGPLH415	Preoperative treatment naïve	WGS	Healthy	100	7240754200	4162208800	1.65
CGPLH416	Preoperative treatment naïve	WGS	Healthy	100	7745658600	4670226000	1.85
CGPLH417	Preoperative treatment naïve	WGS	Healthy	100	7627498600	4403085600	1.75
CGPLH418	Preoperative treatment naïve	WGS	Healthy	100	9090285000	5094814000	2.02
CGPLH419	Preoperative treatment naïve	WGS	Healthy	100	7914120200	5078389800	2.02
CGPLH42	Preoperative treatment naïve	WGS	Healthy	100	39492040600	3901039400	10.32
CGPLH420	Preoperative treatment naïve	WGS	Healthy	100	7014307800	4711393600	1.87
CGPLH422	Preoperative treatment naïve	WGS	Healthy	100	9103972800	6053559800	2.40
CGPLH423	Preoperative treatment naïve	WGS	Healthy	100	10154714200	6128800200	2.43
CGPLH424	Preoperative treatment naïve	WGS	Healthy	100	11002394000	6573756000	2.61
CGPLH425	Preoperative treatment naïve	WGS	Healthy	100	14681352600	9272557000	3.68
CGPLH426	Preoperative treatment naïve	WGS	Healthy	100	8336731000	5177430800	2.05
CGPLH427	Preoperative treatment naïve	WGS	Healthy	100	8242924400	5632991800	2.24

CGPLH428	Preoperative treatment naïve	WGS	Healthy	100	8512550400	5604756600	2.22
CGPLH429	Preoperative treatment naïve	WGS	Healthy	100	8369802800	5477121400	2.17
CGPLH43	Preoperative treatment naïve	WGS	Healthy	100	38513193400	3815698400	10.10
CGPLH430	Preoperative treatment naïve	WGS	Healthy	100	10357365400	6841611000	2.71
CGPLH431	Preoperative treatment naïve	WGS	Healthy	100	7599875800	5006909000	1.99
CGPLH432	Preoperative treatment naïve	WGS	Healthy	100	7932532400	4932304200	1.96
CGPLH434	Preoperative treatment naïve	WGS	Healthy	100	10417028600	6965998800	2.76
CGPLH435	Preoperative treatment naïve	WGS	Healthy	100	8747793800	5677115200	2.25
CGPLH436	Preoperative treatment naïve	WGS	Healthy	100	7990589400	5228737800	2.07
CGPLH437	Preoperative treatment naïve	WGS	Healthy	100	10156991200	6935537200	2.75
CGPLH438	Preoperative treatment naïve	WGS	Healthy	100	9473604000	6445455600	2.56
CGPLH439	Preoperative treatment naïve	WGS	Healthy	100	8303723400	5439877200	2.16
CGPLH440	Preoperative treatment naïve	WGS	Healthy	100	9055233800	6018631400	2.39
CGPLH441	Preoperative treatment naïve	WGS	Healthy	100	10290682000	6896415200	2.74
CGPLH442	Preoperative treatment naïve	WGS	Healthy	100	9876551600	6591249800	2.62
CGPLH443	Preoperative treatment naïve	WGS	Healthy	100	9837225800	6360740800	2.52
CGPLH444	Preoperative treatment naïve	WGS	Healthy	100	9199271400	5755941600	2.28
CGPLH445	Preoperative treatment naïve	WGS	Healthy	100	8089236400	5218259800	2.07
CGPLH446	Preoperative treatment naïve	WGS	Healthy	100	7890664200	5181606000	2.06
CGPLH447	Preoperative treatment naïve	WGS	Healthy	100	7775775000	5120239800	2.03
CGPLH448	Preoperative treatment naïve	WGS	Healthy	100	8686964800	5605079200	2.22
CGPLH449	Preoperative treatment naïve	WGS	Healthy	100	8604545400	5527726600	2.19
CGPLH45	Preoperative treatment naïve	WGS	Healthy	100	39029653000	3771601200	9.98
CGPLH450	Preoperative treatment naïve	WGS	Healthy	100	8428254800	5439950000	2.16
CGPLH451	Preoperative treatment naïve	WGS	Healthy	100	8128977600	5186265600	2.06
CGPLH452	Preoperative treatment naïve	WGS	Healthy	100	6474313400	4216316400	1.67
CGPLH453	Preoperative treatment naïve	WGS	Healthy	100	9831832800	6224917600	2.47
CGPLH455	Preoperative treatment naïve	WGS	Healthy	100	7373753000	4593473600	1.82

CGPLH456	Preoperative treatment naïve	WGS	Healthy	100	8455416200	5457148200	2.17
CGPLH457	Preoperative treatment naïve	WGS	Healthy	100	8647618000	5534503800	2.20
CGPLH458	Preoperative treatment naïve	WGS	Healthy	100	6633156400	4415186000	1.75
CGPLH459	Preoperative treatment naïve	WGS	Healthy	100	8361048200	5497193800	2.18
CGPLH46	Preoperative treatment naïve	WGS	Healthy	100	35361484600	3516232800	9.30
CGPLH460	Preoperative treatment naïve	WGS	Healthy	100	6788835400	4472282800	1.77
CGPLH463	Preoperative treatment naïve	WGS	Healthy	100	8534880800	5481759200	2.18
CGPLH464	Preoperative treatment naïve	WGS	Healthy	100	6692520000	4184463400	1.66
CGPLH465	Preoperative treatment naïve	WGS	Healthy	100	7772884600	4878430800	1.94
CGPLH466	Preoperative treatment naïve	WGS	Healthy	100	9056275000	5830877400	2.31
CGPLH467	Preoperative treatment naïve	WGS	Healthy	100	6931419200	4585861000	1.82
CGPLH468	Preoperative treatment naïve	WGS	Healthy	100	9334067400	6314830400	2.51
CGPLH469	Preoperative treatment naïve	WGS	Healthy	100	7376691000	4545246600	1.80
CGPLH47	Preoperative treatment naïve	WGS	Healthy	100	38485647600	3534883600	9.35
CGPLH470	Preoperative treatment naïve	WGS	Healthy	100	7899727600	5221650600	2.07
CGPLH471	Preoperative treatment naïve	WGS	Healthy	100	9200430600	6102371000	2.42
CGPLH472	Preoperative treatment naïve	WGS	Healthy	100	8143742400	5399946600	2.14
CGPLH473	Preoperative treatment naïve	WGS	Healthy	100	8123924600	5419825400	2.15
CGPLH474	Preoperative treatment naïve	WGS	Healthy	100	8853071400	6084059400	2.41
CGPLH475	Preoperative treatment naïve	WGS	Healthy	100	8115374000	5291718000	2.10
CGPLH476	Preoperative treatment naïve	WGS	Healthy	100	8163162600	5096869600	2.02
CGPLH477	Preoperative treatment naïve	WGS	Healthy	100	8350093200	5465468600	2.17
CGPLH478	Preoperative treatment naïve	WGS	Healthy	100	8259642200	5406516200	2.15
CGPLH479	Preoperative treatment naïve	WGS	Healthy	100	8027598600	5417376800	2.15
CGPLH48	Preoperative treatment naïve	WGS	Healthy	100	42232410000	4165893400	11.02
CGPLH480	Preoperative treatment naïve	WGS	Healthy	100	7832983200	5020127000	1.99
CGPLH481	Preoperative treatment naïve	WGS	Healthy	100	7578518800	4883280800	1.94
CGPLH482	Preoperative treatment naïve	WGS	Healthy	100	8279364800	5652263600	2.24

CGPLH483	Preoperative treatment naïve	WGS	Healthy	100	8660338800	5823859200	2.31
CGPLH484	Preoperative treatment naïve	WGS	Healthy	100	8445420000	5794328000	2.30
CGPLH485	Preoperative treatment naïve	WGS	Healthy	100	8371255400	5490207800	2.18
CGPLH486	Preoperative treatment naïve	WGS	Healthy	100	8216712200	5506871000	2.19
CGPLH487	Preoperative treatment naïve	WGS	Healthy	100	7936294200	5309250200	2.11
CGPLH488	Preoperative treatment naïve	WGS	Healthy	100	8355603600	5453160000	2.16
CGPLH49	Preoperative treatment naïve	WGS	Healthy	100	33912191800	3310056000	8.76
CGPLH490	Preoperative treatment naïve	WGS	Healthy	100	7768712400	5175567800	2.05
CGPLH491	Preoperative treatment naïve	WGS	Healthy	100	9070904000	6011275000	2.39
CGPLH492	Preoperative treatment naïve	WGS	Healthy	100	7208727200	4753213800	1.89
CGPLH493	Preoperative treatment naïve	WGS	Healthy	100	10542882600	7225870800	2.87
CGPLH494	Preoperative treatment naïve	WGS	Healthy	100	10908197600	7046645000	2.80
CGPLH495	Preoperative treatment naïve	WGS	Healthy	100	8945040400	5891697800	2.34
CGPLH496	Preoperative treatment naïve	WGS	Healthy	100	10859729400	7549608000	3.00
CGPLH497	Preoperative treatment naïve	WGS	Healthy	100	9630507400	6473162800	2.57
CGPLH498	Preoperative treatment naïve	WGS	Healthy	100	10060232600	6744622800	2.68
CGPLH499	Preoperative treatment naïve	WGS	Healthy	100	10221293600	6951282800	2.76
CGPLH50	Preoperative treatment naïve	WGS	Healthy	100	41248860600	4073272800	10.78
CGPLH500	Preoperative treatment naïve	WGS	Healthy	100	9703168200	6239893800	2.48
CGPLH501	Preoperative treatment naïve	WGS	Healthy	100	9104779800	6161602800	2.45
CGPLH502	Preoperative treatment naïve	WGS	Healthy	100	8514467400	5290881400	2.10
CGPLH503	Preoperative treatment naïve	WGS	Healthy	100	9019992200	6100383400	2.42
CGPLH504	Preoperative treatment naïve	WGS	Healthy	100	9320330200	6199750200	2.46
CGPLH505	Preoperative treatment naïve	WGS	Healthy	100	7499497400	4914559000	1.95
CGPLH506	Preoperative treatment naïve	WGS	Healthy	100	10526142000	6963312600	2.76
CGPLH507	Preoperative treatment naïve	WGS	Healthy	100	9091018400	6146678600	2.44
CGPLH508	Preoperative treatment naïve	WGS	Healthy	100	10989315600	7360201400	2.92
CGPLH509	Preoperative treatment naïve	WGS	Healthy	100	9729084600	6702691600	2.66

CGPLH51	Preoperative treatment naïve	WGS	Healthy	100	35967451400	3492833200	9.24
CGPLH510	Preoperative treatment naïve	WGS	Healthy	100	11162691600	7626795400	3.03
CGPLH511	Preoperative treatment naïve	WGS	Healthy	100	11888619600	8110427600	3.22
CGPLH512	Preoperative treatment naïve	WGS	Healthy	100	10726438400	7110078000	2.82
CGPLH513	Preoperative treatment naïve	WGS	Healthy	100	10701564200	7155271400	2.84
CGPLH514	Preoperative treatment naïve	WGS	Healthy	100	8822067000	5958773800	2.36
CGPLH515	Preoperative treatment naïve	WGS	Healthy	100	7792074800	5317464600	2.11
CGPLH516	Preoperative treatment naïve	WGS	Healthy	100	8642620000	5846439400	2.32
CGPLH517	Preoperative treatment naïve	WGS	Healthy	100	11915929600	8013937000	3.18
CGPLH518	Preoperative treatment naïve	WGS	Healthy	100	12804517400	8606661600	3.42
CGPLH519	Preoperative treatment naïve	WGS	Healthy	100	11513222200	7922798400	3.14
CGPLH52	Preoperative treatment naïve	WGS	Healthy	100	49247304200	4849631400	12.83
CGPLH520	Preoperative treatment naïve	WGS	Healthy	100	8942102400	6030683400	2.39
CGPLH54	Preoperative treatment naïve	WGS	Healthy	100	45399346400	4466164600	11.82
CGPLH55	Preoperative treatment naïve	WGS	Healthy	100	42547725000	4283337600	11.33
CGPLH56	Preoperative treatment naïve	WGS	Healthy	100	33460308000	3226338000	8.53
CGPLH57	Preoperative treatment naïve	WGS	Healthy	100	36504735200	3509125000	9.28
CGPLH59	Preoperative treatment naïve	WGS	Healthy	100	39642810600	3820011000	10.11
CGPLH625	Preoperative treatment naïve	WGS	Healthy	100	6408225000	4115487600	1.63
CGPLH626	Preoperative treatment naïve	WGS	Healthy	100	9915193600	6391657000	2.54
CGPLH63	Preoperative treatment naïve	WGS	Healthy	100	37447047600	3506737000	9.28
CGPLH639	Preoperative treatment naïve	WGS	Healthy	100	8158965800	5216049600	2.07
CGPLH64	Preoperative treatment naïve	WGS	Healthy	100	34275506800	3264508000	8.63
CGPLH640	Preoperative treatment naïve	WGS	Healthy	100	8058876800	5333551800	2.12
CGPLH642	Preoperative treatment naïve	WGS	Healthy	100	7545555600	4909732800	1.95
CGPLH643	Preoperative treatment naïve	WGS	Healthy	100	7865776800	5254772000	2.09
CGPLH644	Preoperative treatment naïve	WGS	Healthy	100	6890139000	4599387400	1.83
CGPLH646	Preoperative treatment naïve	WGS	Healthy	100	7757219400	5077408200	2.01

CGPLH75	Preoperative treatment naïve	WGS	Healthy	100	23882926000	2250344400	5.95
CGPLH76	Preoperative treatment naïve	WGS	Healthy	100	30631483600	3086042200	8.16
CGPLH77	Preoperative treatment naïve	WGS	Healthy	100	31651741400	3041290200	8.04
CGPLH78	Preoperative treatment naïve	WGS	Healthy	100	31165831200	3130079800	8.28
CGPLH79	Preoperative treatment naïve	WGS	Healthy	100	31935043000	3128488200	8.27
CGPLH80	Preoperative treatment naïve	WGS	Healthy	100	32965093000	3311371800	8.76
CGPLH81	Preoperative treatment naïve	WGS	Healthy	100	27035311200	2455084400	6.49
CGPLH82	Preoperative treatment naïve	WGS	Healthy	100	28447051200	2893358200	7.65
CGPLH83	Preoperative treatment naïve	WGS	Healthy	100	26702240200	2459494000	6.50
CGPLH84	Preoperative treatment naïve	WGS	Healthy	100	25176861400	2524467400	6.68
CGPLLU13	Pre-treatment, Day -2	WGS	Lung Cancer	100	9126585600	5915061800	2.35
CGPLLU13	Post-treatment, Day 5	WGS	Lung Cancer	100	7739120200	5071745800	2.01
CGPLLU13	Post-treatment, Day 28	WGS	Lung Cancer	100	9081585400	5764371600	2.29
CGPLLU13	Post-treatment, Day 91	WGS	Lung Cancer	100	9576557000	6160760200	2.44
CGPLLU14	Pre-treatment, Day -38	WGS	Lung Cancer	100	13659198400	9033455800	3.58
CGPLLU14	Pre-treatment, Day -16	WGS	Lung Cancer	100	7178855800	4856648600	1.93
CGPLLU14	Pre-treatment, Day -3	WGS	Lung Cancer	100	7653473000	4816193600	1.91
CGPLLU14	Pre-treatment, Day 0	WGS	Lung Cancer	100	7851997400	5193256600	2.06
CGPLLU14	Post-treatment, Day 0.33	WGS	Lung Cancer	100	7193040800	4869701600	1.93
CGPLLU14	Post-treatment, Day 7	WGS	Lung Cancer	100	7102050000	4741432600	1.88
CGPLLU144	Preoperative treatment naïve	WGS	Lung Cancer	100	4934813600	3415936400	1.36
CGPLLU147	Preoperative treatment naïve	WGS	Lung Cancer	100	24409561000	2118672800	5.61
CGPLLU161	Preoperative treatment naïve	WGS	Lung Cancer	100	8998813400	6016145000	2.39
CGPLLU162	Preoperative treatment naïve	WGS	Lung Cancer	100	9709792400	6407866400	2.54
CGPLLU163	Preoperative treatment naïve	WGS	Lung Cancer	100	9150620200	6063569800	2.41
CGPLLU165	Preoperative treatment naïve	WGS	Lung Cancer	100	28374436400	2651138600	7.01
CGPLLU168	Preoperative treatment naïve	WGS	Lung Cancer	100	5692739400	3695191000	1.47
CGPLLU169	Preoperative treatment naïve	WGS	Lung Cancer	100	9093975600	5805320800	2.30

CGPLLU175	Preoperative treatment naïve	WGS	Lung Cancer	100	33794816800	3418750400	9.04
CGPLLU176	Preoperative treatment naïve	WGS	Lung Cancer	100	8778553800	5794950200	2.30
CGPLLU177	Preoperative treatment naïve	WGS	Lung Cancer	100	3734614800	2578696200	1.02
CGPLLU180	Preoperative treatment naïve	WGS	Lung Cancer	100	28305936600	2756034200	7.29
CGPLLU198	Preoperative treatment naïve	WGS	Lung Cancer	100	23244959200	2218577200	5.86
CGPLLU202	Preoperative treatment naïve	WGS	Lung Cancer	100	21110128200	1831279400	4.84
CGPLLU203	Preoperative treatment naïve	WGS	Lung Cancer	100	4304235600	2896429000	1.15
CGPLLU205	Preoperative treatment naïve	WGS	Lung Cancer	100	10502467000	7386984800	2.93
CGPLLU206	Preoperative treatment naïve	WGS	Lung Cancer	100	21888248200	2026666000	5.36
CGPLLU207	Preoperative treatment naïve	WGS	Lung Cancer	100	10806230600	7363049000	2.92
CGPLLU208	Preoperative treatment naïve	WGS	Lung Cancer	100	7795426800	5199545800	2.06
CGPLLU209	Preoperative treatment naïve	WGS	Lung Cancer	100	26174542000	2621961800	6.93
CGPLLU244	Pre-treatment, Day -7	WGS	Lung Cancer	100	9967531400	6704365800	2.66
CGPLLU244	Pre-treatment, Day -1	WGS	Lung Cancer	100	9547119200	5785172600	2.30
CGPLLU244	Post-treatment, Day 6	WGS	Lung Cancer	100	9535898600	6452174000	2.56
CGPLLU244	Post-treatment, Day 62	WGS	Lung Cancer	100	8783628600	5914149000	2.35
CGPLLU245	Pre-treatment, Day -32	WGS	Lung Cancer	100	10025823200	6313303800	2.51
CGPLLU245	Pre-treatment, Day 0	WGS	Lung Cancer	100	9462480400	6612867800	2.62
CGPLLU245	Post-treatment, Day 7	WGS	Lung Cancer	100	9143825000	6431013200	2.55
CGPLLU245	Post-treatment, Day 21	WGS	Lung Cancer	100	9072713800	6368533000	2.53
CGPLLU246	Pre-treatment, Day -21	WGS	Lung Cancer	100	9579787000	6458003400	2.56
CGPLLU246	Pre-treatment, Day 0	WGS	Lung Cancer	100	9512703600	6440535600	2.56
CGPLLU246	Post-treatment, Day 9	WGS	Lung Cancer	100	9512646000	6300939200	2.50
CGPLLU246	Post-treatment, Day 42	WGS	Lung Cancer	100	11136103000	7358747400	2.92
CGPLLU264	Pre-treatment, Day -1	WGS	Lung Cancer	100	9196305000	6239803600	2.48
CGPLLU264	Post-treatment, Day 6	WGS	Lung Cancer	100	8247416600	5600454200	2.22
CGPLLU264	Post-treatment, Day 27	WGS	Lung Cancer	100	8681022200	5856109000	2.32
CGPLLU264	Post-treatment, Day 69	WGS	Lung Cancer	100	8931976400	5974246000	2.37

CGPLLU265	Pre-treatment, Day 0	WGS	Lung Cancer	100	9460534000	6111185200	2.43
CGPLLU265	Post-treatment, Day 3	WGS	Lung Cancer	100	8051601200	4984166600	1.98
CGPLLU265	Post-treatment, Day 7	WGS	Lung Cancer	100	8082224600	5110092600	2.03
CGPLLU265	Post-treatment, Day 84	WGS	Lung Cancer	100	8368637400	5369526400	2.13
CGPLLU266	Pre-treatment, Day 0	WGS	Lung Cancer	100	8583766400	5846473600	2.32
CGPLLU266	Post-treatment, Day 16	WGS	Lung Cancer	100	8795793600	5984531400	2.37
CGPLLU266	Post-treatment, Day 83	WGS	Lung Cancer	100	9157947600	6227735000	2.47
CGPLLU266	Post-treatment, Day 328	WGS	Lung Cancer	100	7299455400	5049379000	2.00
CGPLLU267	Pre-treatment, Day -1	WGS	Lung Cancer	100	10658657800	6892067000	2.73
CGPLLU267	Post-treatment, Day 34	WGS	Lung Cancer	100	8492833400	5101097800	2.02
CGPLLU267	Post-treatment, Day 90	WGS	Lung Cancer	100	12030314800	7757930400	3.08
CGPLLU269	Pre-treatment, Day 0	WGS	Lung Cancer	100	9170168000	5830454400	2.31
CGPLLU269	Post-treatment, Day 9	WGS	Lung Cancer	100	8905640400	5298461400	2.10
CGPLLU269	Post-treatment, Day 28	WGS	Lung Cancer	100	8455306600	5387927400	2.14
CGPLLU271	Post-treatment, Day 259	WGS	Lung Cancer	100	8112060400	5404979000	2.14
CGPLLU271	Pre-treatment, Day 0	WGS	Lung Cancer	100	13150818200	8570453400	3.40
CGPLLU271	Post-treatment, Day 6	WGS	Lung Cancer	100	9008880600	5854051400	2.32
CGPLLU271	Post-treatment, Day 20	WGS	Lung Cancer	100	8670913000	5461577000	2.17
CGPLLU271	Post-treatment, Day 104	WGS	Lung Cancer	100	8887441400	5609039000	2.23
CGPLLU43	Pre-treatment, Day -1	WGS	Lung Cancer	100	8407811200	5203486400	2.06
CGPLLU43	Post-treatment, Day 6	WGS	Lung Cancer	100	9264335200	5626714400	2.23
CGPLLU43	Post-treatment, Day 27	WGS	Lung Cancer	100	8902283000	5485656200	2.18
CGPLLU43	Post-treatment, Day 83	WGS	Lung Cancer	100	9201509200	5875084200	2.33
CGPLLU86	Pre-treatment, Day 0	WGS	Lung Cancer	100	9152729200	6248173200	2.48
CGPLLU86	Post-treatment, Day 0.5	WGS	Lung Cancer	100	6703253000	4663026800	1.85
CGPLLU86	Post-treatment, Day 7	WGS	Lung Cancer	100	6590121400	4559562400	1.81
CGPLLU86	Post-treatment, Day 17	WGS	Lung Cancer	100	8653551800	5900136000	2.34
CGPLLU88	Pre-treatment, Day 0	WGS	Lung Cancer	100	8096528000	5505475400	2.18

CGPLLU88	Post-treatment, Day 7	WGS	Lung Cancer	100	8283192200	5784217600	2.30
CGPLLU88	Post-treatment, Day 297	WGS	Lung Cancer	100	9297110800	6407258000	2.54
CGPLLU89	Pre-treatment, Day 0	WGS	Lung Cancer	100	7842145200	5356095400	2.13
CGPLLU89	Post-treatment, Day 7	WGS	Lung Cancer	100	7234220200	4930375200	1.96
CGPLLU89	Post-treatment, Day 22	WGS	Lung Cancer	100	6242889800	4057361000	1.61
CGPLOV11	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8985130400	5871959600	2.33
CGPLOV12	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9705820000	6430505400	2.55
CGPLOV13	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10307949400	7029712000	2.79
CGPLOV15	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8472829400	5562142400	2.21
CGPLOV16	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10977781000	7538581600	2.99
CGPLOV19	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8800876200	5855304000	2.32
CGPLOV20	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8714443600	5695165800	2.26
CGPLOV21	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10180394800	7120260400	2.83
CGPLOV22	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10107760000	6821916800	2.71
CGPLOV23	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10643399800	7206330800	2.86
CGPLOV24	Preoperative treatment naïve	WGS	Ovarian Cancer	100	6780929000	4623300400	1.83
CGPLOV25	Preoperative treatment naïve	WGS	Ovarian Cancer	100	7817548600	5359975200	2.13
CGPLOV26	Preoperative treatment naïve	WGS	Ovarian Cancer	100	11763101400	8178024400	3.25
CGPLOV28	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9522546400	6259423400	2.48
CGPLOV31	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9104831200	6109358400	2.42
CGPLOV32	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9222073600	6035150000	2.39
CGPLOV37	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8898328600	5971018200	2.37
CGPLOV38	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8756825200	5861536600	2.33
CGPLOV40	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9709391600	6654707200	2.64
CGPLOV41	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8923625000	5973070400	2.37
CGPLOV42	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10719380400	7353214200	2.92
CGPLOV43	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10272189000	6423288600	2.55
CGPLOV44	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9861862600	6769185800	2.69

CGPLOV46	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8788956400	5789863400	2.30
CGPLOV47	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9380561800	6480763600	2.57
CGPLOV48	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9258552600	6380106400	2.53
CGPLOV49	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8787025400	6134503600	2.43
CGPLOV50	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10144154400	6984721400	2.77
CGPLPA112	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	12740651400	9045622000	3.59
CGPLPA113	Preoperative treatment naïve	WGS	Duodenal Cancer	100	8802479000	5909030800	2.34
CGPLPA114	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8792313600	6019061000	2.39
CGPLPA115	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8636551400	5958809000	2.36
CGPLPA117	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9128885200	6288833200	2.50
CGPLPA118	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7931485800	5407532800	2.15
CGPLPA122	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	10888985000	7530118800	2.99
CGPLPA124	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8562012400	5860171000	2.33
CGPLPA125	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9715576600	6390321000	2.54
CGPLPA126	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8056768800	5651600800	2.24
CGPLPA127	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8000301000	5382987600	2.14
CGPLPA128	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	6165751600	4256521400	1.69
CGPLPA129	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7143147400	4917370400	1.95
CGPLPA130	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	5664335000	3603919400	1.43
CGPLPA131	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8292982000	5844942000	2.32
CGPLPA134	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7088917000	5048887600	2.00
CGPLPA135	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8759665600	5800618200	2.30
CGPLPA136	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7539715800	5248227600	2.08
CGPLPA137	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8391815400	5901273800	2.34
CGPLPA139	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8992280200	6328314400	2.51
CGPLPA14	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8787706200	5731317600	2.27
CGPLPA140	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	16365641800	11216732000	4.45
CGPLPA141	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	15086298000	10114790200	4.01

CGPLPA15	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8255566800	5531677600	2.20
CGPLPA155	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9457155800	6621881800	2.63
CGPLPA156	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9845385800	6728653000	2.67
CGPLPA165	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8356604600	5829895800	2.31
CGPLPA168	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	10365661600	7048115600	2.80
CGPLPA17	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8073547400	4687808000	1.86
CGPLPA184	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9014218400	6230922200	2.47
CGPLPA187	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8883536200	6140874400	2.44
CGPLPA23	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9835452000	6246525400	2.48
CGPLPA25	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10077515400	6103322200	2.42
CGPLPA26	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8354272400	5725781000	2.27
CGPLPA28	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8477461600	5688846800	2.26
CGPLPA33	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7287615600	4596723800	1.82
CGPLPA34	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	6122902400	4094828000	1.62
CGPLPA37	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	12714888200	8527779200	3.38
CGPLPA38	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8525500600	5501341400	2.18
CGPLPA39	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10502663600	6812333000	2.70
CGPLPA40	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9083670000	5394717800	2.14
CGPLPA42	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	5972126600	3890395200	1.54
CGPLPA46	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	4720090200	2626298800	1.04
CGPLPA47	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7317385800	4543833000	1.80
CGPLPA48	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7553856200	5022695600	1.99
CGPLPA52	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	5655875000	3551861600	1.41
CGPLPA53	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9504749000	6323344800	2.51
CGPLPA58	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8088090200	5118138200	2.03
CGPLPA59	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	14547364600	9617778600	3.82
CGPLPA67	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8222177400	5351172600	2.12
CGPLPA69	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7899181400	5006114800	1.99

CGPLPA71	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7349620400	4955417400	1.97
CGPLPA74	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	6666371400	4571394200	1.81
CGPLPA76	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9755658600	6412606800	2.54
CGPLPA85	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10856223000	7309498600	2.90
CGPLPA86	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8744365400	5514523200	2.19
CGPLPA92	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8073791200	5390492800	2.14
CGPLPA93	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10390273000	7186589400	2.85
CGPLPA94	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	11060347600	7641336400	3.03
CGPLPA95	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	12416627200	7206503800	2.86
CGST102	Preoperative treatment naïve	WGS	Gastric cancer	100	6637004600	4545072600	1.80
CGST11	Preoperative treatment naïve	WGS	Gastric cancer	100	9718427800	6259679600	2.48
CGST110	Preoperative treatment naïve	WGS	Gastric cancer	100	9319661600	6359317400	2.52
CGST114	Preoperative treatment naïve	WGS	Gastric cancer	100	6865213000	4841171600	1.92
CGST13	Preoperative treatment naïve	WGS	Gastric cancer	100	9284554800	6360843800	2.52
CGST131	Preoperative treatment naïve	WGS	Gastric cancer	100	5924382000	3860677200	1.53
CGST141	Preoperative treatment naïve	WGS	Gastric cancer	100	8486380800	5860491000	2.33
CGST16	Preoperative treatment naïve	WGS	Gastric cancer	100	13820725800	9377828000	3.72
CGST18	Preoperative treatment naïve	WGS	Gastric cancer	100	7781288000	5278862400	2.09
CGST21	Preoperative treatment naïve	WGS	Gastric cancer	100	7171165400	4103970800	1.63
CGST26	Preoperative treatment naïve	WGS	Gastric cancer	100	8983961800	6053405600	2.40
CGST28	Preoperative treatment naïve	WGS	Gastric cancer	100	9683035400	6745116400	2.68
CGST30	Preoperative treatment naïve	WGS	Gastric cancer	100	8684086600	5741416000	2.28
CGST32	Preoperative treatment naïve	WGS	Gastric cancer	100	8568194600	5783369200	2.29
CGST33	Preoperative treatment naïve	WGS	Gastric cancer	100	9351699600	6448718400	2.56
CGST38	Preoperative treatment naïve	WGS	Gastric cancer	100	8409876400	5770989200	2.29
CGST39	Preoperative treatment naïve	WGS	Gastric cancer	100	10573763000	7597016000	3.01
CGST41	Preoperative treatment naïve	WGS	Gastric cancer	100	9434854200	6609415400	2.62
CGST45	Preoperative treatment naïve	WGS	Gastric cancer	100	8203868600	5625223000	2.23

CGST47	Preoperative treatment naïve	WGS	Gastric cancer	100	8938597600	6178990600	2.45
CGST48	Preoperative treatment naïve	WGS	Gastric cancer	100	9106628800	6517085200	2.59
CGST53	Preoperative treatment naïve	WGS	Gastric cancer	100	9005374200	5854996200	2.32
CGST58	Preoperative treatment naïve	WGS	Gastric cancer	100	10020368600	6133458400	2.43
CGST67	Preoperative treatment naïve	WGS	Gastric cancer	100	9198135600	5911071000	2.35
CGST77	Preoperative treatment naïve	WGS	Gastric cancer	100	8228789400	5119116800	2.03
CGST80	Preoperative treatment naïve	WGS	Gastric cancer	100	10596963400	7283152800	2.89
CGST81	Preoperative treatment naïve	WGS	Gastric cancer	100	8494881200	5838064000	2.32

Table 4.5. Summary of high coverage whole genome cfDNA analyses.

Patient	Patient Type	Analysis Type	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals*	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals*	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Lymphocytes*	Correlation of Fragment Ratio Profile to Lymphocyte Nucleosome Distances*
CGPLH75	Healthy	WGS	NA	168	0.977	0.952	0.920	-0.886
CGPLH77	Healthy	WGS	NA	166	0.970	0.960	0.904	-0.912
CGPLH80	Healthy	WGS	NA	168	0.955	0.949	0.960	-0.917
CGPLH81	Healthy	WGS	NA	167	0.949	0.953	0.869	-0.883
CGPLH82	Healthy	WGS	NA	166	0.969	0.949	0.954	-0.917
CGPLH83	Healthy	WGS	NA	167	0.949	0.939	0.919	-0.904
CGPLH84	Healthy	WGS	NA	168	0.967	0.948	0.951	-0.913
CGPLH52	Healthy	WGS	NA	167	0.946	0.968	0.952	-0.924
CGPLH35	Healthy	WGS	NA	166	0.981	0.973	0.945	-0.921
CGPLH37	Healthy	WGS	NA	168	0.968	0.970	0.951	-0.922
CGPLH54	Healthy	WGS	NA	167	0.968	0.976	0.948	-0.925
CGPLH55	Healthy	WGS	NA	166	0.947	0.964	0.948	-0.917
CGPLH48	Healthy	WGS	NA	168	0.959	0.965	0.960	-0.923
CGPLH50	Healthy	WGS	NA	167	0.960	0.968	0.952	-0.921
CGPLH36	Healthy	WGS	NA	168	0.955	0.954	0.955	-0.919
CGPLH42	Healthy	WGS	NA	167	0.973	0.963	0.948	-0.918
CGPLH43	Healthy	WGS	NA	166	0.952	0.958	0.953	-0.928
CGPLH59	Healthy	WGS	NA	168	0.970	0.965	0.951	-0.925
CGPLH45	Healthy	WGS	NA	168	0.965	0.950	0.949	-0.911
CGPLH47	Healthy	WGS	NA	167	0.952	0.944	0.954	-0.921
CGPLH46	Healthy	WGS	NA	168	0.966	0.965	0.953	-0.923
CGPLH63	Healthy	WGS	NA	168	0.977	0.968	0.939	-0.920

CGPLH51	Healthy	WGS	NA	168	0.935	0.955	0.957	-0.914
CGPLH57	Healthy	WGS	NA	169	0.965	0.954	0.955	-0.917
CGPLH49	Healthy	WGS	NA	168	0.958	0.951	0.950	-0.924
CGPLH56	Healthy	WGS	NA	166	0.940	0.957	0.959	-0.911
CGPLH64	Healthy	WGS	NA	169	0.960	0.940	0.949	-0.918
CGPLH78	Healthy	WGS	NA	166	0.956	0.936	0.958	-0.911
CGPLH79	Healthy	WGS	NA	168	0.960	0.957	0.953	-0.917
CGPLH76	Healthy	WGS	NA	167	0.969	0.965	0.953	-0.917
CGPLLU175	Lung Cancer	WGS	I	165	0.316	0.284	0.244	-0.262
CGPLLU180	Lung Cancer	WGS	I	166	0.907	0.846	0.826	-0.819
CGPLLU198	Lung Cancer	WGS	I	166	0.972	0.946	0.928	-0.911
CGPLLU202	Lung Cancer	WGS	I	163	0.821	0.605	0.905	-0.843
CGPLLU165	Lung Cancer	WGS	II	163	0.924	0.961	0.815	-0.851
CGPLLU209	Lung Cancer	WGS	II	163	0.578	0.526	0.513	-0.534
CGPLLU147	Lung Cancer	WGS	III	166	0.953	0.919	0.939	-0.912
CGPLLU206	Lung Cancer	WGS	III	158	0.488	0.343	0.460	-0.481

*Pearson correlation.

Table 4.6. Summary of monitoring response to therapy using whole genome and targeted analyses.

Patient	Patient Type	Timepoint	Stage	Progression-free Survival (months)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals*	Correlation of Fragment Ratio Profile to Lymphocyte Nucleosome Distances*	Targeted Mutation[1]	Maximum Mutant Allele Fraction[1]
CGPLLU14	Lung Cancer	Pre-treatment, Day -38	IV	15.4	0.941	-0.841	EGFR 861L>Q	0.89%
CGPLLU14	Lung Cancer	Pre-treatment, Day -16	IV	15.4	0.933	-0.833	EGFR 861L>Q	0.18%
CGPLLU14	Lung Cancer	Pre-treatment, Day -3	IV	15.4	0.908	-0.814	EGFR 719G>S	0.49%
CGPLLU14	Lung Cancer	Pre-treatment, Day 0	IV	15.4	0.883	-0.752	EGFR 861L>Q	1.39%
CGPLLU14	Lung Cancer	Post-treatment, Day 0.33	IV	15.4	0.820	-0.692	EGFR 719G>S	1.05%
CGPLLU14	Lung Cancer	Post-treatment, Day 7	IV	15.4	0.927	-0.887	EGFR 861L>Q	0.00%
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	IV	18.0	0.657	-0.584	EGFR 745KELREA>T	9.06%
CGPLLU88	Lung Cancer	Post-treatment, Day 7	IV	18.0	0.939	-0.799	EGFR 790T>M	0.15%
CGPLLU88	Lung Cancer	Post-treatment, Day 297	IV	18.0	0.946	-0.869	EGFR 745KELREA>T	0.93%
CGPLLU244	Lung Cancer	Pre-treatment, Day -7	IV	1.2	0.850	-0.706	EGFR 858L>R	4.98%
CGPLLU244	Lung Cancer	Pre-treatment, Day -1	IV	1.2	0.867	-0.764	EGFR 62L>R	3.41%
CGPLLU244	Lung Cancer	Post-treatment, Day 6	IV	1.2	0.703	-0.639	EGFR 858L>R	5.57%
CGPLLU244	Lung Cancer	Post-treatment, Day 62	IV	1.2	0.659	-0.660	EGFR 858L>R	11.80%
CGPLLU245	Lung Cancer	Pre-treatment, Day -32	IV	1.7	0.871	-0.724	EGFR 745KELREA>K	10.60%
CGPLLU245	Lung Cancer	Pre-treatment, Day 0	IV	1.7	0.738	-0.608	EGFR 745KELREA>K	14.10%
CGPLLU245	Lung Cancer	Post-treatment, Day 7	IV	1.7	0.731	-0.559	EGFR 745KELREA>K	8.56%
CGPLLU245	Lung Cancer	Post-treatment, Day 21	IV	1.7	0.613	-0.426	EGFR 745KELREA>K	10.69%
CGPLLU246	Lung Cancer	Pre-treatment, Day -21	IV	1.3	0.897	-0.757	EGFR 790T>M	0.49%
CGPLLU246	Lung Cancer	Pre-treatment, Day 0	IV	1.3	0.469	-0.376	EGFR 858L>R	6.17%
CGPLLU246	Lung Cancer	Post-treatment, Day 9	IV	1.3	0.874	-0.746	EGFR 858L>R	1.72%
CGPLLU246	Lung Cancer	Post-treatment, Day 42	IV	1.3	0.775	-0.665	EGFR 858L>R	5.29%
CGPLLU86	Lung Cancer	Pre-treatment, Day 0	IV	12.4	0.817	-0.630	EGFR 746ELREATS>D	0.00%
CGPLLU86	Lung Cancer	Post-treatment, Day 0.5	IV	12.4	0.916	-0.811	EGFR 746ELREATS>D	0.19%

CGPLLU86	Lung Cancer	Post-treatment, Day 7	IV	12.4	0.859	-0.694	EGFR 746ELREATS>D	0.00%
CGPLLU86	Lung Cancer	Post-treatment, Day 17	IV	12.4	0.932	-0.848	EGFR 746ELREATS>D	0.00%
CGPLLU89	Lung Cancer	Pre-treatment, Day 0	IV	6.7	0.864	-0.729	EGFR 747LREATS>-	0.42%
CGPLLU89	Lung Cancer	Post-treatment, Day 7	IV	6.7	0.908	-0.803	EGFR 747LREATS>-	0.20%
CGPLLU89	Lung Cancer	Post-treatment, Day 22	IV	6.7	0.853	-0.881	EGFR 747LREATS>-	0.00%
CGLU316	Lung Cancer	Pre-treatment, Day -53	IV	1.4	0.331	-0.351	EGFR L861Q	15.72%
CGLU316	Lung Cancer	Pre-treatment, Day -4	IV	1.4	0.225	-0.253	EGFR L861Q	45.67%
CGLU316	Lung Cancer	Post-treatment, Day 18	IV	1.4	0.336	-0.364	EGFR G719A	33.38%
CGLU316	Lung Cancer	Post-treatment, Day 87	IV	1.4	0.340	-0.364	EGFR L861Q	66.01%
CGLU344	Lung Cancer	Pre-treatment, Day -21	IV	Ongoing	0.935	-0.818	EGFR E746_A750del	0.00%
CGLU344	Lung Cancer	Pre-treatment, Day 0	IV	Ongoing	0.919	-0.774	EGFR E746_A750del	0.22%
CGLU344	Lung Cancer	Post-treatment, Day 0.1875	IV	Ongoing	0.953	-0.860	EGFR E746_A750del	0.40%
CGLU344	Lung Cancer	Post-treatment, Day 59	IV	Ongoing	0.944	-0.832	EGFR E746_A750del	0.00%
CGLU369	Lung Cancer	Pre-treatment, Day -2	IV	7.5	0.825	-0.826	EGFR L858R	20.61%
CGLU369	Lung Cancer	Post-treatment, Day 12	IV	7.5	0.950	-0.903	EGFR L858R	0.22%
CGLU369	Lung Cancer	Post-treatment, Day 68	IV	7.5	0.945	-0.889	EGFR L858R	0.16%
CGLU369	Lung Cancer	Post-treatment, Day 110	IV	7.5	0.886	-0.883	EGFR L858R	0.10%
CGLU373	Lung Cancer	Pre-treatment, Day -2	IV	Ongoing	0.922	-0.804	EGFR E746_A750del	0.82%
CGLU373	Lung Cancer	Post-treatment, Day 0.125	IV	Ongoing	0.959	-0.853	EGFR E746_A750del	0.00%
CGLU373	Lung Cancer	Post-treatment, Day 7	IV	Ongoing	0.967	-0.886	EGFR E746_A750del	0.15%
CGLU373	Lung Cancer	Post-treatment, Day 47	IV	Ongoing	0.951	-0.890	EGFR E746_A750del	0.00%
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	IV	1.5	0.425	-0.400	EGFR E746_A750del	7.66%
CGPLLU13	Lung Cancer	Post-treatment, Day 5	IV	1.5	0.272	-0.257	EGFR E746_A750del	13.10%
CGPLLU13	Lung Cancer	Post-treatment, Day 28	IV	1.5	0.584	-0.536	EGFR E746_A750del	6.09%
CGPLLU13	Lung Cancer	Post-treatment, Day 91	IV	1.5	0.530	-0.513	EGFR E746_A750del	9.28%
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	IV	Ongoing	0.946	-0.824	EGFR D761N	0.00%
CGPLLU264	Lung Cancer	Post-treatment, Day 6	IV	Ongoing	0.927	-0.788	EGFR D761N	0.16%
CGPLLU264	Lung Cancer	Post-treatment, Day 27	IV	Ongoing	0.962	-0.856	EGFR D761N	0.00%

CGPLLU264	Lung Cancer	Post-treatment, Day 69	IV	Ongoing	0.960	-0.894	EGFR D761N	0.00%
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	IV	Ongoing	0.953	-0.859	EGFR L858R	0.21%
CGPLLU265	Lung Cancer	Post-treatment, Day 3	IV	Ongoing	0.949	-0.842	EGFR L858R	0.21%
CGPLLU265	Lung Cancer	Post-treatment, Day 7	IV	Ongoing	0.955	-0.844	EGFR T790M	0.21%
CGPLLU265	Lung Cancer	Post-treatment, Day 84	IV	Ongoing	0.946	-0.825	EGFR L858R	0.00%
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	IV	9.6	0.961	-0.904	NA	0.00%
CGPLLU266	Lung Cancer	Post-treatment, Day 16	IV	9.6	0.959	-0.886	NA	0.00%
CGPLLU266	Lung Cancer	Post-treatment, Day 83	IV	9.6	0.961	-0.880	NA	0.00%
CGPLLU266	Lung Cancer	Post-treatment, Day 328	IV	9.6	0.958	-0.855	NA	0.00%
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	IV	3.9	0.919	-0.863	EGFR L858R	1.93%
CGPLLU267	Lung Cancer	Post-treatment, Day 34	IV	3.9	0.863	-0.889	EGFR L858R	0.14%
CGPLLU267	Lung Cancer	Post-treatment, Day 90	IV	3.9	0.962	-0.876	EGFR L858R	0.38%
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	IV	Ongoing	0.951	-0.864	EGFR L858R	0.10%
CGPLLU269	Lung Cancer	Post-treatment, Day 9	IV	Ongoing	0.941	-0.894	EGFR L858R	0.00%
CGPLLU269	Lung Cancer	Post-treatment, Day 28	IV	Ongoing	0.957	-0.876	EGFR L858R	0.00%
CGPLLU271	Lung Cancer	Pre-treatment, Day 0	IV	8.2	0.371	-0.284	EGFR E746_A750del	3.36%
CGPLLU271	Lung Cancer	Post-treatment, Day 6	IV	8.2	0.947	-0.826	EGFR E746_A750del	0.17%
CGPLLU271	Lung Cancer	Post-treatment, Day 20	IV	8.2	0.952	-0.839	EGFR E746_A750del	0.00%
CGPLLU271	Lung Cancer	Post-treatment, Day 104	IV	8.2	0.944	-0.810	EGFR E746_A750del	0.00%
CGPLLU271	Lung Cancer	Post-treatment, Day 259	IV	8.2	0.950	-0.831	EGFR E746_A750del	0.44%
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	IV	Ongoing	0.944	-0.903	NA	0.00%
CGPLLU43	Lung Cancer	Post-treatment, Day 6	IV	Ongoing	0.956	-0.899	NA	0.00%
CGPLLU43	Lung Cancer	Post-treatment, Day 27	IV	Ongoing	0.959	-0.901	NA	0.00%
CGPLLU43	Lung Cancer	Post-treatment, Day 83	IV	Ongoing	0.965	-0.896	NA	0.00%

*Pearson correlation. [1]Please see reference 36 for more information on targeted mutation analyses.

Table 4.7. Summary of whole genome cfDNA analyses in healthy individuals and cancer patients.

Patient	Patient Type	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals*	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals*	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Alelle Fraction Detected using Targeted sequencing[‡]
CGPLPA114	Bile Duct Cancer	II	166	0.9098	0.9246	0.0836%	0.7598	Y	Y	-
CGPLPA115	Bile Duct Cancer	IV	165	0.8053	0.8310	0.0763%	0.9974	Y	Y	-
CGPLPA117	Bile Duct Cancer	II	165	0.9395	0.8767	0.1084%	0.9049	Y	Y	-
CGPLPA118	Bile Duct Cancer	I	167	0.9406	0.9001	0.1842%	0.9859	Y	Y	0.14%
CGPLPA122	Bile Duct Cancer	II	164	0.8231	0.8058	0.2047%	0.9983	Y	Y	37.22%
CGPLPA124	Bile Duct Cancer	II	166	0.9108	0.9238	0.1542%	0.8791	Y	Y	0.62%
CGPLPA125	Bile Duct Cancer	II	166	0.9675	0.9373	0.0273%	0.0228	N	N	-
CGPLPA126	Bile Duct Cancer	II	166	0.9155	0.9139	0.4349%	0.9908	Y	Y	ND
CGPLPA127	Bile Duct Cancer	IV	167	0.8916	0.8117	0.4371%	0.9789	Y	Y	-
CGPLPA128	Bile Duct Cancer	II	167	0.9262	0.9003	0.1317%	0.9812	Y	Y	ND
CGPLPA129	Bile Duct Cancer	II	166	0.9220	0.9155	0.0642%	0.9839	Y	Y	ND
CGPLPA130	Bile Duct Cancer	II	169	0.8586	0.8499	0.1005%	0.9895	Y	Y	ND
CGPLPA131	Bile Duct Cancer	II	165	0.7707	0.9195	0.0780%	0.9885	Y	Y	0.21%
CGPLPA134	Bile Duct Cancer	II	160	0.7502	0.8847	0.0260%	0.9896	Y	Y	0.93%
CGPLPA135	Bile Duct Cancer	I	165	0.9495	0.9184	0.0558%	0.6594	Y	N	-
CGPLPA136	Bile Duct Cancer	II	164	0.9289	0.9050	0.0769%	0.9596	Y	Y	0.10%
CGPLPA137	Bile Duct Cancer	II	166	0.9568	0.9320	0.0499%	0.7282	Y	N	-
CGPLPA139	Bile Duct Cancer	IV	166	0.9511	0.9374	0.0465%	0.0743	N	N	-
CGPLPA140	Bile Duct Cancer	II	166	0.9215	0.9548	0.0330%	0.9761	Y	Y	0.21%
CGPLPA141	Bile Duct Cancer	II	165	0.9172	0.9381	0.0920%	0.9988	Y	Y	-
CGPLPA155	Bile Duct Cancer	II	165	0.9496	0.9313	0.0260%	0.8013	Y	Y	-
CGPLPA165	Bile Duct Cancer	I	168	0.9596	0.9309	0.0558%	0.2158	N	N	-
CGPLPA168	Bile Duct Cancer	II	162	0.7838	0.7757	0.3123%	0.9878	Y	Y	-

CGPLPA184	Bile Duct Cancer	II	165	0.9100	0.9203	0.0897%	0.9926	Y	Y	-
CGPLPA187	Bile Duct Cancer	II	165	0.8577	0.8968	0.0658%	0.9675	Y	Y	-
CGPLBR100	Breast Cancer	III	166	0.9440	0.8946	0.1234%	0.8664	Y	Y	ND
CGPLBR101	Breast Cancer	II	169	0.8864	0.9304	0.0709%	0.9385	Y	Y	ND
CGPLBR102	Breast Cancer	II	169	0.9617	0.9345	0.4742%	0.9052	Y	Y	0.25%
CGPLBR103	Breast Cancer	II	168	0.9498	0.9251	0.0775%	0.5994	N	N	ND
CGPLBR104	Breast Cancer	II	167	0.8490	0.9192	0.0532%	0.9950	Y	Y	0.13%
CGPLBR12	Breast Cancer	III	164	0.8350	0.7760	0.1407%	0.7598	Y	Y	-
CGPLBR18	Breast Cancer	III	163	0.8411	0.9534	0.0267%	0.3886	N	N	-
CGPLBR23	Breast Cancer	II	166	0.9714	0.9312	0.0144%	0.1235	N	N	-
CGPLBR24	Breast Cancer	II	156	0.8402	0.8766	0.0210%	0.7480	Y	Y	-
CGPLBR28	Breast Cancer	III	166	0.9584	0.9120	0.1456%	0.9630	Y	Y	-
CGPLBR30	Breast Cancer	II	161	0.6951	0.6611	0.0952%	0.9956	Y	Y	-
CGPLBR31	Breast Cancer	II	167	0.9719	0.9556	0.0427%	0.2227	N	N	-
CGPLBR32	Breast Cancer	II	166	0.9590	0.9229	0.0306%	0.9815	Y	Y	-
CGPLBR33	Breast Cancer	II	166	0.9706	0.9432	0.0617%	0.2863	N	N	-
CGPLBR34	Breast Cancer	II	163	0.8735	0.9425	0.0115%	0.1637	N	N	-
CGPLBR35	Breast Cancer	II	168	0.9655	0.9348	0.1371%	0.5057	N	N	-
CGPLBR36	Breast Cancer	II	169	0.9394	0.8884	0.0813%	0.4017	N	N	-
CGPLBR37	Breast Cancer	II	167	0.9691	0.9496	0.0518%	0.0314	N	N	-
CGPLBR38	Breast Cancer	I	165	0.9105	0.9349	0.1352%	0.8983	Y	Y	0.53%
CGPLBR40	Breast Cancer	III	167	0.9273	0.9244	0.0929%	0.9046	Y	Y	ND
CGPLBR41	Breast Cancer	III	168	0.9626	0.9346	0.0544%	0.9416	Y	Y	0.32%
CGPLBR45	Breast Cancer	II	164	0.9615	0.9286	0.0296%	0.3860	N	N	-
CGPLBR46	Breast Cancer	III	168	0.9322	0.9005	0.0345%	0.7270	Y	N	-
CGPLBR47	Breast Cancer	I	166	0.9461	0.9028	0.0591%	0.8247	Y	Y	-
CGPLBR48	Breast Cancer	II	169	0.7686	0.8246	0.0504%	0.9973	Y	Y	0.18%
CGPLBR49	Breast Cancer	II	171	0.8867	0.7887	0.0377%	0.9946	Y	Y	ND

CGPLBR50	Breast Cancer	I	160	0.8593	0.9332	0.0137%	0.6820	Y	N	-
CGPLBR51	Breast Cancer	II	165	0.9359	0.9160	0.0863%	0.6915	Y	N	-
CGPLBR52	Breast Cancer	III	164	0.8688	0.9196	0.0165%	0.6390	Y	N	-
CGPLBR55	Breast Cancer	III	165	0.9634	0.9341	0.0356%	0.9494	Y	Y	0.68%
CGPLBR56	Breast Cancer	II	163	0.9469	0.9428	0.2025%	0.4700	N	N	-
CGPLBR57	Breast Cancer	III	166	0.9672	0.9416	0.0902%	0.9090	Y	Y	ND
CGPLBR59	Breast Cancer	I	168	0.9438	0.9130	0.0761%	0.5828	N	N	ND
CGPLBR60	Breast Cancer	II	167	0.9479	0.8916	0.0626%	0.8779	Y	Y	-
CGPLBR61	Breast Cancer	II	165	0.9611	0.9422	0.0601%	0.4417	N	N	0.44%
CGPLBR63	Breast Cancer	II	168	0.9555	0.9132	0.0514%	0.8788	Y	Y	ND
CGPLBR65	Breast Cancer	II	167	0.9506	0.8970	0.0264%	0.9048	Y	Y	-
CGPLBR68	Breast Cancer	III	163	0.9154	0.9532	0.0164%	0.7863	Y	Y	ND
CGPLBR69	Breast Cancer	II	165	0.9460	0.9474	0.0279%	0.0600	N	N	ND
CGPLBR70	Breast Cancer	II	168	0.9651	0.9388	0.0171%	0.6447	Y	N	0.36%
CGPLBR71	Breast Cancer	II	165	0.9577	0.9368	0.0271%	0.6706	Y	N	0.10%
CGPLBR72	Breast Cancer	II	167	0.9786	0.9640	0.0263%	0.6129	N	N	ND
CGPLBR73	Breast Cancer	II	167	0.9576	0.9421	0.0142%	0.0746	N	N	0.27%
CGPLBR76	Breast Cancer	II	170	0.9410	0.9254	0.0775%	0.9334	Y	Y	0.12%
CGPLBR81	Breast Cancer	II	170	0.9043	0.8193	0.0241%	0.9899	Y	Y	-
CGPLBR82	Breast Cancer	I	166	0.9254	0.9288	0.1640%	0.9834	Y	Y	0.12%
CGPLBR83	Breast Cancer	II	169	0.9451	0.9138	0.0419%	0.9810	Y	Y	0.28%
CGPLBR84	Breast Cancer	III	169	0.9315	0.8659	0.0274%	0.9901	Y	Y	-
CGPLBR87	Breast Cancer	II	166	0.9154	0.8797	0.0294%	0.9968	Y	Y	0.45%
CGPLBR88	Breast Cancer	II	169	0.9370	0.8547	0.0181%	0.9988	Y	Y	0.38%
CGPLBR90	Breast Cancer	II	169	0.9002	0.8330	0.0417%	0.9667	Y	Y	-
CGPLBR91	Breast Cancer	III	164	0.7955	0.9408	0.0799%	0.8710	Y	Y	ND
CGPLBR92	Breast Cancer	II	162	0.6774	0.8835	0.1042%	0.9866	Y	Y	0.20%
CGPLBR93	Breast Cancer	II	164	0.8773	0.9072	0.0352%	0.7253	Y	N	ND

CGCRC291	Colorectal Cancer	IV	163	0.1972	0.5268	0.0484%	0.9976	Y	Y	22.85%
CGCRC292	Colorectal Cancer	IV	166	0.7804	0.8835	0.0270%	0.7299	Y	N	1.41%
CGCRC293	Colorectal Cancer	IV	166	0.9335	0.9206	0.0748%	0.5234	N	N	0.35%
CGCRC294	Colorectal Cancer	II	166	0.6531	0.8904	0.0188%	0.8757	Y	Y	0.17%
CGCRC296	Colorectal Cancer	II	166	0.8161	0.8695	0.0369%	0.9951	Y	Y	ND
CGCRC299	Colorectal Cancer	I	162	0.7325	0.9268	0.0392%	0.9648	Y	Y	ND
CGCRC300	Colorectal Cancer	I	167	0.9382	0.9303	0.0235%	0.4447	N	N	ND
CGCRC301	Colorectal Cancer	I	165	0.8252	0.9151	0.0310%	0.2190	N	N	0.21%
CGCRC302	Colorectal Cancer	II	163	0.7499	0.9243	0.0112%	0.9897	Y	Y	0.12%
CGCRC304	Colorectal Cancer	II	162	0.4642	0.9360	0.0093%	0.9358	Y	Y	0.27%
CGCRC305	Colorectal Cancer	II	165	0.8909	0.9250	0.0120%	0.8988	Y	Y	0.19%
CGCRC306	Colorectal Cancer	II	165	0.8523	0.8186	0.0781%	0.9466	Y	Y	8.02%
CGCRC307	Colorectal Cancer	II	165	0.9140	0.9342	0.0181%	0.7042	Y	N	0.56%
CGCRC308	Colorectal Cancer	III	165	0.8734	0.9324	0.0078%	0.9082	Y	Y	0.11%
CGCRC311	Colorectal Cancer	I	166	0.8535	0.9156	0.0173%	0.1867	N	N	ND
CGCRC315	Colorectal Cancer	III	167	0.6083	0.8846	0.0241%	0.6422	Y	N	0.27%
CGCRC316	Colorectal Cancer	III	161	0.1546	0.5879	0.0315%	0.9971	Y	Y	6.52%
CGCRC317	Colorectal Cancer	III	163	0.6242	0.8944	0.0184%	0.9855	Y	Y	0.36%
CGCRC318	Colorectal Cancer	I	166	0.8824	0.9140	0.0156%	0.5615	N	N	ND
CGCRC319	Colorectal Cancer	III	160	0.5979	0.8230	0.1259%	0.9925	Y	Y	0.11%
CGCRC320	Colorectal Cancer	I	167	0.7949	0.9101	0.0383%	0.8019	Y	Y	0.64%
CGCRC321	Colorectal Cancer	I	164	0.7804	0.9091	0.0829%	0.9759	Y	Y	0.20%
CGCRC333	Colorectal Cancer	IV	163	0.4263	0.4355	0.4284%	0.9974	Y	Y	43.03%
CGCRC336	Colorectal Cancer	IV	162	0.6466	0.6856	0.1154%	0.9887	Y	Y	81.61%
CGCRC338	Colorectal Cancer	IV	162	0.7740	0.7573	0.1436%	0.9976	Y	Y	36.00%
CGCRC341	Colorectal Cancer	IV	164	0.8995	0.9191	0.0197%	0.9670	Y	Y	ND
CGCRC342	Colorectal Cancer	IV	158	0.2524	0.1845	0.1732%	0.9987	Y	Y	30.72%
CGPLPA113	Duodenal Cancer	I	170	0.8751	0.7674	1.0116%	0.9935	Y	Y	-

CGST102	Gastric cancer	II	167	0.9496	0.9057	0.0704%	0.8581	Y	Y	0.43%
CGST11	Gastric cancer	IV	169	0.9419	0.9161	0.0651%	0.1435	N	N	-
CGST110	Gastric cancer	III	167	0.9626	0.9232	0.0817%	0.8900	Y	Y	ND
CGST114	Gastric cancer	III	164	0.9535	0.9038	0.0317%	0.5893	N	N	ND
CGST13	Gastric cancer	II	166	0.9369	0.9156	0.0321%	0.9754	Y	Y	ND
CGST131	Gastric cancer	III	171	0.9428	0.8886	0.2752%	0.9409	Y	Y	-
CGST141	Gastric cancer	III	168	0.9621	0.9206	0.0388%	0.2008	N	N	ND
CGST16	Gastric cancer	III	166	0.7804	0.8355	0.1744%	0.9974	Y	Y	0.93%
CGST18	Gastric cancer	II	169	0.9523	0.9111	0.0299%	0.3842	N	N	0.14%
CGST21	Gastric cancer	II	165	-0.4778	0.2687	0.2299%	0.9910	Y	Y	-
CGST26	Gastric cancer	IV	166	0.9554	0.9140	0.0399%	0.5009	N	N	-
CGST28	Gastric cancer	X	169	0.9076	0.7832	0.1295%	0.9955	Y	Y	1.62%
CGST30	Gastric cancer	III	169	0.9246	0.9121	0.0338%	0.9183	Y	Y	0.42%
CGST32	Gastric cancer	II	169	0.9431	0.8639	0.0247%	0.9612	Y	Y	2.99%
CGST33	Gastric cancer	I	168	0.7999	0.7770	0.0799%	0.9805	Y	Y	2.32%
CGST38	Gastric cancer	X	168	0.9368	0.8758	0.0640%	0.9416	Y	Y	-
CGST39	Gastric cancer	IV	164	0.8742	0.9401	0.0287%	0.8480	Y	Y	ND
CGST41	Gastric cancer	IV	168	0.8194	0.9284	0.0398%	0.9263	Y	Y	ND
CGST45	Gastric cancer	II	168	0.9576	0.9036	0.0220%	0.9713	Y	Y	ND
CGST47	Gastric cancer	I	168	0.9611	0.9096	0.0157%	0.9687	Y	Y	0.45%
CGST48	Gastric cancer	IV	167	0.7469	0.5445	0.0220%	0.9975	Y	Y	4.21%
CGST53	Gastric cancer	X	173	-0.0019	0.7888	0.1140%	0.9914	Y	Y	-
CGST58	Gastric cancer	III	169	0.9470	0.9094	0.0696%	0.9705	Y	Y	ND
CGST67	Gastric cancer	I	170	0.9352	0.8853	0.3245%	0.9032	Y	Y	-
CGST77	Gastric cancer	IV	170	0.0043	0.8295	0.1851%	0.9981	Y	Y	-
CGST80	Gastric cancer	III	168	0.9313	0.8846	0.0490%	0.9513	Y	Y	1.04%
CGST81	Gastric cancer	I	168	0.9480	0.8851	0.0138%	0.9748	Y	Y	0.20%
CGPLH189	Healthy	NA	168	0.9325	0.8947	0.0591%	0.1748	N	N	-

CGPLH190	Healthy	NA	167	0.9433	0.9369	0.1193%	0.5168	N	N	-
CGPLH192	Healthy	NA	167	0.9646	0.9487	0.0276%	0.0178	N	N	-
CGPLH193	Healthy	NA	167	0.9423	0.9442	0.0420%	0.5794	N	N	-
CGPLH194	Healthy	NA	168	0.9567	0.9289	0.0407%	0.1616	N	N	-
CGPLH196	Healthy	NA	167	0.9709	0.9512	0.0266%	0.0999	N	N	-
CGPLH197	Healthy	NA	166	0.9605	0.9416	0.0334%	0.4699	N	N	-
CGPLH198	Healthy	NA	167	0.9238	0.9457	0.0302%	0.6571	Y	N	-
CGPLH199	Healthy	NA	165	0.9618	0.9439	0.0170%	0.5564	N	N	-
CGPLH200	Healthy	NA	167	0.9183	0.9391	0.0362%	0.3833	N	N	-
CGPLH201	Healthy	NA	168	0.9548	0.9180	0.0470%	0.8395	Y	Y	-
CGPLH202	Healthy	NA	168	0.9471	0.9436	0.0501%	0.1088	N	N	-
CGPLH203	Healthy	NA	167	0.9534	0.9575	0.0455%	0.2485	N	N	-
CGPLH205	Healthy	NA	168	0.9075	0.9283	0.0409%	0.4401	N	N	-
CGPLH208	Healthy	NA	168	0.9422	0.9409	0.0371%	0.2706	N	N	-
CGPLH209	Healthy	NA	169	0.9556	0.9367	0.0427%	0.2213	N	N	-
CGPLH210	Healthy	NA	169	0.9447	0.9181	0.0279%	0.3500	N	N	-
CGPLH211	Healthy	NA	169	0.9538	0.9410	0.0317%	0.1752	N	N	-
CGPLH300	Healthy	NA	168	0.9019	0.9200	0.0397%	0.0226	N	N	-
CGPLH307	Healthy	NA	168	0.9576	0.9167	0.0388%	0.1789	N	N	-
CGPLH308	Healthy	NA	168	0.9481	0.9352	0.0311%	0.0185	N	N	-
CGPLH309	Healthy	NA	168	0.9672	0.9451	0.0226%	0.0441	N	N	-
CGPLH310	Healthy	NA	165	0.9547	0.9527	0.0145%	0.7135	Y	N	-
CGPLH311	Healthy	NA	167	0.9302	0.9348	0.0202%	0.2589	N	N	-
CGPLH314	Healthy	NA	167	0.9482	0.9491	0.0212%	0.1632	N	N	-
CGPLH315	Healthy	NA	167	0.8659	0.9427	0.0071%	0.3450	N	N	-
CGPLH316	Healthy	NA	165	0.9374	0.9552	0.0191%	0.4697	N	N	-
CGPLH317	Healthy	NA	169	0.9542	0.9352	0.0232%	0.1330	N	N	-
CGPLH319	Healthy	NA	167	0.9578	0.9189	0.0263%	0.2232	N	N	-

CGPLH320	Healthy	NA	164	0.8913	0.9166	0.0222%	0.1095	N	N	-
CGPLH322	Healthy	NA	167	0.8751	0.9411	0.0248%	0.0749	N	N	-
CGPLH324	Healthy	NA	169	0.9519	0.9133	0.0402%	0.0128	N	N	-
CGPLH325	Healthy	NA	167	0.9124	0.9202	0.0711%	0.0102	N	N	-
CGPLH326	Healthy	NA	166	0.9574	0.9408	0.0213%	0.0475	N	N	-
CGPLH327	Healthy	NA	168	0.9533	0.9071	0.1275%	0.4891	N	N	-
CGPLH328	Healthy	NA	166	0.9643	0.9332	0.0256%	0.0234	N	N	-
CGPLH329	Healthy	NA	167	0.9609	0.9396	0.0269%	0.0139	N	N	-
CGPLH330	Healthy	NA	167	0.9118	0.9403	0.0203%	0.2642	N	N	-
CGPLH331	Healthy	NA	166	0.9679	0.9377	0.0314%	0.0304	N	N	-
CGPLH333	Healthy	NA	169	0.9474	0.9132	0.0350%	0.1633	N	N	-
CGPLH335	Healthy	NA	167	0.8909	0.9333	0.0285%	0.0096	N	N	-
CGPLH336	Healthy	NA	169	0.9248	0.9159	0.0159%	0.3872	N	N	-
CGPLH337	Healthy	NA	167	0.9533	0.9262	0.0367%	0.2976	N	N	-
CGPLH338	Healthy	NA	165	0.9388	0.9303	0.0103%	0.0431	N	N	-
CGPLH339	Healthy	NA	167	0.9396	0.9338	0.0280%	0.0379	N	N	-
CGPLH340	Healthy	NA	167	0.9488	0.9321	0.0210%	0.0379	N	N	-
CGPLH341	Healthy	NA	166	0.9533	0.9187	0.0448%	0.1775	N	N	-
CGPLH342	Healthy	NA	166	0.7858	0.8986	0.0283%	0.0904	N	N	-
CGPLH343	Healthy	NA	167	0.9421	0.9067	0.0632%	0.0160	N	N	-
CGPLH344	Healthy	NA	169	0.9192	0.8998	0.0257%	0.0120	N	N	-
CGPLH345	Healthy	NA	169	0.9345	0.9107	0.0445%	0.0031	N	N	-
CGPLH346	Healthy	NA	169	0.9475	0.9074	0.0208%	0.0686	N	N	-
CGPLH350	Healthy	NA	171	0.9570	0.9288	0.0284%	0.0071	N	N	-
CGPLH351	Healthy	NA	168	0.8176	0.9294	0.0223%	0.0207	N	N	-
CGPLH352	Healthy	NA	168	0.9521	0.9190	0.0613%	0.0512	N	N	-
CGPLH353	Healthy	NA	167	0.9435	0.9130	0.0408%	0.0132	N	N	-
CGPLH354	Healthy	NA	168	0.9481	0.9121	0.0318%	0.0082	N	N	-

CGPLH355	Healthy	NA	167	0.9613	0.9308	0.0400%	0.6407	Y	N	-
CGPLH356	Healthy	NA	168	0.9474	0.9312	0.0427%	0.2437	N	N	-
CGPLH357	Healthy	NA	167	0.9255	0.9540	0.0217%	0.0070	N	N	-
CGPLH358	Healthy	NA	167	0.7777	0.9372	0.0174%	0.1451	N	N	-
CGPLH360	Healthy	NA	168	0.8500	0.8775	0.0395%	0.0048	N	N	-
CGPLH361	Healthy	NA	167	0.9261	0.9283	0.0268%	0.1524	N	N	-
CGPLH362	Healthy	NA	167	0.9236	0.9503	0.0309%	0.4832	N	N	-
CGPLH363	Healthy	NA	167	0.9488	0.9187	0.0620%	0.0199	N	N	-
CGPLH364	Healthy	NA	168	0.9311	0.9480	0.0282%	0.8719	Y	Y	-
CGPLH365	Healthy	NA	165	0.9371	0.9051	0.1740%	0.9683	Y	Y	-
CGPLH366	Healthy	NA	167	0.9536	0.9170	0.0344%	0.0952	N	N	-
CGPLH367	Healthy	NA	166	0.8748	0.9181	0.0353%	0.1235	N	N	-
CGPLH368	Healthy	NA	169	0.9490	0.9076	0.1073%	0.1252	N	N	-
CGPLH369	Healthy	NA	167	0.9428	0.9541	0.0246%	0.2821	N	N	-
CGPLH370	Healthy	NA	167	0.9642	0.9423	0.0410%	0.0989	N	N	-
CGPLH371	Healthy	NA	168	0.9621	0.9414	0.0734%	0.2173	N	N	-
CGPLH380	Healthy	NA	170	0.9662	0.9424	0.0523%	0.0128	N	N	-
CGPLH381	Healthy	NA	169	0.9541	0.9501	0.0435%	0.0152	N	N	-
CGPLH382	Healthy	NA	167	0.9380	0.9584	0.0340%	0.0326	N	N	-
CGPLH383	Healthy	NA	168	0.9700	0.9407	0.0389%	0.0035	N	N	-
CGPLH384	Healthy	NA	169	0.8061	0.9043	0.0207%	0.0258	N	N	-
CGPLH385	Healthy	NA	167	0.8866	0.9246	0.0165%	0.0566	N	N	-
CGPLH386	Healthy	NA	167	0.6920	0.8859	0.0502%	0.2677	N	N	-
CGPLH387	Healthy	NA	169	0.9583	0.9223	0.0375%	0.0081	N	N	-
CGPLH388	Healthy	NA	167	0.9348	0.9266	0.0527%	0.0499	N	N	-
CGPLH389	Healthy	NA	168	0.9409	0.9035	0.0667%	0.6565	Y	N	-
CGPLH390	Healthy	NA	167	0.9216	0.9182	0.0229%	0.0837	N	N	-
CGPLH391	Healthy	NA	166	0.9334	0.9162	0.0223%	0.0716	N	N	-

CGPLH392	Healthy	NA	167	0.9165	0.9014	0.0424%	0.1305	N	N	-
CGPLH393	Healthy	NA	169	0.9256	0.9045	0.0407%	0.0037	N	N	-
CGPLH394	Healthy	NA	167	0.9257	0.9292	0.0522%	0.1073	N	N	-
CGPLH395	Healthy	NA	166	0.8611	0.9254	0.0424%	0.0171	N	N	-
CGPLH396	Healthy	NA	167	0.7884	0.8928	0.0393%	0.0303	N	N	-
CGPLH398	Healthy	NA	167	0.9463	0.9578	0.0242%	0.3195	N	N	-
CGPLH399	Healthy	NA	169	0.8780	0.9195	0.0679%	0.0685	N	N	-
CGPLH400	Healthy	NA	168	0.6862	0.9047	0.0300%	0.2103	N	N	-
CGPLH401	Healthy	NA	167	0.9428	0.9339	0.0146%	0.0620	N	N	-
CGPLH402	Healthy	NA	167	0.9353	0.8800	0.1516%	0.0395	N	N	-
CGPLH403	Healthy	NA	168	0.9329	0.8829	0.0515%	0.0223	N	N	-
CGPLH404	Healthy	NA	169	0.9402	0.8948	0.0528%	0.0027	N	N	-
CGPLH405	Healthy	NA	166	0.9579	0.9204	0.0359%	0.0188	N	N	-
CGPLH406	Healthy	NA	167	0.8188	0.8592	0.0667%	0.0206	N	N	-
CGPLH407	Healthy	NA	169	0.9527	0.9099	0.0229%	0.0040	N	N	-
CGPLH408	Healthy	NA	167	0.9584	0.9192	0.0415%	0.1257	N	N	-
CGPLH409	Healthy	NA	168	0.9220	0.8950	0.0302%	0.0056	N	N	-
CGPLH410	Healthy	NA	168	0.9102	0.9006	0.0453%	0.0019	N	N	-
CGPLH411	Healthy	NA	167	0.9392	0.8857	0.0621%	0.0188	N	N	-
CGPLH412	Healthy	NA	167	0.9561	0.9191	0.0140%	0.0417	N	N	-
CGPLH413	Healthy	NA	167	0.9461	0.9145	0.0355%	0.0084	N	N	-
CGPLH414	Healthy	NA	168	0.9258	0.9127	0.0290%	0.0284	N	N	-
CGPLH415	Healthy	NA	169	0.9217	0.9025	0.0296%	0.0131	N	N	-
CGPLH416	Healthy	NA	167	0.9672	0.9388	0.0198%	0.0645	N	N	-
CGPLH417	Healthy	NA	168	0.9578	0.9192	0.0241%	0.0836	N	N	-
CGPLH418	Healthy	NA	169	0.9376	0.9234	0.0306%	0.0052	N	N	-
CGPLH419	Healthy	NA	167	0.9228	0.9295	0.0280%	0.0469	N	N	-
CGPLH420	Healthy	NA	169	0.9164	0.9108	0.0187%	0.0420	N	N	-

CGPLH422	Healthy	NA	166	0.9069	0.9006	0.0209%	0.0324	N	N	-
CGPLH423	Healthy	NA	169	0.9606	0.9289	0.0832%	0.0139	N	N	-
CGPLH424	Healthy	NA	167	0.9553	0.9265	0.1119%	0.0864	N	N	-
CGPLH425	Healthy	NA	168	0.9722	0.9488	0.0722%	0.0156	N	N	-
CGPLH426	Healthy	NA	168	0.9560	0.9080	0.0548%	0.1075	N	N	-
CGPLH427	Healthy	NA	167	0.9594	0.9257	0.0182%	0.0470	N	N	-
CGPLH428	Healthy	NA	167	0.9591	0.9272	0.0346%	0.0182	N	N	-
CGPLH429	Healthy	NA	168	0.9358	0.8757	0.0593%	0.8143	Y	Y	-
CGPLH430	Healthy	NA	167	0.9639	0.9307	0.0258%	0.0369	N	N	-
CGPLH431	Healthy	NA	167	0.9570	0.9185	0.0234%	0.0174	N	N	-
CGPLH432	Healthy	NA	168	0.9485	0.9082	0.0433%	0.0181	N	N	-
CGPLH434	Healthy	NA	168	0.9671	0.9442	0.0297%	0.0060	N	N	-
CGPLH435	Healthy	NA	170	0.9133	0.9097	0.0179%	0.0441	N	N	-
CGPLH436	Healthy	NA	168	0.9360	0.9158	0.0290%	0.0958	N	N	-
CGPLH437	Healthy	NA	170	0.9445	0.9245	0.0156%	0.0136	N	N	-
CGPLH438	Healthy	NA	170	0.9537	0.9138	0.0169%	0.1041	N	N	-
CGPLH439	Healthy	NA	171	0.9547	0.9028	0.0226%	0.0078	N	N	-
CGPLH440	Healthy	NA	169	0.9562	0.9295	0.0330%	0.0867	N	N	-
CGPLH441	Healthy	NA	167	0.9660	0.9430	0.0178%	0.0085	N	N	-
CGPLH442	Healthy	NA	167	0.9569	0.9406	0.0169%	0.0562	N	N	-
CGPLH443	Healthy	NA	170	0.9431	0.8801	0.0207%	0.0578	N	N	-
CGPLH444	Healthy	NA	171	0.9429	0.9066	0.0464%	0.0097	N	N	-
CGPLH445	Healthy	NA	171	0.9446	0.8750	0.0267%	0.1939	N	N	-
CGPLH446	Healthy	NA	167	0.9502	0.9257	0.0281%	0.0340	N	N	-
CGPLH447	Healthy	NA	169	0.9421	0.8968	0.0167%	0.0017	N	N	-
CGPLH448	Healthy	NA	167	0.9553	0.9191	0.0401%	0.0389	N	N	-
CGPLH449	Healthy	NA	167	0.9550	0.9254	0.0236%	0.0116	N	N	-
CGPLH450	Healthy	NA	167	0.9572	0.9195	0.0331%	0.0597	N	N	-

CGPLH451	Healthy	NA	169	0.9548	0.9167	0.0262%	0.0104	N	N	-
CGPLH452	Healthy	NA	167	0.9498	0.8948	0.0480%	0.4722	N	N	-
CGPLH453	Healthy	NA	166	0.9572	0.9339	0.0186%	0.3419	N	N	-
CGPLH455	Healthy	NA	166	0.9626	0.9322	0.0455%	0.4536	N	N	-
CGPLH456	Healthy	NA	168	0.9537	0.9098	0.0207%	0.0365	N	N	-
CGPLH457	Healthy	NA	167	0.9429	0.9022	0.0298%	0.0364	N	N	-
CGPLH458	Healthy	NA	167	0.9511	0.9275	0.0298%	0.1891	N	N	-
CGPLH459	Healthy	NA	168	0.9609	0.9209	0.0281%	0.0371	N	N	-
CGPLH460	Healthy	NA	168	0.9331	0.8863	0.0227%	0.1157	N	N	-
CGPLH463	Healthy	NA	167	0.9506	0.9372	0.0130%	0.0865	N	N	-
CGPLH464	Healthy	NA	170	0.9133	0.8511	0.0659%	0.2040	N	N	-
CGPLH465	Healthy	NA	167	0.9251	0.9164	0.0325%	0.0124	N	N	-
CGPLH466	Healthy	NA	167	0.9679	0.9408	0.0155%	0.1733	N	N	-
CGPLH467	Healthy	NA	168	0.9273	0.9024	0.0229%	0.2303	N	N	-
CGPLH468	Healthy	NA	167	0.8353	0.9345	0.0247%	0.5427	N	N	-
CGPLH469	Healthy	NA	169	0.8225	0.8799	0.0201%	0.5351	N	N	-
CGPLH470	Healthy	NA	168	0.9073	0.9228	0.0715%	0.0327	N	N	-
CGPLH471	Healthy	NA	167	0.9354	0.9333	0.0150%	0.0406	N	N	-
CGPLH472	Healthy	NA	166	0.8509	0.8915	0.0481%	0.6152	N	N	-
CGPLH473	Healthy	NA	167	0.9206	0.9128	0.0443%	0.2995	N	N	-
CGPLH474	Healthy	NA	168	0.8474	0.9245	0.0316%	0.6246	Y	N	-
CGPLH475	Healthy	NA	167	0.9155	0.9233	0.0269%	0.0736	N	N	-
CGPLH476	Healthy	NA	169	0.8807	0.9059	0.0236%	0.0143	N	N	-
CGPLH477	Healthy	NA	169	0.9129	0.9376	0.0382%	0.1111	N	N	-
CGPLH478	Healthy	NA	167	0.9588	0.9344	0.0256%	0.0828	N	N	-
CGPLH479	Healthy	NA	167	0.9303	0.9207	0.0221%	0.0648	N	N	-
CGPLH480	Healthy	NA	169	0.9522	0.9046	0.0672%	0.7473	Y	N	-
CGPLH481	Healthy	NA	168	0.9568	0.9113	0.0311%	0.0282	N	N	-

CGPLH482	Healthy	NA	168	0.9379	0.9336	0.0162%	0.0058	N	N	-
CGPLH483	Healthy	NA	168	0.9518	0.9275	0.0251%	0.0495	N	N	-
CGPLH484	Healthy	NA	166	0.9630	0.9366	0.0261%	0.0048	N	N	-
CGPLH485	Healthy	NA	168	0.9547	0.9128	0.0291%	0.1064	N	N	-
CGPLH486	Healthy	NA	169	0.9199	0.9042	0.0220%	0.0820	N	N	-
CGPLH487	Healthy	NA	169	0.9575	0.9098	0.0594%	0.2154	N	N	-
CGPLH488	Healthy	NA	167	0.9618	0.9298	0.0409%	0.0903	N	N	-
CGPLH490	Healthy	NA	167	0.8950	0.8794	0.0432%	0.0424	N	N	-
CGPLH491	Healthy	NA	168	0.9631	0.9332	0.0144%	0.0223	N	N	-
CGPLH492	Healthy	NA	170	0.9335	0.8799	0.0322%	0.0311	N	N	-
CGPLH493	Healthy	NA	168	0.8718	0.9330	0.0065%	0.0280	N	N	-
CGPLH494	Healthy	NA	169	0.9623	0.9303	0.0232%	0.0824	N	N	-
CGPLH495	Healthy	NA	166	0.8777	0.8908	0.0513%	0.0465	N	N	-
CGPLH496	Healthy	NA	166	0.8788	0.9398	0.0208%	0.0572	N	N	-
CGPLH497	Healthy	NA	167	0.9576	0.9330	0.0335%	0.0404	N	N	-
CGPLH498	Healthy	NA	167	0.9526	0.9315	0.0403%	0.0752	N	N	-
CGPLH499	Healthy	NA	167	0.9733	0.9442	0.0198%	0.0149	N	N	-
CGPLH500	Healthy	NA	168	0.9542	0.9240	0.0433%	0.0754	N	N	-
CGPLH501	Healthy	NA	169	0.9526	0.9308	0.0300%	0.0159	N	N	-
CGPLH502	Healthy	NA	167	0.9512	0.9200	0.0351%	0.0841	N	N	-
CGPLH503	Healthy	NA	169	0.8947	0.8939	0.0398%	0.0649	N	N	-
CGPLH504	Healthy	NA	167	0.9561	0.9324	0.0440%	0.1231	N	N	-
CGPLH505	Healthy	NA	166	0.9554	0.9243	0.0605%	0.1869	N	N	-
CGPLH506	Healthy	NA	167	0.9733	0.9498	0.0284%	0.0180	N	N	-
CGPLH507	Healthy	NA	168	0.9222	0.9192	0.0186%	0.0848	N	N	-
CGPLH508	Healthy	NA	167	0.9674	0.9410	0.0150%	0.1077	N	N	-
CGPLH509	Healthy	NA	167	0.9475	0.9323	0.0163%	0.0828	N	N	-
CGPLH510	Healthy	NA	167	0.9459	0.9548	0.0128%	0.0378	N	N	-

CGPLH511	Healthy	NA	168	0.9714	0.9493	0.0224%	0.1779	N	N	-
CGPLH512	Healthy	NA	168	0.9442	0.9244	0.0094%	0.0076	N	N	-
CGPLH513	Healthy	NA	166	0.9705	0.9595	0.0441%	0.5250	N	N	-
CGPLH514	Healthy	NA	167	0.9690	0.9369	0.0114%	0.3131	N	N	-
CGPLH515	Healthy	NA	167	0.9568	0.9283	0.0352%	0.4936	N	N	-
CGPLH516	Healthy	NA	168	0.9508	0.9298	0.0175%	0.0916	N	N	-
CGPLH517	Healthy	NA	168	0.9635	0.9494	0.0161%	0.0059	N	N	-
CGPLH518	Healthy	NA	168	0.9647	0.9432	0.0274%	0.0130	N	N	-
CGPLH519	Healthy	NA	166	0.9366	0.9351	0.0171%	0.0949	N	N	-
CGPLH520	Healthy	NA	166	0.9649	0.9476	0.0241%	0.0944	N	N	-
CGPLH625	Healthy	NA	166	0.8766	0.9231	0.0697%	0.4977	N	N	-
CGPLH626	Healthy	NA	170	0.9011	0.9269	0.0231%	0.3100	N	N	-
CGPLH639	Healthy	NA	165	0.9482	0.9410	0.0549%	0.0773	N	N	-
CGPLH640	Healthy	NA	166	0.9131	0.9264	0.0232%	0.0327	N	N	-
CGPLH642	Healthy	NA	167	0.9641	0.9376	0.0768%	0.0555	N	N	-
CGPLH643	Healthy	NA	169	0.9450	0.9271	0.0579%	0.1325	N	N	-
CGPLH644	Healthy	NA	170	0.9398	0.8948	0.0621%	0.3819	N	N	-
CGPLH646	Healthy	NA	172	0.9296	0.8691	0.0462%	0.2423	N	N	-
CGPLLU144	Lung Cancer	II	164	0.8702	0.8681	0.0423%	0.9892	Y	Y	5.10%
CGPLLU161	Lung Cancer	II	165	0.9128	0.9187	0.0273%	0.9955	Y	Y	0.20%
CGPLLU162	Lung Cancer	II	165	0.7753	0.8836	0.1410%	0.9986	Y	Y	0.22%
CGPLLU163	Lung Cancer	II	166	0.4770	0.3033	0.0724%	0.9940	Y	Y	0.21%
CGPLLU168	Lung Cancer	I	163	0.9164	0.8842	0.0712%	0.9861	Y	Y	0.07%
CGPLLU169	Lung Cancer	I	163	0.9326	0.9189	0.0846%	0.9866	Y	Y	0.13%
CGPLLU176	Lung Cancer	I	168	0.9572	0.9081	0.0626%	0.8769	Y	Y	ND
CGPLLU177	Lung Cancer	II	166	0.8472	0.6790	0.0564%	0.9924	Y	Y	3.22%
CGPLLU203	Lung Cancer	II	164	0.9119	0.8741	0.0568%	0.9178	Y	Y	0.11%
CGPLLU205	Lung Cancer	II	163	0.9518	0.9476	0.0495%	0.9877	Y	Y	ND

CGPLLU207	Lung Cancer	II	166	0.9344	0.9379	0.0421%	0.9908	Y	Y	0.32%
CGPLLU208	Lung Cancer	II	164	0.9091	0.8942	0.0815%	0.9273	Y	Y	1.33%
CGPLOV11	Ovarian Cancer	IV	166	0.8902	0.8872	0.0469%	0.9343	Y	Y	0.87%
CGPLOV12	Ovarian Cancer	I	167	0.8779	0.8973	0.2767%	0.9764	Y	Y	ND
CGPLOV13	Ovarian Cancer	IV	166	0.7560	0.9146	0.1017%	0.9690	Y	Y	0.35%
CGPLOV15	Ovarian Cancer	III	165	0.8585	0.8552	0.0876%	0.9945	Y	Y	3.54%
CGPLOV16	Ovarian Cancer	III	165	0.9052	0.9046	0.0400%	0.9983	Y	Y	1.12%
CGPLOV19	Ovarian Cancer	II	165	0.7854	0.7578	0.1089%	0.9989	Y	Y	46.35%
CGPLOV20	Ovarian Cancer	II	165	0.8711	0.9154	0.0581%	0.9749	Y	Y	0.21%
CGPLOV21	Ovarian Cancer	IV	167	0.8942	0.8889	0.0677%	0.9961	Y	Y	14.36%
CGPLOV22	Ovarian Cancer	III	164	0.8944	0.9355	0.0251%	0.9775	Y	Y	0.49%
CGPLOV23	Ovarian Cancer	I	169	0.8510	0.8850	0.1520%	0.9916	Y	Y	1.39%
CGPLOV24	Ovarian Cancer	I	166	0.9449	0.8995	0.0303%	0.9856	Y	Y	ND
CGPLOV25	Ovarian Cancer	I	166	0.9590	0.9228	0.0141%	0.8544	Y	Y	ND
CGPLOV26	Ovarian Cancer	I	161	0.8148	0.9351	0.0646%	0.9946	Y	Y	ND
CGPLOV28	Ovarian Cancer	I	167	0.9635	0.9378	0.0647%	0.8160	Y	Y	ND
CGPLOV31	Ovarian Cancer	III	167	0.9461	0.9293	0.1606%	0.9795	Y	Y	ND
CGPLOV32	Ovarian Cancer	I	168	0.9582	0.9338	0.1351%	0.8609	Y	Y	ND
CGPLOV37	Ovarian Cancer	I	170	0.9397	0.8831	0.0986%	0.9849	Y	Y	0.29%
CGPLOV38	Ovarian Cancer	I	166	0.5779	0.6502	0.0490%	0.9990	Y	Y	4.89%
CGPLOV40	Ovarian Cancer	IV	170	0.6097	0.8127	0.6145%	0.9983	Y	Y	6.73%
CGPLOV41	Ovarian Cancer	IV	167	0.9403	0.8929	0.1110%	0.9484	Y	Y	0.60%
CGPLOV42	Ovarian Cancer	I	166	0.9265	0.9086	0.0489%	0.9979	Y	Y	1.24%
CGPLOV43	Ovarian Cancer	I	167	0.9626	0.9342	0.0432%	0.6042	N	N	ND
CGPLOV44	Ovarian Cancer	I	164	0.9536	0.9173	0.1946%	0.9962	Y	Y	0.37%
CGPLOV46	Ovarian Cancer	I	166	0.9622	0.9291	0.0801%	0.9128	Y	Y	ND
CGPLOV47	Ovarian Cancer	I	165	0.9704	0.9461	0.0270%	0.3410	N	N	3.20%
CGPLOV48	Ovarian Cancer	I	167	0.9675	0.9429	0.0422%	0.4874	N	N	10.70%

CGPLOV49	Ovarian Cancer	III	164	0.8998	0.8083	0.1527%	0.9897	Y	Y	2.03%
CGPLOV50	Ovarian Cancer	III	165	0.9682	0.9382	0.0807%	0.9955	Y	Y	ND
CGPLPA112	Pancreatic Cancer	II	164	0.8914	0.9429	0.0268%	0.0856	N	N	-
CGPLPA14	Pancreatic Cancer	II	167	0.8718	0.9069	0.0515%	0.9824	Y	Y	-
CGPLPA15	Pancreatic Cancer	II	167	0.9111	0.8927	0.0160%	0.8737	Y	Y	-
CGPLPA156	Pancreatic Cancer	II	167	0.9479	0.9432	0.0290%	0.0159	N	N	-
CGPLPA17	Pancreatic Cancer	II	166	0.8624	0.6771	1.2600%	0.9956	Y	Y	-
CGPLPA23	Pancreatic Cancer	II	165	0.7887	0.6938	0.5785%	0.9984	Y	Y	-
CGPLPA25	Pancreatic Cancer	II	166	0.9549	0.9239	0.0380%	0.8103	Y	Y	-
CGPLPA26	Pancreatic Cancer	II	166	0.9598	0.9356	0.0247%	0.8231	Y	Y	-
CGPLPA28	Pancreatic Cancer	II	165	0.9069	0.8938	0.0546%	0.9036	Y	Y	-
CGPLPA33	Pancreatic Cancer	II	166	0.8361	0.8553	0.0894%	0.9967	Y	Y	-
CGPLPA34	Pancreatic Cancer	II	168	0.8946	0.8885	0.0439%	0.7977	Y	Y	-
CGPLPA37	Pancreatic Cancer	II	165	0.8840	0.9294	0.0410%	0.9924	Y	Y	-
CGPLPA38	Pancreatic Cancer	II	167	0.8746	0.8941	0.0372%	0.9851	Y	Y	-
CGPLPA39	Pancreatic Cancer	II	167	0.8562	0.7972	0.5058%	0.9951	Y	Y	-
CGPLPA40	Pancreatic Cancer	II	165	0.8563	0.8865	0.2268%	0.9920	Y	Y	-
CGPLPA42	Pancreatic Cancer	II	167	0.9126	0.8863	0.0283%	0.3544	N	N	-
CGPLPA46	Pancreatic Cancer	II	169	0.8274	0.7525	1.0982%	0.9952	Y	Y	-
CGPLPA47	Pancreatic Cancer	II	166	0.8376	0.8439	0.1596%	0.9946	Y	Y	-
CGPLPA48	Pancreatic Cancer	I	167	0.9391	0.9207	1.0232%	0.2251	N	N	-
CGPLPA52	Pancreatic Cancer	II	167	0.9452	0.8863	0.0154%	0.0963	N	N	-
CGPLPA53	Pancreatic Cancer	I	163	0.9175	0.8776	0.1824%	0.8946	Y	Y	-
CGPLPA58	Pancreatic Cancer	II	165	0.9587	0.9224	0.0803%	0.9056	Y	Y	-
CGPLPA59	Pancreatic Cancer	II	163	0.9230	0.9193	0.1479%	0.9759	Y	Y	-
CGPLPA67	Pancreatic Cancer	III	166	0.9574	0.9248	0.0329%	0.6716	Y	N	-
CGPLPA69	Pancreatic Cancer	I	168	0.9172	0.8592	0.0459%	0.1245	N	N	-
CGPLPA71	Pancreatic Cancer	II	167	0.9424	0.8888	0.0479%	0.0524	N	N	-

CGPLPA74	Pancreatic Cancer	II	166	0.9688	0.9372	0.0292%	0.0108	N	N	-
CGPLPA76	Pancreatic Cancer	II	163	0.9681	0.9441	0.0345%	0.0897	N	N	-
CGPLPA85	Pancreatic Cancer	II	165	0.9137	0.9337	0.0363%	0.0508	N	N	-
CGPLPA86	Pancreatic Cancer	II	165	0.8875	0.8042	0.7564%	0.9864	Y	Y	-
CGPLPA92	Pancreatic Cancer	II	167	0.9389	0.9003	0.1458%	0.7061	Y	N	-
CGPLPA93	Pancreatic Cancer	II	166	0.8585	0.8023	0.6250%	0.9978	Y	Y	-
CGPLPA94	Pancreatic Cancer	II	162	0.9365	0.9433	0.0180%	0.9025	Y	Y	-
CGPLPA95	Pancreatic Cancer	II	163	0.8542	0.8571	0.0815%	0.9941	Y	Y	-

*Pearson correlation. [1]ND indicates not detected. Please see reference 10 for additional information on targeted sequencing analyes. DELFI cancer detection at 95% and 98% specificity is based on scores greater than 0.6200 and 0.7500, respectively.

Table 4.8. Summary of whole genome cfDNA analyses of chromosomal copy number changes.

Patient	Z Score Chromosome Arm																			
	chr1p	chr1q	chr2p	chr2q	chr3p	chr3q	chr4p	chr4q	chr5p	chr5q	chr6p	chr6q	chr7p	chr7q	chr8p	chr8q	chr9p	chr9q	chr10p	chr10q
CGCRC291	-20.27	-18.19	25.09	26.20	-102.97	24.14	-17.90	-33.11	-13.32	-42.14	3.90	7.19	39.64	32.59	-72.09	93.57	13.16	23.03	-13.87	-19.62
CGCRC292	-1.36	-1.69	-1.42	-1.35	-2.31	-2.02	1.11	0.47	1.57	-3.57	-1.69	-0.63	2.53	-0.07	-1.22	0.00	-0.40	-0.59	-1.14	-0.98
CGCRC293	5.38	5.64	5.38	5.56	6.74	5.42	3.75	4.92	2.42	8.51	2.63	-3.51	-2.68	0.67	-2.27	-2.18	-1.39	-0.98	-1.37	-1.08
CGCRC294	-1.43	-1.59	-0.84	-1.04	-3.69	-3.10	0.82	-1.98	0.69	-4.36	-1.69	-1.82	0.88	-0.37	0.01	-0.26	-1.51	-0.17	0.22	-0.46
CGCRC296	-1.99	-1.63	-0.16	-0.60	-0.92	-3.45	1.62	-0.42	2.83	-2.37	-1.74	-0.75	2.85	0.60	0.32	1.03	-1.15	-0.67	0.80	0.04
CGCRC299	1.36	2.15	1.37	0.55	-2.17	1.12	-1.57	-1.00	-1.66	-0.11	2.41	-1.16	2.49	-2.14	-2.33	0.12	-2.50	1.76	2.69	0.94
CGCRC300	1.58	1.20	1.06	0.39	-0.11	0.60	-1.44	-0.97	-1.40	1.92	1.35	-1.36	0.70	-2.47	0.36	1.47	-1.06	2.45	0.58	1.03
CGCRC301	1.05	0.08	1.35	-0.49	-2.17	-0.78	0.41	-0.03	-0.84	-1.44	0.96	-1.33	-0.67	-1.95	0.12	0.26	-1.25	1.63	0.60	0.83
CGCRC302	-0.37	0.39	1.03	0.49	-3.76	-0.60	-1.06	-2.12	-1.40	-2.12	0.51	0.10	3.58	-2.24	-1.80	-0.41	-3.49	2.37	1.68	1.49
CGCRC304	0.05	1.23	2.03	1.19	-2.95	-1.01	-0.62	-1.81	-0.80	-1.89	1.46	-0.49	3.76	-2.02	-1.94	-0.80	-4.10	2.76	1.46	1.12
CGCRC305	-0.51	0.28	0.15	-0.53	-1.53	-0.52	0.16	-0.57	-0.10	-2.89	-0.09	-1.28	-1.25	-0.82	-0.71	-1.40	-0.88	0.82	0.77	0.09
CGCRC306	-1.33	-0.99	-0.57	-0.85	-1.51	-0.04	0.87	-0.20	1.19	-1.25	-1.28	0.14	0.07	0.25	0.43	-0.15	-0.34	-1.72	-1.55	-1.14
CGCRC307	0.36	0.26	0.35	0.29	-1.14	-0.37	1.56	-0.39	0.73	-2.22	-0.25	-0.85	0.56	-1.02	-0.87	0.34	-0.53	0.56	0.41	-0.45
CGCRC308	-1.45	-1.03	-0.11	-0.30	-2.31	-2.19	1.94	-1.29	1.23	-2.40	-2.35	0.69	1.15	-0.44	2.27	0.65	-1.38	-0.95	-0.06	-0.23
CGCRC311	-0.48	0.75	0.97	-0.37	-1.21	-0.62	0.63	0.49	1.00	-0.27	0.09	1.06	-0.32	-0.74	2.00	0.29	0.31	0.84	-0.15	0.59
CGCRC315	-0.97	-0.91	-1.48	-1.27	-4.08	-2.63	0.16	-1.80	0.58	-5.40	-0.74	0.46	-0.37	-0.75	-0.47	-1.84	-0.81	0.05	0.09	-1.32
CGCRC316	-17.67	-10.90	9.05	0.74	-49.91	-24.51	-8.57	-10.51	11.54	-15.05	-3.79	-27.22	3.89	55.18	-49.45	36.06	20.38	11.90	33.86	-16.28
CGCRC317	-3.34	-1.43	-0.82	-0.47	-3.99	-2.29	1.01	-1.36	0.30	-3.49	-1.26	0.01	3.95	0.40	8.64	14.60	-3.20	-0.24	0.99	-1.16
CGCRC318	-1.99	-2.70	-1.10	-1.84	-3.82	-3.74	0.63	-1.51	2.50	-5.10	-2.28	-0.51	4.14	-1.62	-0.59	-1.35	-1.82	-0.24	0.03	-0.40
CGCRC319	-1.60	0.24	0.03	-0.55	-3.81	-1.74	-0.04	-0.71	0.41	-3.65	0.13	0.01	3.66	0.59	-2.34	-0.67	-2.70	-0.30	1.45	-0.76
CGCRC320	-1.14	-1.89	0.18	0.82	-3.74	-1.40	0.26	0.24	1.01	-1.73	-1.51	2.63	2.93	-1.92	0.18	-0.12	-2.63	1.36	0.66	-0.04
CGCRC321	-1.64	-0.37	-0.14	-0.30	0.01	-1.03	1.49	-0.38	1.84	-0.91	-0.78	-0.05	0.60	0.85	-0.38	0.34	0.10	-0.38	-0.17	-0.25
CGCRC333	-10.99	7.54	31.44	57.46	-109.86	-86.92	-10.67	-79.07	60.37	-64.37	15.86	75.31	-7.50	82.29	-79.21	176.22	-58.84	-69.05	-13.05	17.55

CGCRC336	-1.71	1.38	30.93	23.56	-19.48	-9.92	-16.06	-30.59	-17.64	-42.34	39.01	103.82	93.53	76.11	-15.78	27.73	3.97	6.93	68.25	-2.00
CGCRC338	-21.29	9.04	27.36	30.26	-31.15	-28.63	-16.13	-28.70	-11.91	-38.27	-15.12	-35.38	49.64	41.37	12.65	57.75	-16.52	-24.11	13.68	-9.74
CGCRC341	-2.63	-0.72	-1.69	-1.58	-3.63	-1.60	1.11	-1.27	1.41	-2.53	-1.87	0.01	3.10	0.65	0.50	-0.99	-0.38	-1.34	-0.38	-1.25
CGCRC342	-22.85	-17.62	-22.09	-26.52	-27.22	-26.44	-33.61	-53.05	-5.40	-30.70	21.70	38.60	242.92	202.28	-150.81	98.92	44.48	61.88	14.05	16.66
CGPLBR100	-1.08	-0.27	-1.04	-0.27	0.93	0.65	1.25	2.97	2.13	1.19	-0.91	1.12	0.05	2.58	1.49	0.62	1.94	-1.29	-0.85	-0.89
CGPLBR101	-0.45	-1.07	-1.30	-0.53	-0.48	-1.11	1.49	0.81	1.82	-1.11	-1.83	0.05	0.84	0.83	0.37	0.50	0.87	-1.66	-0.87	-0.28
CGPLBR102	-0.35	-0.60	-0.08	-0.27	-0.47	-0.12	0.76	0.32	1.26	-0.84	-0.54	0.67	0.88	0.26	1.29	2.80	1.14	0.36	-1.52	-0.60
CGPLBR103	-0.15	-1.17	-1.07	-0.96	0.14	-0.98	0.93	0.92	1.58	-1.82	-1.90	-0.78	-0.59	-0.27	1.09	-0.14	2.14	-0.69	-1.56	-0.41
CGPLBR104	-1.76	-0.02	-0.22	1.33	0.22	0.79	2.68	2.30	2.70	2.13	-1.80	3.50	2.07	1.76	2.55	3.17	1.45	-0.61	-1.50	0.18
CGPLBR12	0.44	4.71	3.71	-0.12	-2.21	0.09	-2.94	0.28	-0.10	-3.04	2.94	2.37	-0.77	-0.71	-5.56	-2.08	-0.69	0.32	1.30	0.63
CGPLBR18	1.24	1.31	0.86	-0.71	-1.29	0.19	-1.74	-1.04	-1.77	-2.69	2.21	-1.86	-0.31	-1.07	-1.67	-1.52	-1.43	0.93	0.71	-0.36
CGPLBR23	0.04	0.45	0.93	-0.78	-0.91	-1.56	0.10	-1.23	0.09	-1.48	-0.10	-1.36	-0.98	-1.38	0.45	-1.17	-0.55	0.58	0.31	1.14
CGPLBR24	-1.02	-0.45	-0.29	-0.79	-2.66	-0.64	0.02	-1.49	0.19	-2.49	-0.45	0.10	1.55	-0.59	-0.80	-0.28	-1.27	0.53	0.78	-0.42
CGPLBR28	-0.80	0.34	-1.42	-0.82	-0.48	1.06	1.54	2.73	1.94	0.93	-1.05	1.08	-0.35	1.98	0.66	1.95	2.15	-2.36	-0.78	-1.10
CGPLBR30	17.04	19.77	21.37	20.63	-50.27	21.81	-24.45	-25.93	53.83	-92.42	-12.81	-43.32	24.81	29.62	-46.58	150.52	-4.47	-9.73	9.12	-15.62
CGPLBR31	0.56	0.98	-0.51	0.29	0.00	1.53	0.09	0.52	-0.54	0.10	0.36	0.94	-0.47	0.01	-1.04	0.26	-0.47	0.37	-0.38	-0.33
CGPLBR32	-0.60	1.36	1.01	2.68	0.92	2.92	0.94	4.91	1.12	4.15	-0.28	5.45	0.62	1.78	1.01	3.65	0.95	-0.59	-0.72	0.58
CGPLBR33	-0.52	0.65	-0.06	-0.59	0.12	-0.07	0.82	0.14	1.03	-1.10	-0.97	0.93	0.34	0.46	0.70	-0.04	0.91	-1.55	-1.36	0.06
CGPLBR34	-0.01	1.16	1.00	0.56	-0.25	-0.09	0.57	0.39	0.11	-0.54	0.50	0.03	-0.62	0.26	-0.71	0.00	-0.86	-0.86	1.47	-0.02
CGPLBR35	0.25	-0.04	-0.25	-0.83	-0.31	0.37	0.84	1.55	2.12	-1.79	-0.89	0.39	0.21	0.33	1.38	-0.01	0.83	-0.73	-0.19	-0.65
CGPLBR36	-1.38	-1.10	-3.11	-4.53	-2.33	-2.39	-0.54	-1.10	1.90	-5.36	-2.28	-2.40	-1.67	-1.10	1.19	1.51	1.05	-2.07	-1.08	-2.13
CGPLBR37	-0.76	-0.14	-0.24	-1.08	-0.53	0.22	0.26	0.56	0.88	-1.27	-0.17	0.93	0.11	0.56	-0.31	-0.24	0.04	-0.50	-0.76	-0.13
CGPLBR38	1.12	1.55	1.34	0.21	-0.30	1.46	-0.53	0.46	-1.49	0.82	1.28	-0.02	1.74	-0.14	-1.84	0.54	-1.59	1.29	1.87	1.72
CGPLBR40	-0.49	-1.20	-1.00	-0.35	-0.58	-1.04	1.63	1.45	3.30	-0.85	-2.25	-0.05	2.86	0.78	2.85	0.49	1.07	-0.33	-0.69	0.49
CGPLBR41	-0.66	0.03	-0.36	-0.86	-1.49	-0.58	1.24	-0.43	1.40	-0.97	-1.05	-0.93	1.49	0.28	0.49	0.11	0.47	-1.52	-0.53	-0.30
CGPLBR45	1.38	2.47	1.70	-0.27	-1.31	1.46	-1.88	-0.77	-0.99	-0.75	2.33	-1.34	-0.73	-0.46	-2.34	-0.99	-1.11	1.14	0.51	0.90
CGPLBR46	-0.93	1.93	-0.99	0.49	0.52	1.76	0.59	2.51	1.01	1.35	-0.82	3.24	0.24	0.57	0.27	5.43	1.10	-0.78	0.29	-0.46
CGPLBR47	0.71	2.23	1.84	1.36	-0.68	0.88	-1.19	0.82	-1.32	0.30	1.43	0.04	0.11	-1.67	0.12	0.68	-0.76	0.97	0.83	1.18

CGPLBR48	0.80	5.04	0.43	6.12	-0.71	7.96	-0.45	6.24	-3.09	10.19	1.15	12.92	3.72	3.24	-0.38	7.95	-0.34	1.33	2.56	0.73
CGPLBR49	1.71	4.54	-0.98	5.51	-1.97	7.73	-2.30	6.63	-4.89	9.84	2.03	11.07	3.75	4.03	-1.71	4.71	-1.33	1.51	2.09	-1.05
CGPLBR50	-0.75	-0.40	-0.84	-0.05	-0.47	-0.23	1.54	0.53	1.62	-1.44	-1.10	0.52	1.77	0.38	0.93	1.61	0.55	0.31	-0.86	-0.17
CGPLBR51	1.13	2.07	0.42	0.53	0.93	1.33	1.20	0.19	-0.84	0.87	0.82	0.61	-2.34	-0.89	-1.13	2.72	-0.87	1.08	-0.82	0.56
CGPLBR52	-0.54	-0.84	-2.45	-2.54	-1.46	-1.48	0.51	-5.05	1.55	-3.74	-1.90	-2.25	0.14	-1.27	-0.74	0.83	0.14	-1.41	-1.35	-1.43
CGPLBR55	-0.54	2.24	-0.32	-0.29	0.44	-0.57	3.15	0.55	1.83	-0.18	-1.29	0.92	-0.16	1.19	0.52	2.15	1.28	-0.54	-0.83	0.47
CGPLBR56	-0.37	0.66	0.05	0.11	-0.27	-0.61	-0.15	-1.29	0.24	-0.66	0.48	-0.91	0.27	-1.30	-2.06	0.33	-1.28	-0.01	0.29	0.31
CGPLBR57	-0.68	-0.04	-1.00	-0.41	-0.35	-0.87	0.07	0.94	1.34	0.65	-1.50	0.26	-0.50	0.93	0.33	1.34	0.82	-1.07	0.22	-0.22
CGPLBR59	0.19	0.18	-0.07	-0.70	-0.47	0.16	0.72	-0.85	0.43	-0.43	-0.31	-1.33	0.31	0.45	-1.61	0.67	0.11	-0.62	-0.49	0.46
CGPLBR60	-0.32	0.73	0.28	1.59	0.73	-0.05	1.09	1.08	0.25	0.72	-0.53	0.84	-0.43	-0.01	1.53	1.39	1.14	-0.87	-1.21	0.28
CGPLBR61	-0.09	0.88	0.52	0.63	-0.33	-0.35	0.28	-0.93	0.18	0.07	0.01	0.18	-1.40	-0.73	0.28	-0.37	-0.41	0.79	-0.47	0.49
CGPLBR63	0.78	0.59	0.04	0.94	0.30	2.86	0.45	2.81	0.58	2.42	-0.55	3.15	0.79	1.23	0.29	2.68	1.21	-0.32	0.38	-0.39
CGPLBR65	0.58	1.54	-0.59	1.00	-0.15	2.96	0.40	3.27	0.32	2.09	-0.37	2.70	0.02	2.05	0.70	2.00	1.04	0.16	0.55	-0.85
CGPLBR68	1.38	2.13	2.11	0.53	0.69	0.02	-1.47	-2.01	-0.99	-0.52	2.73	-1.75	0.69	-2.68	-0.10	0.13	-2.00	2.49	1.06	2.41
CGPLBR69	0.27	0.56	2.08	-0.51	-0.23	0.35	0.45	0.21	0.94	-0.62	-0.26	-0.37	1.04	-0.61	-0.03	0.89	-0.01	-0.38	-0.32	0.42
CGPLBR70	-1.04	-0.87	-0.51	-0.77	-0.36	-1.29	1.31	0.77	2.21	-1.02	-0.94	0.27	1.16	0.05	1.01	0.24	1.16	-0.52	-0.58	0.13
CGPLBR71	-1.06	0.37	-0.08	-0.51	0.49	0.68	1.55	1.11	1.69	0.16	-0.18	1.63	0.72	0.91	-0.29	1.58	0.18	-0.84	-1.38	-0.18
CGPLBR72	-1.20	-0.49	-1.03	-1.88	-1.17	-1.68	-0.07	-0.89	0.99	-1.90	-0.82	-1.27	0.07	-0.01	0.26	-0.80	-0.18	-0.98	-0.78	-0.88
CGPLBR73	0.21	-0.41	-0.75	-1.52	-1.15	-1.28	0.64	-0.64	0.68	-1.79	-0.35	-0.89	0.26	-1.68	0.60	1.26	0.02	0.13	-1.08	0.91
CGPLBR76	-0.32	-1.39	-1.33	0.30	-0.44	0.24	1.81	2.26	2.00	-1.81	-2.13	0.93	1.81	1.36	2.87	2.07	1.98	-0.15	-0.04	0.26
CGPLBR81	0.73	3.17	-0.25	4.93	0.97	6.20	0.41	7.32	-0.78	8.60	1.01	8.61	2.88	3.60	1.59	5.96	-0.12	0.83	1.12	0.90
CGPLBR82	-0.21	0.57	0.48	1.78	-1.00	0.86	-0.06	0.77	-0.20	0.46	0.47	2.25	1.96	0.18	0.69	1.36	-2.10	1.05	1.77	0.43
CGPLBR83	0.66	1.06	0.20	2.15	0.66	2.36	-0.20	2.52	-0.42	1.16	0.65	2.79	1.76	0.38	1.34	2.84	0.30	0.40	1.86	0.36
CGPLBR84	1.39	2.34	-0.91	4.14	1.26	5.40	0.80	5.69	0.07	7.09	-0.29	7.01	2.43	3.19	1.21	7.04	1.98	0.02	-0.27	0.27
CGPLBR87	1.47	2.50	-1.31	4.83	-0.82	5.43	-0.55	6.92	-2.13	8.22	0.40	9.23	1.81	3.80	3.19	6.73	0.31	1.30	1.74	0.54
CGPLBR88	-2.25	0.28	-0.49	4.05	-2.17	2.55	0.63	5.78	1.05	4.70	-0.40	9.82	5.89	3.37	5.22	6.97	0.10	-0.21	2.42	0.65
CGPLBR90	0.96	1.78	-0.68	3.72	-0.43	6.04	0.03	5.93	-0.89	7.21	0.52	9.34	1.91	3.84	0.56	4.26	1.86	0.11	2.06	0.43
CGPLBR91	-0.06	0.34	0.40	-0.46	0.03	0.42	0.88	0.12	1.11	-0.27	-0.42	0.92	0.93	0.42	1.06	0.56	0.01	-0.04	0.02	0.48

CGPLBR92	-1.92	-1.03	-0.04	-1.69	-5.51	-4.59	-0.68	-4.02	0.44	-6.77	-0.09	-2.73	3.49	-2.36	0.61	-1.80	-4.10	0.07	3.89	0.46
CGPLBR93	0.22	0.06	-0.13	-0.46	-0.10	-0.20	1.06	0.23	0.92	-1.31	-0.05	-1.26	1.67	0.38	-0.16	0.97	-0.91	0.06	0.68	0.36
CGPLH189	0.87	0.62	1.69	0.70	0.95	0.35	-0.24	0.64	-0.04	0.40	0.42	0.11	0.64	-1.17	0.11	0.40	-0.03	1.33	-0.22	0.73
CGPLH190	-0.59	-0.63	0.10	0.62	1.47	-0.04	0.98	0.44	2.06	-0.22	-0.96	0.14	1.31	-0.24	0.60	1.68	0.68	0.03	-0.62	0.36
CGPLH192	0.56	0.58	0.44	0.52	-0.13	0.53	-0.55	0.81	-0.30	0.75	0.36	-0.70	0.27	0.38	-1.13	-0.12	-1.00	-0.22	-0.42	0.38
CGPLH193	-0.35	-0.15	0.29	0.13	0.64	0.32	1.08	0.14	0.26	-0.63	-0.38	1.18	0.11	-0.39	-0.19	0.60	0.23	-0.40	-1.42	-1.32
CGPLH194	1.45	2.35	3.16	3.03	-0.44	1.15	-1.62	-0.18	-1.32	1.10	2.11	0.54	1.54	-1.87	-0.13	0.29	-1.94	2.42	1.51	2.60
CGPLH196	0.13	1.20	0.89	-0.72	0.45	-0.08	-0.27	-0.48	-0.44	0.12	0.92	-0.58	0.65	-1.78	-1.35	-0.36	-0.77	0.52	-0.11	0.46
CGPLH197	-0.89	1.12	0.75	0.92	0.76	1.75	0.81	2.55	0.97	1.25	-0.60	2.31	0.33	2.43	0.24	1.48	1.35	-1.14	-1.13	-0.38
CGPLH198	-0.57	0.28	0.72	-0.34	1.00	-1.25	0.25	-1.31	0.90	-0.61	0.55	-1.31	0.17	-1.31	0.38	0.00	-0.43	0.37	0.35	0.40
CGPLH199	-0.39	-0.20	-1.74	-1.70	1.14	-0.86	1.00	-0.33	0.75	-0.76	0.03	-0.54	-3.50	-0.94	0.95	-0.13	0.38	-0.01	-1.17	-0.26
CGPLH200	-0.97	-0.42	-0.96	-1.55	0.03	-0.61	0.80	0.24	0.63	-0.90	-0.96	-1.25	-0.52	1.19	0.28	-0.86	0.21	-0.82	-0.82	-1.06
CGPLH201	-1.10	-0.69	-0.77	-1.00	-0.22	-0.42	1.21	0.91	0.81	-0.16	-0.97	-0.24	-2.02	0.74	5.42	0.30	1.28	-1.46	-2.08	-0.70
CGPLH202	0.41	0.32	0.84	-0.19	0.13	0.62	-0.43	0.74	-0.04	0.39	0.22	-0.39	-0.34	-0.67	0.05	0.18	-0.32	-0.03	-0.30	0.91
CGPLH203	1.54	1.76	0.77	0.99	-0.41	1.39	-0.70	0.78	-1.22	0.58	1.21	0.02	0.86	-1.78	-1.38	1.21	-1.31	1.23	-0.31	0.45
CGPLH205	1.66	1.74	2.37	1.33	0.62	1.44	-1.40	-0.02	-1.52	0.65	2.19	0.20	1.08	-0.20	-1.79	0.42	-1.27	1.17	1.31	1.73
CGPLH208	-0.23	0.21	0.06	0.29	1.86	-0.29	0.63	-0.08	0.68	-0.08	-0.36	0.21	1.23	0.39	1.01	0.41	-0.11	-0.65	-1.17	0.15
CGPLH209	-0.70	-0.31	-0.36	-0.30	0.31	-0.52	1.25	-0.33	1.47	-0.08	-1.51	0.76	0.73	0.02	1.52	0.68	0.31	-0.22	-1.36	0.42
CGPLH210	-0.02	-0.07	0.14	0.44	0.85	0.21	1.02	0.81	1.00	1.71	-0.82	0.05	1.92	0.33	1.67	1.22	0.73	0.56	-0.11	0.75
CGPLH211	0.58	0.84	0.07	1.02	-0.08	1.34	-0.41	1.24	-0.43	0.85	0.23	0.49	0.62	0.23	0.09	0.61	-0.14	0.65	0.33	0.80
CGPLH300	0.88	1.03	-0.11	-0.04	0.41	1.01	-0.15	1.24	0.80	1.85	0.13	0.81	-0.60	-0.15	0.60	0.01	-0.56	0.27	-0.95	0.40
CGPLH307	0.35	1.03	0.01	0.54	-0.85	1.61	0.50	0.97	0.26	1.35	0.48	2.52	0.96	1.19	0.50	1.10	0.90	-0.03	-0.14	0.03
CGPLH308	1.04	1.47	0.57	0.73	-0.33	0.72	0.32	0.95	0.25	0.12	1.06	0.06	-1.46	-0.53	-1.14	0.25	-0.06	0.25	-0.12	0.88
CGPLH309	1.23	1.23	1.11	0.16	-0.46	0.13	-0.79	-0.04	-0.13	-0.89	1.10	0.12	-0.50	-0.36	-0.57	-0.12	-0.20	1.48	0.74	1.05
CGPLH310	-0.54	-0.34	0.70	0.26	0.31	-1.10	1.97	1.17	1.68	-1.12	-0.88	-0.57	1.43	-0.30	0.25	0.86	-0.36	0.12	-0.12	0.86
CGPLH311	-0.02	0.58	-0.33	-0.74	-0.63	-0.23	0.13	-0.12	0.59	-0.79	-0.48	-0.28	-0.46	0.06	-0.04	-0.73	0.75	-0.79	-0.44	-0.31
CGPLH314	0.98	0.80	0.92	-0.63	-0.18	-0.76	-0.88	-1.86	-0.19	-2.07	1.08	-2.12	-0.89	-2.15	0.39	-0.65	-0.11	1.56	0.44	1.01
CGPLH315	-0.84	-0.32	-0.21	-1.20	-1.39	-1.61	0.82	-1.84	0.36	-2.77	-0.48	-0.72	-0.64	-0.37	-1.38	-0.68	-0.98	0.13	-0.73	-1.11

CGPLH316	-0.41	0.58	0.94	-0.35	0.31	-1.05	-0.08	-2.53	0.55	-0.67	-0.07	-0.95	0.10	-2.28	-0.18	0.06	-0.82	0.81	-0.43	1.12
CGPLH317	1.02	0.48	0.15	0.82	0.71	0.55	-0.05	1.18	1.25	-0.38	-0.81	0.95	0.52	0.14	1.34	1.53	0.51	0.58	-0.85	0.52
CGPLH319	-0.38	0.29	-0.17	-0.41	0.85	0.22	1.16	1.69	1.63	0.23	-1.29	1.47	0.61	2.09	1.59	0.85	0.77	-0.56	-0.58	-0.16
CGPLH320	0.23	0.37	-0.83	-0.20	-0.53	-0.19	0.51	-0.55	0.61	0.72	-0.14	-0.34	0.54	-0.34	0.42	0.38	0.18	-0.39	-1.27	-0.37
CGPLH322	0.73	0.95	0.18	-0.24	-0.75	-0.16	-1.04	-0.80	-0.58	-0.89	1.19	-1.78	0.16	-1.05	-1.28	-0.16	-0.38	0.69	-0.15	1.40
CGPLH324	0.59	0.48	0.32	-0.52	-0.38	-0.49	0.12	0.08	-0.08	-1.36	0.34	-1.17	0.36	-0.57	0.19	0.89	0.04	-0.68	0.60	0.99
CGPLH325	-0.08	0.79	-0.74	-0.08	0.01	0.73	0.57	0.93	0.68	-0.66	0.51	0.60	0.33	0.75	1.09	0.33	-0.48	-1.14	-0.41	-0.12
CGPLH326	-0.16	0.66	0.86	0.57	-1.09	0.24	0.31	0.99	-0.33	-0.98	0.56	-0.31	-0.71	-0.74	0.33	1.29	-0.97	1.10	-0.05	0.36
CGPLH327	-0.35	0.23	-0.57	-0.51	-0.40	-0.28	0.67	0.62	0.56	-1.30	-1.12	0.81	-0.04	0.63	0.28	-0.02	0.56	-1.56	-1.19	-0.37
CGPLH328	-1.48	0.24	-0.93	-1.03	-0.53	-0.22	1.21	0.88	1.87	-1.49	-1.60	0.16	-0.47	1.29	-1.04	0.23	-0.60	-1.70	-1.43	-1.28
CGPLH329	0.65	1.73	0.55	0.59	-0.92	0.87	-0.25	0.67	-0.07	0.34	0.33	0.85	1.13	-0.16	-0.45	0.07	0.07	0.80	-0.24	0.05
CGPLH330	0.01	0.29	-0.25	-1.33	-0.60	-0.03	0.40	0.92	0.10	-1.54	-0.81	0.36	0.74	0.61	-0.24	-0.80	-0.05	-0.25	-0.57	-1.62
CGPLH331	0.43	1.03	-0.18	-1.05	-2.32	-0.78	-0.47	-0.65	-0.96	-1.59	0.08	-1.04	-1.01	-0.16	-0.69	-1.17	-0.39	-1.12	0.58	-0.63
CGPLH333	0.74	-0.01	-0.25	0.10	-0.01	0.88	0.28	1.75	0.75	-1.25	-0.89	0.46	-1.53	0.02	-0.86	0.63	0.98	-0.09	-0.77	0.51
CGPLH335	0.09	0.75	-0.48	0.00	0.05	0.55	-0.45	0.33	0.12	0.19	-0.41	0.69	-0.41	0.18	-0.30	-0.04	0.01	0.56	-0.34	0.30
CGPLH336	0.52	-0.49	-0.57	-0.38	-0.06	0.79	0.46	1.54	0.51	-0.35	-0.58	-0.10	-0.67	0.96	0.21	0.34	1.36	-0.92	-1.41	-0.31
CGPLH337	0.75	1.49	0.65	0.44	-0.11	0.94	-0.76	1.38	-0.84	-0.25	0.64	-0.16	-0.11	-0.48	-0.32	0.29	0.16	0.43	0.15	0.61
CGPLH338	-0.69	1.08	0.49	0.37	-0.23	-0.40	1.79	-0.12	1.10	0.34	-0.15	0.17	1.10	-1.33	1.31	0.81	-0.67	0.20	-1.41	0.26
CGPLH339	1.33	1.10	0.71	0.28	0.50	1.20	-0.34	0.43	0.02	0.08	0.25	0.23	-1.88	-0.27	-0.27	1.20	-0.45	-0.66	-0.49	-0.04
CGPLH340	0.26	0.95	0.30	0.17	0.64	1.61	0.63	-0.19	0.30	-0.55	0.13	0.19	-0.98	-0.51	-1.25	-0.58	-0.55	-0.08	-0.92	-0.51
CGPLH341	-0.60	-0.81	-1.38	-0.73	0.64	1.41	2.31	2.99	2.15	0.15	-1.62	2.03	-0.12	1.48	2.11	1.33	1.62	-2.79	-1.52	-0.77
CGPLH342	-0.58	0.60	0.00	-0.45	0.44	-0.71	0.61	-0.16	1.40	-0.36	-1.10	0.19	0.03	0.10	0.18	-0.65	0.19	-0.19	-1.49	0.18
CGPLH343	-0.15	0.27	-1.01	-1.54	-2.05	-0.70	-0.54	-0.14	-0.03	-2.57	-0.11	-1.77	-1.10	-1.97	0.00	-0.48	1.00	-0.87	-0.26	-0.63
CGPLH344	1.14	0.83	-0.02	0.17	-0.66	-0.70	0.18	0.96	1.17	1.52	-0.80	0.74	1.11	-0.96	1.51	1.09	0.86	0.16	0.15	0.88
CGPLH345	1.87	-0.10	-1.35	-0.44	-1.75	-0.55	-0.08	1.46	0.39	-1.80	-0.49	0.03	-0.98	-0.93	0.22	0.45	0.31	-0.47	-1.35	0.62
CGPLH346	0.90	1.12	-0.41	-0.31	-0.51	0.70	0.23	1.09	0.50	-0.80	0.20	-0.26	-1.35	0.51	-0.31	0.53	0.40	-0.65	-0.20	-0.22
CGPLH350	0.69	-0.05	-0.50	0.41	-2.41	-0.52	0.47	0.49	-0.30	-0.86	-1.42	-0.94	0.65	-1.98	1.18	0.98	-0.64	1.50	-0.10	1.41
CGPLH351	-0.45	-0.68	-1.49	-1.69	-2.28	-1.69	-0.42	0.03	0.48	-3.05	-1.14	-0.76	-0.19	0.67	-0.05	-1.22	-0.47	-0.45	-0.56	-1.20

CGPLH352	0.78	0.59	1.32	-1.30	-1.66	-0.62	-0.76	-1.15	0.32	-2.36	0.24	-1.02	-1.96	-1.60	-0.64	-1.82	0.19	0.58	0.54	0.89
CGPLH353	2.01	1.85	0.60	0.64	-0.19	1.71	-0.76	1.33	-0.90	0.09	1.42	0.47	-1.48	-0.91	-0.98	-0.42	-0.04	0.36	-0.01	0.80
CGPLH354	0.56	0.41	0.18	-1.33	0.04	-1.21	0.39	-0.80	0.86	-0.81	-0.51	-0.93	-0.99	-0.20	1.30	-0.91	-0.63	0.30	-0.62	-0.14
CGPLH355	0.73	2.65	0.68	0.20	-1.15	2.57	-0.67	0.82	-1.20	1.77	1.12	1.71	0.13	-0.20	-0.96	0.10	0.29	-0.27	-0.28	-0.39
CGPLH356	4.03	3.94	2.87	1.73	-0.29	3.89	-2.66	0.47	-3.08	0.65	3.96	0.63	-0.05	-1.31	-1.43	0.05	-1.90	2.35	1.29	2.16
CGPLH357	-1.07	-0.04	-0.95	-1.70	-2.96	-2.13	0.86	-0.07	0.65	-2.28	-1.38	-0.99	-0.17	0.02	0.06	-1.27	0.38	-1.11	-0.71	-1.31
CGPLH358	-0.33	0.45	1.15	0.26	-1.53	-0.09	0.52	1.15	0.43	-1.41	-0.01	1.31	1.62	-0.02	1.32	0.57	-0.54	0.33	0.48	-0.02
CGPLH360	1.17	0.19	0.29	0.28	-0.10	1.25	-0.16	0.56	0.12	0.03	-0.08	-0.13	-0.21	-0.35	0.35	-0.52	1.05	-0.14	-0.85	-0.17
CGPLH361	0.86	0.42	0.13	-0.24	-1.47	-0.26	-1.13	0.29	-0.40	-2.03	0.32	-0.36	0.85	-0.97	-0.74	-0.86	-0.69	1.37	-0.81	0.67
CGPLH362	-0.69	-0.36	-0.16	-0.04	-1.62	-0.15	0.53	0.63	0.85	-2.08	-0.94	1.11	0.87	0.10	-0.25	-0.44	-0.42	-0.36	0.12	-0.60
CGPLH363	0.00	-0.71	0.63	0.40	1.06	0.01	1.03	0.71	1.94	-0.69	-0.60	0.67	1.35	0.12	0.61	0.55	0.08	-0.52	-2.09	0.28
CGPLH364	-1.59	-1.29	-0.51	-0.42	-1.18	-2.23	0.92	0.24	1.51	-2.20	-1.85	0.05	1.30	0.29	0.69	-0.24	-0.43	-0.44	0.28	-0.40
CGPLH365	1.04	2.04	1.18	2.28	-0.86	3.92	-1.17	3.29	0.04	1.48	1.43	3.40	0.81	1.05	-1.40	1.80	0.16	0.26	0.70	0.91
CGPLH366	1.02	1.46	1.33	1.29	-0.61	0.42	-0.30	0.45	0.39	0.71	1.14	1.36	0.83	-0.70	-0.21	-0.15	-0.53	1.24	0.43	1.35
CGPLH367	0.07	-0.36	-0.15	-0.28	-1.19	-0.70	1.37	-1.04	1.18	-1.50	-0.88	-0.64	-1.02	-1.87	-0.10	0.14	-0.33	-0.99	-0.94	0.34
CGPLH368	0.33	0.53	-0.56	-0.05	-0.88	-0.50	0.88	1.34	1.19	0.06	-0.10	1.16	-1.14	0.01	0.35	0.73	0.34	0.17	-0.62	0.33
CGPLH369	-1.20	-0.47	-0.53	-0.20	-1.42	-1.35	1.67	-0.84	0.72	-2.41	-1.08	-0.44	1.08	-1.34	0.78	-0.23	-0.83	-0.07	-0.83	-0.24
CGPLH370	0.15	0.17	-0.11	-0.53	0.21	-0.95	1.48	-1.38	1.07	-1.10	-0.24	-0.11	1.14	-1.47	-0.35	0.37	-0.51	0.13	-0.87	1.10
CGPLH371	0.20	0.18	0.82	-0.26	0.51	-0.59	0.63	-0.56	1.53	0.41	-0.56	0.66	0.92	-0.85	1.52	0.84	-0.05	0.60	-0.79	0.56
CGPLH380	0.63	-0.04	0.29	-1.63	-3.28	-0.58	-1.23	-0.16	-0.31	-3.32	-0.47	-1.23	-1.31	0.01	-0.75	-2.26	-0.82	-0.21	1.07	-0.50
CGPLH381	-1.10	-1.02	-0.31	-1.16	-2.26	-1.41	0.14	-0.15	1.02	-4.35	-1.67	-0.02	0.65	0.74	1.15	-0.57	-0.31	-0.34	-0.23	-0.57
CGPLH382	-0.61	-0.04	-0.36	-0.56	-1.43	-0.29	-0.10	1.14	0.74	-4.25	-1.00	0.17	0.08	0.00	-1.52	-0.30	0.09	-0.25	-0.01	-0.42
CGPLH383	1.65	1.12	0.78	-1.44	-3.48	-2.08	-2.32	-1.69	-0.96	-3.70	0.84	-3.26	-0.76	-2.43	-0.88	-2.98	-2.56	0.39	1.32	0.43
CGPLH384	1.50	1.36	0.84	0.70	-0.94	1.43	-0.11	1.06	-0.33	0.48	0.68	0.06	-0.51	-0.62	-0.98	1.14	-0.21	0.88	-0.35	0.82
CGPLH385	0.40	0.02	-0.64	-0.48	-0.76	-0.83	-0.52	0.18	0.14	-2.06	0.12	-0.56	-1.22	-1.44	-0.09	-1.74	-1.12	0.68	-0.35	-0.40
CGPLH386	0.91	0.99	0.76	0.14	-0.97	0.57	0.45	1.77	0.72	0.04	-0.26	0.69	0.32	-0.02	0.46	1.70	0.09	0.03	-0.41	0.91
CGPLH387	1.17	-0.09	-0.61	-0.76	-0.57	-0.24	0.39	0.75	0.97	-1.35	-0.94	0.16	-1.38	0.08	2.11	0.87	0.54	-0.36	-0.82	0.12
CGPLH388	1.51	1.68	1.39	-0.52	-0.84	0.43	-1.52	-0.76	-1.20	-1.33	1.74	-0.75	0.36	-0.73	-1.34	-2.00	-0.87	0.18	1.60	-0.69

CGPLH389	-0.76	0.21	0.37	-0.59	-0.56	-0.70	2.14	0.89	2.11	-0.38	-1.46	0.49	-1.07	2.35	1.08	0.36	1.14	-2.23	-1.00	-0.53
CGPLH390	1.48	1.42	0.49	-0.02	-1.32	-2.12	-1.92	-3.25	-0.92	-2.68	1.00	-1.79	1.31	-3.36	-0.95	-0.78	-2.58	1.37	0.47	0.68
CGPLH391	-1.23	0.36	-0.25	-0.52	-0.84	-0.15	1.03	1.75	2.36	-0.20	-0.81	0.44	-1.03	1.05	0.13	0.58	0.88	-1.67	-1.87	-1.03
CGPLH392	-0.13	0.33	-0.35	0.29	-0.71	2.31	0.33	3.25	0.40	0.30	-0.27	2.31	1.02	1.51	-0.07	-0.07	0.68	-0.85	-0.40	-1.17
CGPLH393	1.76	1.09	0.93	-0.52	0.11	0.19	-0.35	-0.10	-0.08	0.19	0.32	-0.99	-1.88	-0.11	0.08	-0.25	-0.35	0.38	0.31	0.96
CGPLH394	1.38	2.02	0.71	0.13	-1.41	1.32	-0.76	0.49	-1.06	0.24	1.28	-0.49	-0.19	-0.13	-0.64	-0.24	-0.59	0.85	-0.09	0.22
CGPLH395	-0.03	0.60	-0.24	-1.51	-1.94	-0.56	0.42	-0.02	0.73	-1.52	-0.28	-0.78	-1.12	-0.02	-1.74	-0.95	-0.52	-0.76	-0.73	-0.64
CGPLH396	0.39	0.71	0.40	0.47	-0.79	-0.63	0.47	1.42	0.90	-0.30	-0.36	0.91	-0.84	-0.63	1.02	0.34	0.42	-0.29	0.22	0.54
CGPLH398	-0.36	0.21	-0.31	0.19	-0.16	-1.15	1.90	-0.51	1.57	-1.59	-0.97	-0.13	1.10	-1.16	0.11	1.48	-1.51	0.53	-1.04	0.53
CGPLH399	0.25	0.62	0.54	0.27	-0.63	1.66	0.72	2.76	0.90	-0.69	-0.34	1.25	0.02	1.91	-0.13	0.87	0.57	-1.33	0.00	-0.31
CGPLH400	4.06	3.28	2.01	1.77	-1.72	2.15	-2.47	0.85	-2.20	0.61	2.91	0.07	0.49	-3.61	-1.45	-0.06	-1.91	2.34	2.35	1.51
CGPLH401	0.10	0.74	0.85	-0.62	-1.34	-1.38	-0.05	-1.63	-0.02	-2.08	0.14	-1.21	0.11	-1.50	-0.09	0.44	-1.89	0.48	-0.33	1.50
CGPLH402	1.26	1.33	0.03	-1.33	-2.98	-0.68	-1.00	0.32	-0.60	-1.44	0.20	-0.56	-2.25	-0.32	-0.93	-0.19	-0.34	-0.98	-0.22	-1.33
CGPLH403	0.28	1.34	0.24	-2.31	-4.15	-0.76	-0.98	-0.31	-0.07	-3.94	-0.22	-1.87	-2.12	-0.47	2.48	3.41	-0.14	-1.05	-0.49	-0.47
CGPLH404	-0.20	0.72	-0.72	-0.85	-1.89	0.52	-0.32	1.61	1.36	-1.98	-1.03	-0.05	0.40	1.92	0.47	-0.33	0.52	-1.36	-1.52	-1.14
CGPLH405	0.39	2.44	0.35	0.34	-1.58	0.90	-0.16	0.57	-0.29	0.51	0.68	0.69	-0.75	0.27	-1.44	0.29	-1.27	-1.00	-0.21	0.55
CGPLH406	0.26	1.79	-0.19	-1.67	-1.78	0.60	-0.86	0.81	0.32	-0.59	-0.73	-0.36	1.61	1.14	-1.28	-0.98	-0.92	-1.30	-1.62	-1.01
CGPLH407	1.76	1.14	1.19	-0.19	-1.37	0.51	0.31	1.07	-0.42	-0.92	0.25	-0.39	-0.67	0.42	-0.69	-0.19	-0.69	0.20	-0.55	-0.33
CGPLH408	-0.15	-0.20	-0.94	-2.68	-1.02	-2.09	0.58	-1.60	0.57	-3.06	-1.03	-2.36	-0.90	-0.52	-0.51	-1.97	0.86	-0.46	-1.26	-0.38
CGPLH409	1.14	1.20	0.57	-1.24	-1.33	0.18	-0.92	-0.11	-0.42	-0.84	0.50	-2.07	-0.83	0.36	-1.12	-0.69	-0.66	-0.57	0.50	0.02
CGPLH410	0.91	1.45	0.30	-0.83	-0.97	-0.22	-0.09	0.24	0.06	-1.55	-0.77	0.23	0.32	-0.60	-0.73	0.00	-0.08	-0.26	-0.41	-1.06
CGPLH411	-0.17	0.40	-0.24	-1.37	-2.10	-0.53	-0.02	1.13	1.23	-1.69	-0.85	0.20	-0.34	0.60	0.79	0.37	0.96	-1.64	-1.56	-0.44
CGPLH412	0.25	1.44	-0.24	-0.69	-1.54	0.21	0.05	0.01	-0.27	-1.14	-0.61	-0.34	-1.82	0.23	-0.25	-0.83	-0.28	-1.20	-0.52	-0.97
CGPLH413	-0.43	0.00	-1.47	-1.97	-2.25	-0.36	0.85	-0.92	1.08	-1.92	-1.81	0.26	-1.85	-0.64	0.50	-0.27	0.38	-0.61	-2.28	-1.35
CGPLH414	0.75	0.42	0.28	0.14	-1.86	0.36	0.43	0.08	0.07	-0.57	-0.77	0.12	0.27	0.65	0.66	0.33	-0.35	-0.14	-0.40	-0.17
CGPLH415	0.50	0.75	-0.34	-1.35	-2.31	0.18	0.04	0.63	0.92	-1.73	-1.41	-0.60	-2.30	0.31	0.75	-0.96	-0.08	-0.54	-1.01	-0.11
CGPLH416	1.98	3.55	1.88	1.25	-1.14	1.51	-3.41	2.40	-2.70	-0.28	2.36	-0.07	-0.86	-1.42	-1.38	0.35	-2.46	1.26	1.26	1.28
CGPLH417	2.06	3.57	1.93	0.74	-2.34	2.41	-2.09	0.33	-2.49	0.90	2.47	1.24	-1.38	-1.57	-1.32	-0.09	-2.02	0.99	-0.39	1.08

CGPLH418	0.75	1.42	0.70	0.53	-1.51	0.74	-1.28	1.13	0.48	-0.61	-0.18	0.46	-0.73	0.64	-0.51	-0.07	-0.50	-0.09	-0.25	0.82
CGPLH419	0.91	1.12	0.27	-0.03	-1.95	0.44	-0.41	0.46	-0.24	-1.38	0.44	1.06	-1.51	-0.56	0.24	0.23	0.19	0.23	0.26	0.23
CGPLH420	0.82	0.24	-0.77	-0.58	-0.49	-0.08	0.35	0.44	0.67	-0.57	-0.84	-0.33	-0.46	0.31	0.33	0.85	0.44	0.12	-1.03	0.63
CGPLH422	1.49	2.05	1.24	-0.01	-1.02	1.65	-1.79	-0.45	-1.47	-0.28	1.84	-0.48	-0.95	-0.78	-1.83	-1.80	-0.69	-0.30	1.03	0.47
CGPLH423	1.47	0.67	0.07	-0.66	-1.81	0.58	-0.88	0.49	-1.09	-1.64	0.53	-0.56	-1.79	0.13	-0.70	-1.17	-0.82	-0.53	0.92	-0.18
CGPLH424	-0.51	0.44	-0.75	-1.51	-1.75	-0.18	-0.41	-0.31	-0.09	-2.13	-0.31	-0.31	-1.32	0.38	0.26	-1.93	-0.09	-1.90	-0.07	-0.97
CGPLH425	0.54	0.96	0.52	-0.10	-0.64	0.57	-0.63	0.11	0.02	-1.16	0.45	-0.38	0.40	0.16	0.14	-0.79	-0.82	-0.10	0.59	-0.07
CGPLH426	0.67	1.38	0.20	0.26	-0.76	0.34	0.15	0.87	-0.34	-0.20	0.37	0.08	-1.43	-0.61	-0.01	-0.58	-0.23	-0.26	0.35	0.62
CGPLH427	0.51	1.41	0.12	-0.03	0.14	0.18	-0.30	1.08	0.03	-0.29	-0.12	0.15	-1.50	0.35	0.00	-0.61	-0.06	-0.58	-1.05	-0.56
CGPLH428	0.80	0.46	-0.30	-0.13	-0.06	-0.56	0.05	0.08	-0.02	-0.62	-0.42	0.32	-0.58	-0.62	0.00	-0.35	0.12	-0.24	-0.41	-0.44
CGPLH429	1.51	2.10	1.56	1.27	0.23	2.80	-1.06	2.01	-0.09	1.73	1.18	1.66	0.84	0.02	-0.63	2.02	-0.36	-0.07	1.87	1.72
CGPLH430	-0.48	0.56	0.23	-0.67	-0.85	-0.40	-0.24	0.36	-0.30	-0.69	-0.16	1.17	0.54	-0.24	0.92	-0.86	-0.32	-0.40	0.15	0.00
CGPLH431	0.75	1.05	-0.32	-0.52	-1.76	0.43	-1.25	-0.77	-0.56	-1.03	0.77	-0.55	-1.21	-0.94	-1.42	-1.23	-1.41	-0.60	0.15	-0.40
CGPLH432	1.30	0.90	-0.63	-0.34	0.09	0.56	-0.76	2.35	0.03	0.78	-0.13	0.62	0.03	1.00	-1.45	0.12	0.32	-0.79	-0.88	-0.48
CGPLH434	0.68	0.85	0.23	-0.03	-0.82	-0.30	-0.92	-0.20	-0.08	0.01	-0.16	-0.51	0.15	-0.99	-0.80	0.15	-0.88	-0.29	0.08	0.02
CGPLH435	0.22	0.26	-0.20	-0.53	-1.86	-1.19	0.42	-0.09	0.76	-2.55	-0.48	-1.14	1.31	-2.07	0.66	-0.13	-1.73	0.16	-0.45	0.94
CGPLH436	-0.06	0.11	-0.53	-0.58	0.10	0.44	0.86	1.67	0.30	0.47	-0.82	0.90	-1.18	1.44	0.24	-0.17	1.06	-1.18	-0.34	-0.63
CGPLH437	0.00	0.48	-0.04	-0.97	-0.56	-0.01	0.46	-0.81	0.54	-1.75	-0.90	-0.95	-1.44	-0.58	0.24	-0.70	-0.49	-0.95	-0.65	-0.08
CGPLH438	0.19	-0.02	-0.56	0.07	-0.29	-0.01	0.75	1.38	0.96	-0.42	-1.13	0.81	0.03	0.70	-0.40	0.13	1.15	-0.47	-1.07	-0.54
CGPLH439	1.01	-0.70	-1.26	-1.06	-0.91	0.76	0.74	2.43	1.29	-2.18	-1.68	0.45	-1.57	1.47	-0.15	-0.28	2.17	-0.92	-0.86	-0.48
CGPLH440	0.65	1.15	0.59	-0.25	-1.87	1.21	-0.52	0.87	-0.31	0.46	-0.57	0.36	-0.49	0.74	0.36	-0.33	0.10	-1.20	-0.37	-0.12
CGPLH441	0.79	-0.03	-1.18	-0.63	-1.07	0.31	-0.31	0.84	0.06	-1.16	-0.29	0.60	0.37	0.50	-0.54	-0.48	0.55	-0.45	-0.64	-0.55
CGPLH442	0.99	1.62	0.10	0.16	-1.13	1.04	-0.55	-0.33	-0.88	-0.73	0.78	-0.47	-1.76	0.02	-1.89	0.08	-1.70	-0.15	0.23	-0.02
CGPLH443	0.57	0.85	1.84	0.67	0.06	0.61	0.18	2.62	0.30	0.87	-0.20	1.79	0.96	2.10	0.58	-0.49	0.39	-0.17	0.42	1.32
CGPLH444	1.29	1.69	1.00	-0.44	-2.29	0.34	-1.59	1.01	-1.35	-1.06	0.91	-0.65	-1.65	-0.96	-0.47	-1.70	-1.08	0.08	1.72	0.99
CGPLH445	0.33	0.71	-0.40	-0.27	-1.70	1.42	-0.18	1.42	0.58	0.18	-0.70	0.77	0.08	0.57	0.56	0.28	0.82	-1.28	-0.16	0.18
CGPLH446	1.50	1.32	1.56	0.33	-0.56	0.19	-1.60	1.21	-0.18	-0.35	1.06	0.48	-0.50	0.03	-0.55	0.15	-0.45	0.26	1.33	0.17
CGPLH447	1.20	0.66	-0.55	-0.32	-1.35	0.49	-0.53	1.13	0.09	-0.98	-0.74	-0.09	-1.60	0.45	-0.15	-0.11	2.74	-0.05	0.15	-0.80

CGPLH448	-0.03	0.64	-0.05	-1.29	-1.75	0.74	0.68	0.60	0.61	-1.32	-0.22	0.09	-1.34	1.25	-0.04	-0.94	0.69	-0.97	-0.06	-0.49
CGPLH449	2.09	1.10	1.38	-0.13	-2.59	0.71	-1.48	0.41	-2.02	-0.94	1.51	-0.82	-0.66	-1.49	-0.46	-1.95	-1.61	1.39	1.09	0.59
CGPLH450	0.05	0.76	0.11	-1.21	-2.50	-0.48	-0.59	-0.68	-0.13	-1.42	-0.67	-1.65	-1.14	0.25	-1.12	-0.83	-0.22	-0.96	-0.67	-0.55
CGPLH451	1.43	0.78	0.74	-0.36	-1.74	1.04	-0.83	1.17	-0.58	-1.50	0.03	-0.78	-1.65	-0.90	-0.67	-0.16	-0.08	0.63	0.93	1.00
CGPLH452	0.29	1.35	1.20	0.57	-1.08	0.88	-0.38	2.38	-0.01	2.40	-0.06	1.42	-0.43	0.66	-1.19	0.84	0.54	-1.11	0.44	-0.40
CGPLH453	0.26	0.90	0.63	-1.12	-2.14	-0.65	-0.56	-1.75	-0.72	-2.43	1.20	-1.99	-1.73	-1.39	0.24	-0.66	-1.45	0.96	0.61	0.11
CGPLH455	1.22	1.89	0.91	0.65	0.32	2.26	-0.75	0.87	-1.13	2.00	0.82	1.26	0.49	1.49	-1.62	1.44	-1.69	-0.70	-0.58	-0.61
CGPLH456	1.11	-0.20	-0.81	-1.24	-1.93	0.41	0.12	2.26	-0.09	-1.18	-1.20	0.78	-1.21	1.03	0.34	-0.22	1.41	-1.34	-0.63	-1.25
CGPLH457	0.42	0.19	-0.57	-0.86	-1.06	-0.19	-0.37	1.09	1.82	-0.55	-0.97	0.66	-1.34	0.23	-0.20	-0.46	1.14	-1.36	0.72	-0.67
CGPLH458	1.45	2.02	1.44	1.86	-0.53	3.01	-1.21	2.54	-1.19	0.75	1.08	2.56	-1.70	0.17	-2.46	0.59	-0.38	0.15	0.69	0.35
CGPLH459	0.39	1.37	0.83	0.11	-1.90	-0.17	-0.64	0.89	-0.66	-0.34	0.74	0.18	0.20	-0.21	0.08	-0.74	-0.37	0.56	1.01	0.30
CGPLH460	0.19	0.24	-0.55	-2.10	-2.84	-1.19	-0.31	-0.49	-0.16	-3.54	-0.37	-1.29	0.06	-1.10	-0.71	-2.89	-0.71	-1.08	-0.60	-0.79
CGPLH463	-0.43	-0.06	-0.68	-1.57	-1.26	0.33	-0.36	-0.90	0.79	-1.34	-0.05	-1.11	-1.77	-0.79	-0.35	-1.44	0.45	0.14	-0.65	-0.70
CGPLH464	1.22	0.44	-0.73	0.27	-1.47	0.26	0.44	3.48	0.23	-0.82	-0.39	0.26	0.37	1.20	-0.14	-0.09	0.53	-0.87	0.37	-0.18
CGPLH465	1.44	0.42	0.25	-0.27	-0.51	0.09	0.01	1.04	0.01	-0.74	-0.59	-0.03	-2.46	-0.97	-0.47	-0.12	0.81	0.15	0.12	0.16
CGPLH466	0.74	0.62	-0.44	-1.61	-0.63	-0.20	-0.48	-1.66	-0.49	-0.93	0.85	-1.03	-1.31	-1.73	-1.02	-2.23	-0.91	-0.29	0.69	-1.02
CGPLH467	0.53	0.87	-0.11	0.99	0.11	1.55	0.09	2.26	0.60	0.75	-0.30	1.38	-0.63	1.40	1.50	1.26	0.14	-0.67	-0.51	-0.21
CGPLH468	-0.93	-0.18	-0.63	-0.70	-0.95	-0.25	1.10	1.60	1.48	-1.00	-0.92	0.34	0.07	0.35	0.78	0.02	1.09	-0.62	0.05	-1.18
CGPLH469	1.26	0.91	-0.46	0.83	-0.58	1.12	0.15	3.49	0.59	0.64	-0.61	2.77	-0.40	1.92	0.73	1.78	0.96	-0.93	0.18	-0.29
CGPLH470	-0.20	0.47	-0.11	-1.08	-0.07	0.10	0.70	-0.77	0.65	-1.93	-0.45	-0.63	-0.51	-0.52	0.10	0.44	-0.36	0.23	-0.86	-0.03
CGPLH471	-0.35	0.76	-0.70	-0.97	-1.70	-0.76	0.84	-0.84	0.08	-0.82	-0.01	-0.29	-0.96	-0.61	-0.32	-0.16	-1.12	-0.59	0.16	-0.61
CGPLH472	-1.55	0.44	-0.07	-1.28	-0.36	0.09	1.41	1.13	2.29	-1.12	-0.55	0.08	-0.14	0.48	-0.44	0.63	-0.09	-1.44	-0.17	-1.20
CGPLH473	-0.78	-0.05	-0.24	-0.91	-1.24	0.37	1.00	2.46	0.64	0.38	-1.29	1.19	-0.43	0.93	0.03	0.28	1.49	-2.04	-1.05	-1.30
CGPLH474	-1.34	-0.62	-0.65	-0.27	-2.31	-1.70	1.30	0.34	1.70	-1.65	-1.77	1.04	0.06	0.37	1.34	0.21	-0.46	-0.29	-0.39	0.12
CGPLH475	0.08	0.82	-1.40	-0.77	-1.50	0.53	-0.12	1.27	0.52	-0.69	-0.61	0.79	-1.43	1.25	0.17	0.43	0.40	-0.73	-0.32	-0.51
CGPLH476	-0.24	0.54	-1.13	-0.92	-1.27	0.35	0.87	0.89	1.34	-0.13	-1.70	0.39	-0.31	2.07	0.02	-0.13	1.55	-0.31	-0.58	-0.64
CGPLH477	1.64	1.33	1.38	0.45	-0.83	0.37	-0.32	0.28	-1.34	-1.36	1.12	-0.33	-1.09	-0.51	-0.12	-0.92	-0.77	0.86	0.49	0.52
CGPLH478	-0.30	-0.15	0.95	-0.24	1.97	-0.20	0.62	-0.26	1.09	-0.59	-1.02	0.14	0.89	0.72	0.31	0.32	-0.15	0.34	0.90	0.96

CGPLH479	1.93	1.62	0.76	0.47	-0.68	1.64	-1.57	0.43	-0.78	-0.38	1.20	0.04	0.03	-0.65	-1.62	-0.12	-1.23	0.79	1.11	0.93
CGPLH480	0.54	0.87	0.99	0.48	-1.31	0.82	1.19	2.32	1.79	0.39	-0.77	0.32	1.06	1.80	0.46	2.22	0.22	-0.50	0.37	0.87
CGPLH481	0.31	0.53	0.15	-0.75	-1.84	-0.23	-0.54	1.74	0.31	-0.81	-0.24	0.27	-2.06	-0.35	0.32	-0.38	0.14	-0.57	0.24	-0.06
CGPLH482	0.31	0.34	-0.13	0.04	-1.56	-0.68	0.45	0.11	0.37	-0.72	-0.77	-0.47	0.05	-0.21	-0.32	-0.34	-1.18	0.01	-1.22	-0.03
CGPLH483	-0.20	0.54	-0.33	-1.70	-1.48	-0.17	0.38	-0.07	1.08	-0.27	-1.10	0.90	-0.61	1.01	-0.44	-1.47	0.20	-1.16	-1.04	-0.97
CGPLH484	0.63	-0.17	-0.42	-1.67	-0.98	-0.62	-0.19	-0.33	0.47	-2.07	-0.36	-1.39	-0.52	0.05	-0.61	-1.24	-0.19	-0.75	-0.13	-0.37
CGPLH485	-0.63	-0.04	-0.86	-1.47	-1.71	0.38	0.23	1.19	1.09	-1.53	-0.89	0.97	0.05	0.77	0.37	-0.07	0.82	-1.35	-0.04	-1.64
CGPLH486	1.45	1.41	-0.08	1.52	-1.03	1.39	-0.87	2.49	-0.33	-0.25	0.34	2.28	-0.05	0.33	1.13	0.35	0.82	-0.34	1.01	-0.15
CGPLH487	0.87	2.06	0.94	0.93	0.34	1.76	0.13	1.50	-0.35	0.94	1.07	0.52	-1.24	-0.35	1.76	0.39	-0.70	0.63	0.94	0.88
CGPLH488	2.40	0.94	1.58	0.45	-0.05	0.23	-0.58	0.47	-1.27	-1.11	1.71	-0.85	-0.48	-1.17	0.10	-0.90	-1.19	0.72	0.77	1.47
CGPLH490	3.13	3.57	1.44	1.54	0.28	2.47	-3.36	1.72	-2.75	2.02	3.30	1.36	-0.57	-0.66	-1.70	0.65	-0.45	1.82	1.95	1.92
CGPLH491	0.15	1.08	0.16	-0.18	-0.06	-0.38	0.10	1.31	0.86	-0.77	-0.26	1.13	-1.35	-1.12	0.44	0.92	0.02	0.01	-0.21	1.09
CGPLH492	1.16	-0.64	-0.54	-0.27	-0.65	0.27	0.52	2.26	0.87	-1.47	-0.94	0.74	0.28	0.50	0.91	0.96	1.02	-0.69	-0.73	0.21
CGPLH493	0.24	0.02	-1.07	-0.79	-1.52	-1.25	1.24	0.17	0.88	-2.19	-1.10	-1.13	-0.79	-0.61	0.54	-0.26	0.20	-0.04	-0.50	-1.30
CGPLH494	-0.38	-0.05	-0.30	-1.41	-1.03	-1.60	0.76	-0.25	0.62	-1.74	-1.47	-0.82	-1.14	-0.69	0.31	-0.93	0.46	-0.85	-0.30	-0.29
CGPLH495	0.61	0.95	0.46	0.54	-0.42	0.96	-1.55	0.90	-0.48	-0.51	0.85	1.37	-1.13	-1.03	-0.39	-0.91	0.87	0.56	0.20	1.16
CGPLH496	0.11	0.75	1.21	0.82	-0.11	0.82	0.83	1.48	0.63	0.61	0.18	1.51	1.77	-0.43	0.09	0.65	-0.50	-0.09	-0.12	-0.10
CGPLH497	0.12	0.35	0.50	0.12	-1.04	0.32	0.33	0.74	0.22	0.13	-0.01	0.59	-1.65	0.25	0.18	-0.44	0.19	-0.41	-0.24	0.36
CGPLH498	0.87	-0.57	-1.01	-0.44	-1.56	-0.83	-0.58	0.37	0.45	-1.15	-1.46	0.14	-0.21	-0.30	0.64	-0.50	0.74	-0.60	-0.13	0.20
CGPLH499	-0.02	0.38	-0.15	-0.38	-0.73	0.10	0.52	1.22	0.19	-1.16	-0.30	0.53	-0.48	-0.25	0.21	-0.43	0.38	-0.39	-0.60	0.03
CGPLH500	-0.77	-0.39	0.16	-0.44	-0.92	-0.68	0.65	0.39	1.23	-2.36	-1.01	0.41	-0.53	0.11	-0.21	-1.06	0.33	-1.47	-0.74	-0.26
CGPLH501	1.62	0.46	1.13	0.16	0.00	0.02	-0.24	1.30	0.70	-0.84	-0.45	0.17	0.46	-0.06	1.02	0.25	0.53	0.49	0.11	1.45
CGPLH502	-0.15	-0.37	-0.02	-0.84	-1.89	-0.95	-0.31	-0.11	1.03	-2.39	-1.97	-0.05	1.88	-0.95	0.04	-1.21	-0.34	-0.33	-0.58	-0.58
CGPLH503	0.53	-0.15	0.55	0.16	0.48	-0.04	0.91	0.33	1.35	0.24	-0.45	0.40	0.59	-1.71	0.72	1.84	-0.16	0.51	0.13	1.44
CGPLH504	-0.63	-0.21	-0.44	-0.34	-0.55	-0.46	0.69	1.04	1.12	-1.14	-1.19	0.76	0.58	1.14	0.07	-0.61	0.57	-1.33	-0.37	-0.31
CGPLH505	0.61	1.34	1.83	0.30	-1.16	-0.25	-0.60	-0.33	0.12	0.33	1.11	0.58	1.15	-0.76	-0.45	-1.31	-1.02	0.61	-0.10	1.30
CGPLH506	-0.47	-0.01	0.26	-0.60	-0.62	-0.78	0.96	0.49	1.35	-0.70	-1.22	-0.19	0.73	-0.65	0.26	-0.30	0.42	-0.57	-1.21	0.13
CGPLH507	2.67	1.98	2.10	0.57	0.64	1.76	-0.49	0.80	-1.12	1.26	1.18	0.57	1.91	-0.90	-0.23	1.21	-1.66	2.36	1.12	1.85

CGPLH508	1.71	1.51	3.10	0.80	-0.80	-0.60	-1.80	-1.59	-1.33	-0.89	2.01	-1.23	-0.44	-1.95	-0.52	-0.69	-1.31	2.93	1.50	2.82
CGPLH509	0.69	0.85	0.56	-0.17	0.50	0.03	-0.48	-1.12	-0.21	-0.79	0.63	-0.04	0.69	-1.67	-0.95	-0.44	-1.62	0.44	0.54	2.00
CGPLH510	1.08	1.39	1.34	0.99	-0.36	-0.28	-0.94	-0.22	-1.05	-0.55	1.71	-1.37	-0.07	-2.40	-0.81	-0.66	-1.87	1.05	1.05	1.08
CGPLH511	0.46	0.92	1.09	1.89	0.42	0.54	1.59	0.06	1.59	1.97	-1.50	1.32	0.53	-0.72	1.18	2.44	-0.87	0.43	-0.46	1.48
CGPLH512	0.37	1.07	0.57	0.85	-0.19	0.32	0.09	0.76	0.20	-0.21	0.16	0.84	0.74	-0.95	-0.46	0.70	-0.65	0.08	-0.20	0.84
CGPLH513	-0.86	-0.65	1.45	-0.26	0.48	-0.45	0.75	0.10	1.48	-0.98	-0.68	-0.02	1.35	-0.86	0.91	-0.78	-0.53	-0.57	-0.70	0.50
CGPLH514	0.75	0.56	-0.01	0.21	-0.54	0.19	0.08	-0.50	-0.14	-1.23	0.25	0.76	-0.33	-0.83	0.07	0.81	-0.04	0.29	-0.68	-0.13
CGPLH515	-0.03	0.24	1.15	0.78	1.11	0.74	0.54	0.98	1.14	0.94	0.14	0.61	-0.06	-0.68	0.27	1.13	0.20	0.30	-1.07	1.06
CGPLH516	0.26	0.50	0.72	-0.46	-0.27	-0.19	-0.09	0.68	0.32	-0.92	-0.06	0.55	0.09	-0.29	0.22	0.38	0.33	-0.46	-0.46	0.46
CGPLH517	1.02	-0.16	-0.38	-1.29	-0.86	-1.20	0.00	0.15	0.54	-1.50	-0.79	-0.51	-2.46	-0.86	1.41	-0.23	0.32	-0.11	-0.54	-0.55
CGPLH518	0.62	-0.75	0.03	-0.12	-0.20	-0.49	0.29	0.17	1.20	-1.22	-1.33	-0.30	-0.07	-0.49	-0.11	0.17	0.87	-0.35	-0.34	0.45
CGPLH519	-0.02	0.27	-0.44	-0.69	0.16	0.75	1.12	0.54	1.15	-0.95	-0.73	0.23	0.62	-0.22	-0.02	0.84	0.14	-0.76	-0.72	-0.17
CGPLH520	0.08	0.16	-0.10	-1.24	-1.15	-1.49	0.64	-0.44	1.43	-0.85	-0.25	-1.40	0.49	-1.45	-0.09	-1.08	-0.36	-0.76	-0.03	0.47
CGPLH625	-0.18	0.60	-0.50	0.11	-0.32	1.39	0.92	1.28	0.97	0.39	-0.02	0.41	-0.43	0.53	-1.02	1.09	1.24	-0.56	0.24	-0.17
CGPLH626	0.15	-1.68	-1.03	-1.24	-1.10	-1.57	0.97	0.33	2.19	-3.21	-2.08	-0.90	0.82	-1.07	1.50	-1.52	0.88	-0.47	-0.12	0.02
CGPLH639	0.65	1.49	0.43	0.09	0.71	1.35	0.25	1.02	0.70	-0.40	0.13	0.50	-0.75	-0.68	-1.10	0.42	-0.16	0.21	-0.84	0.72
CGPLH640	0.45	-0.20	-1.94	-0.96	0.26	0.25	1.85	0.72	1.77	-1.97	-1.93	-1.31	-0.96	0.01	0.88	0.28	2.03	-0.91	-2.05	-0.18
CGPLH642	0.69	1.02	1.03	0.09	1.12	0.16	0.22	0.74	1.20	0.57	0.13	0.88	1.83	-0.21	0.55	0.87	-0.12	0.70	-0.65	0.24
CGPLH643	-0.24	0.48	-0.72	0.17	0.39	0.67	0.96	0.98	0.95	0.22	-0.59	1.18	-0.40	0.21	0.38	0.71	1.08	0.12	-0.27	-0.13
CGPLH644	1.69	0.83	0.58	0.64	2.01	1.87	1.27	2.32	1.04	1.50	-0.35	1.40	1.11	0.73	0.15	1.40	1.30	0.79	-0.89	0.49
CGPLH646	1.12	-0.73	-1.09	-0.73	-0.03	-0.06	0.04	0.14	0.51	-2.06	-0.42	0.05	-0.64	-0.43	-0.11	0.40	1.13	-0.74	-0.42	-0.17
CGPLLU144	-2.34	2.97	-3.66	-2.71	-8.92	-0.81	4.73	-1.91	9.18	-11.06	-2.04	-7.98	24.38	2.88	-5.74	7.34	4.02	2.59	-3.50	-3.63
CGPLLU161	-0.78	-0.19	-0.15	1.16	-1.59	0.12	1.02	0.56	-0.05	-0.30	-0.36	1.96	3.64	-0.35	0.95	2.16	-1.10	1.21	0.84	0.51
CGPLLU162	-1.78	0.45	0.25	0.38	-0.55	0.50	1.75	1.54	1.44	1.45	-0.26	1.21	2.54	1.42	0.95	2.10	-0.18	-1.28	0.56	-0.26
CGPLLU163	5.82	10.72	12.44	-1.81	-21.42	-3.98	4.82	-8.21	4.24	50.72	-4.70	-22.62	-6.10	20.22	-37.27	22.85	-17.45	-10.59	7.76	27.67
CGPLLU168	-1.64	0.36	-0.74	-0.19	-0.37	0.19	1.60	0.27	0.97	0.38	-0.17	1.07	-0.80	1.09	-0.81	0.19	0.89	-2.24	-1.13	-2.28
CGPLLU169	-1.31	0.81	-0.17	-0.81	0.10	0.24	1.44	0.45	1.36	-1.27	-0.39	0.14	-0.39	0.24	-0.06	0.69	0.54	-1.64	-1.32	-1.02
CGPLLU176	-0.42	0.71	0.42	0.67	-0.29	0.87	0.44	1.10	0.95	0.23	-0.68	1.14	0.64	0.12	0.86	0.56	0.23	-0.79	-0.36	-0.19

CGPLLU177	-2.21	4.18	3.02	1.88	-0.56	0.46	0.19	-3.21	3.59	-4.82	-0.16	-3.71	17.36	-0.01	3.03	11.20	-0.66	-0.53	-0.73	-0.16
CGPLLU203	-1.17	0.35	-0.78	-1.38	0.21	-0.70	1.23	-0.63	1.56	-1.36	-0.49	0.25	-0.70	1.43	0.46	0.07	1.14	-1.15	-0.75	-0.79
CGPLLU205	-1.27	0.50	-0.05	-1.06	0.61	0.57	1.12	-0.10	0.90	-1.06	-0.09	-0.30	0.65	0.59	0.37	0.01	0.51	-1.28	-0.72	-0.82
CGPLLU207	-0.64	0.56	-1.00	-0.96	-0.68	0.46	1.05	1.28	2.19	-1.09	-0.34	-0.24	2.92	1.80	-0.31	1.41	1.50	-2.40	-0.90	-1.47
CGPLLU208	-0.87	0.56	-2.27	-0.20	-1.74	-1.66	2.08	1.37	2.61	4.79	0.54	-1.46	4.10	4.62	-0.41	0.00	-0.20	-1.39	0.27	-2.29
CGPLOV11	1.20	1.67	1.86	1.30	-1.07	8.52	-1.66	-1.38	2.53	-1.91	1.28	-1.00	-7.61	1.16	-1.04	6.40	0.25	1.85	2.36	0.35
CGPLOV12	-1.48	-0.07	0.13	1.09	-0.56	0.21	1.11	1.43	1.64	-0.41	-0.63	0.98	1.50	1.77	0.22	2.02	-0.62	-0.44	0.55	0.48
CGPLOV13	-0.69	-0.84	-0.39	-0.93	-1.50	-0.88	0.49	-0.99	1.58	-2.13	-0.76	-0.51	0.23	0.16	-1.40	1.74	-0.37	-0.09	-0.09	0.25
CGPLOV15	3.32	1.00	-0.37	-0.88	-3.97	15.58	0.49	-7.03	6.64	-13.00	5.05	-5.87	1.45	-4.33	-4.49	10.96	5.50	-2.53	11.48	-5.62
CGPLOV16	-1.60	3.69	3.29	-0.49	-6.81	-1.66	0.09	-4.80	1.03	-5.25	1.81	-3.91	1.97	1.61	-1.61	3.37	2.82	0.08	0.19	0.55
CGPLOV19	-23.77	6.52	37.96	41.52	-38.08	-35.07	-23.07	-36.72	70.28	-122.55	5.31	-25.80	147.22	123.89	-139.74	270.41	10.05	10.50	-4.69	-4.85
CGPLOV20	-2.17	-0.02	-0.06	0.20	0.51	1.08	2.56	2.22	2.61	0.37	-1.49	1.03	0.47	2.84	1.30	2.58	1.86	-1.52	-1.32	-1.25
CGPLOV21	-5.16	-3.11	-2.52	4.58	-6.96	2.39	1.12	-2.29	10.22	-9.45	-1.27	-0.76	3.79	2.59	1.31	-0.21	-3.31	-3.76	3.49	-1.17
CGPLOV22	-0.75	0.96	0.31	0.09	-0.69	-0.29	-0.77	-0.70	0.17	-1.59	0.09	-1.01	1.07	1.50	-0.65	0.05	-1.05	-0.24	-0.23	-0.77
CGPLOV23	-2.35	0.55	-2.86	-1.26	-0.11	-0.26	1.57	-0.76	4.10	-5.00	-0.80	-1.22	0.30	5.08	0.66	2.61	1.07	-2.80	0.83	-0.95
CGPLOV24	-0.06	0.42	-0.25	0.00	0.94	-1.06	1.58	-0.40	1.10	0.85	-0.01	-0.04	-0.03	-0.63	1.56	1.81	1.45	-0.11	-0.97	0.03
CGPLOV25	-0.06	0.98	0.09	-0.51	1.27	0.49	1.58	1.28	0.89	0.08	0.11	-0.26	-1.42	-0.67	0.79	1.26	0.88	0.07	-1.08	-0.08
CGPLOV26	-1.30	0.18	-1.26	-0.55	0.45	0.89	2.40	1.95	2.24	0.64	-1.16	0.17	0.41	1.58	1.41	2.10	1.25	-1.79	-1.22	-1.19
CGPLOV28	-0.55	0.44	-0.70	0.18	-0.42	0.09	0.21	0.77	-0.57	-0.79	-0.59	0.48	0.84	0.89	-0.84	0.00	0.17	-0.60	0.22	-0.70
CGPLOV31	-0.43	-0.20	-0.66	-0.77	-0.44	-0.99	0.08	0.27	0.48	-0.95	-0.71	-1.21	-0.26	1.41	-0.69	0.25	0.36	-1.14	0.57	-0.33
CGPLOV32	-0.58	-0.44	-0.37	0.18	-0.04	-0.04	1.01	0.82	1.00	-0.66	-0.93	0.87	2.33	0.91	-0.15	0.38	0.08	-0.91	0.70	0.43
CGPLOV37	-0.91	-1.01	-1.09	0.47	-1.95	-0.85	1.06	1.30	2.90	-3.94	-1.82	0.62	3.89	3.43	2.34	2.67	1.12	-1.67	0.47	0.68
CGPLOV38	1.00	1.59	3.58	10.24	9.45	28.92	-8.82	-13.11	5.28	-1.17	2.02	-13.32	-3.26	11.27	-10.25	27.00	3.52	1.24	0.63	-0.76
CGPLOV40	-4.89	-2.03	0.73	-0.61	-1.98	-2.15	3.55	2.41	6.68	-2.06	-2.80	0.07	4.71	2.67	2.99	3.15	0.74	-4.31	1.30	-0.43
CGPLOV41	-0.76	-0.27	0.43	0.92	-1.25	2.21	-0.50	-1.12	0.02	-1.89	-0.94	-0.07	2.80	2.80	-0.37	-0.49	-0.56	-0.53	0.20	0.09
CGPLOV42	-1.22	0.41	0.50	-0.80	-1.63	-0.82	1.81	-4.42	0.35	-1.26	-0.93	-4.31	0.73	1.26	-1.26	9.54	-0.10	-0.37	1.05	-1.96
CGPLOV43	0.78	1.14	0.64	0.61	-0.39	1.87	-0.18	2.29	0.17	1.14	0.64	1.73	0.85	1.28	0.37	1.11	0.26	0.47	0.30	0.10
CGPLOV44	-2.11	0.57	-0.45	-0.20	-0.01	-0.03	1.60	2.35	3.25	0.73	-1.19	1.87	1.08	2.61	1.38	1.41	0.93	-2.78	-0.86	-1.06

CGPLOV46	-1.46	-0.28	-0.66	-0.71	-0.99	-0.52	1.47	1.30	2.11	-0.38	-1.92	0.18	-1.24	1.68	0.01	0.57	0.89	-2.38	-0.41	-0.71
CGPLOV47	0.39	0.33	0.58	0.20	-0.36	0.12	0.45	-0.25	0.80	-0.99	-0.41	-1.66	-1.06	-0.37	0.27	0.22	-0.04	-0.08	-0.85	0.99
CGPLOV48	1.02	1.56	1.14	1.18	-0.08	2.90	-1.65	0.42	-0.87	-0.21	1.38	-1.10	-0.56	0.52	-1.37	1.17	-0.46	1.87	1.86	1.42
CGPLOV49	-1.47	-0.32	1.25	5.85	-2.85	2.69	-1.62	-4.03	3.20	-1.10	0.63	-4.05	3.93	2.87	-2.30	17.87	3.93	-0.58	2.68	3.33
CGPLOV50	-1.73	-0.54	-0.66	-0.80	-0.37	-0.27	1.93	1.70	2.65	-0.60	-2.02	0.79	1.40	2.92	2.55	2.29	1.58	-2.35	-0.70	-0.51
CGPLPA112	0.64	0.78	0.74	0.47	-0.25	0.29	0.37	-0.60	0.02	-0.31	0.71	-1.04	-0.14	-1.00	0.67	0.84	-1.12	0.45	0.47	0.99
CGPLPA113	-1.54	-0.21	1.97	1.44	1.80	-0.68	2.48	4.63	3.73	3.89	-1.85	2.75	3.53	1.65	2.87	5.75	1.57	-2.30	0.91	1.42
CGPLPA114	-0.90	-0.03	-0.03	-0.86	-1.08	-1.48	1.15	-0.65	1.52	-1.11	-1.08	-0.25	1.49	-0.25	0.31	0.37	0.41	-1.13	-0.63	-0.68
CGPLPA115	-3.51	5.72	10.03	-2.36	25.33	30.59	-5.73	-8.67	2.07	10.88	-4.18	-11.83	21.42	12.41	2.13	11.85	6.68	1.65	-7.17	-7.87
CGPLPA117	-1.35	0.44	-0.58	-0.54	-1.51	0.68	0.78	3.21	2.06	0.32	-0.80	-0.22	0.39	1.56	-0.40	-0.88	0.29	-2.38	0.31	-2.23
CGPLPA118	-0.09	0.44	1.18	0.51	1.87	0.47	1.88	1.84	1.61	0.99	0.34	0.48	1.70	-0.43	-0.70	2.66	0.88	-1.13	0.30	0.56
CGPLPA122	-2.06	0.16	1.25	0.59	2.97	0.12	4.02	2.52	4.22	2.23	-0.86	2.84	4.30	3.60	-5.16	5.54	0.88	-2.09	-0.14	0.65
CGPLPA124	-0.41	0.50	0.17	0.10	-0.55	-0.69	0.97	1.19	1.44	0.31	-1.41	2.59	-0.80	1.63	0.60	0.81	0.51	-1.55	-0.50	-0.33
CGPLPA125	1.00	1.16	0.25	0.86	1.25	1.25	0.76	1.91	1.09	0.90	-0.30	1.66	-1.32	0.72	-1.23	0.78	0.98	-0.72	-1.04	0.66
CGPLPA126	-2.30	-0.73	-0.44	-0.63	0.55	-1.94	2.47	1.40	3.35	-1.34	-1.87	1.61	2.60	1.36	1.10	1.18	-0.31	-1.51	0.55	0.35
CGPLPA127	-1.50	0.90	1.55	0.75	2.48	0.16	2.57	2.17	2.41	2.72	0.40	2.35	3.23	2.24	-0.49	3.92	0.44	-1.24	-0.14	0.88
CGPLPA128	-0.50	0.14	0.84	0.68	-1.11	0.09	1.01	1.51	1.25	1.19	-0.15	2.04	0.92	0.70	0.00	-0.22	0.50	-0.16	0.72	0.50
CGPLPA129	-2.28	-1.13	-0.25	-0.10	0.19	-1.56	2.33	2.35	2.63	0.61	-1.87	2.33	1.92	1.67	2.86	1.71	0.82	-1.49	0.07	0.06
CGPLPA130	-0.26	-0.08	-0.42	1.16	-0.33	0.46	0.88	2.94	2.20	0.47	-0.65	1.62	1.48	0.26	1.32	2.81	1.30	-0.47	1.30	1.11
CGPLPA131	-0.75	-0.48	-0.98	0.22	-2.80	-1.61	0.79	-1.66	0.50	-0.65	-2.39	-2.42	0.78	-2.45	-0.82	-0.95	-1.61	-0.39	-0.08	0.30
CGPLPA134	-1.13	-0.81	1.48	1.47	-1.28	-1.86	1.59	-1.43	1.65	-0.99	-0.40	0.87	2.80	-2.07	0.96	1.00	-1.53	1.04	0.39	1.53
CGPLPA135	0.62	1.62	1.11	0.97	1.90	0.91	0.52	0.04	0.67	1.40	1.04	0.11	-1.40	-0.54	-0.54	2.19	-0.06	0.14	-0.05	1.85
CGPLPA136	0.16	0.73	2.02	1.83	0.07	0.03	0.04	0.31	0.04	0.80	0.34	2.47	2.35	-1.37	1.95	1.44	-0.90	1.81	0.87	1.66
CGPLPA137	0.58	1.51	1.04	1.33	0.61	1.43	0.74	1.10	1.42	1.57	-0.25	1.49	-0.19	-0.89	0.32	2.23	0.69	-0.84	-0.51	0.11
CGPLPA139	0.75	0.19	1.04	-0.06	0.30	0.16	0.26	-1.57	0.92	0.67	0.04	-1.14	0.48	-1.48	-0.18	1.05	-0.69	1.22	-1.35	1.43
CGPLPA14	-1.53	-0.59	0.24	0.22	4.62	0.24	1.52	1.00	2.00	0.82	-0.69	0.13	0.70	0.38	2.73	2.55	1.50	-0.81	-0.05	-1.15
CGPLPA140	-2.71	-1.54	-0.62	-0.47	-2.22	-2.64	1.61	-0.82	1.98	-3.54	-1.70	-0.35	2.96	-0.21	-0.16	-0.02	-0.80	-0.79	-0.12	-0.20
CGPLPA141	-3.31	-1.59	-0.41	-0.09	1.14	-1.81	1.64	-1.18	1.97	-1.37	-0.41	-0.18	3.76	0.51	1.40	1.73	-1.17	-0.63	0.59	-0.54

CGPLPA15	0.43	0.97	-0.52	1.41	1.39	2.21	1.57	1.25	0.64	0.90	0.44	1.70	0.20	0.64	1.27	2.08	1.38	0.19	-0.81	0.14
CGPLPA155	1.57	0.94	1.42	2.33	1.88	0.29	1.28	0.59	1.09	2.80	0.13	0.28	1.28	-1.19	1.52	3.49	-0.83	1.26	-1.00	2.09
CGPLPA156	0.29	0.52	-0.56	-0.11	-0.95	0.29	0.05	-0.07	0.78	-1.10	-0.58	0.00	-0.08	-0.17	0.79	0.52	-0.05	-0.85	-0.46	0.19
CGPLPA165	0.19	-0.13	0.11	-0.28	1.93	-0.49	1.71	-0.59	1.84	-0.02	-0.47	-0.19	-0.86	-1.08	1.35	-0.16	-0.16	-0.90	-1.40	1.16
CGPLPA168	-4.21	-1.58	-0.13	0.62	1.56	-0.65	4.62	3.48	6.17	1.33	-2.99	2.25	5.94	2.19	2.16	4.74	0.20	-3.09	0.83	1.10
CGPLPA17	-7.74	-3.20	-1.69	-3.24	-0.22	-7.59	2.40	-2.64	9.57	-10.23	-3.41	-0.45	7.03	-2.37	7.13	1.49	-6.00	-3.73	3.15	-3.25
CGPLPA184	-1.25	-0.74	0.61	-0.24	0.18	-1.98	2.11	-1.60	2.07	-0.81	-0.61	-0.98	1.36	-0.87	0.82	2.27	0.09	0.33	-1.06	1.00
CGPLPA187	0.46	1.48	0.43	1.91	1.13	0.68	1.15	0.19	0.88	1.84	0.51	1.21	2.61	-0.39	0.05	3.14	-0.27	0.40	0.46	1.09
CGPLPA23	-4.65	-0.99	-0.90	-1.19	3.76	-1.34	4.84	1.29	4.65	0.93	-1.09	0.33	3.32	1.79	-2.64	7.57	0.76	-3.78	-1.10	-3.13
CGPLPA25	-0.83	0.72	-0.71	-0.39	0.63	-0.59	1.56	-0.54	1.44	1.01	-1.35	-0.02	0.31	0.53	0.47	1.25	0.42	-0.68	-1.14	-0.43
CGPLPA26	-0.12	0.99	0.65	0.13	1.37	0.69	0.06	-0.26	0.04	-0.72	0.21	-0.46	2.42	-0.93	-0.58	-0.26	-0.64	-0.23	-0.30	0.36
CGPLPA28	-1.31	0.57	-1.09	-0.42	1.21	0.01	1.86	1.80	2.06	-0.31	-2.43	1.59	1.17	1.10	1.25	1.85	0.94	-1.67	-1.49	-0.72
CGPLPA33	-2.08	-0.85	-0.09	-0.56	4.22	0.95	3.29	1.94	2.49	2.07	-0.59	-0.08	2.26	2.32	1.65	3.29	1.15	-1.38	0.09	-1.84
CGPLPA34	-1.23	-0.62	-0.60	-0.01	3.30	0.37	1.31	0.04	1.98	0.81	-1.34	-0.37	-0.92	-0.29	1.77	0.26	-1.12	-1.82	-0.82	-0.77
CGPLPA37	-1.34	-0.61	-0.58	0.17	3.06	0.27	2.24	0.01	2.24	-0.70	-0.40	0.04	3.27	-0.21	1.84	3.69	-0.38	0.31	-1.27	-0.60
CGPLPA38	-0.49	-0.82	-0.03	-0.53	3.68	0.76	1.92	0.35	1.28	0.39	-0.64	-1.23	-0.11	0.74	1.38	2.10	0.96	0.01	-1.29	-1.33
CGPLPA39	-2.82	-0.42	-0.55	-0.96	2.13	-0.93	2.44	-0.08	3.26	1.80	-0.66	-0.71	2.15	1.77	-0.35	3.30	0.89	-3.11	-0.58	-1.05
CGPLPA40	-1.93	-0.34	0.45	-0.42	4.21	-0.28	1.91	-0.47	3.07	1.60	-0.49	-0.93	2.77	-0.86	1.97	3.01	-0.54	-1.36	-0.42	-1.01
CGPLPA42	2.12	1.89	0.93	2.19	0.14	3.58	-1.15	0.46	-0.53	2.18	1.86	-0.36	0.44	-0.86	0.47	0.83	-0.11	0.72	0.74	0.27
CGPLPA46	-6.36	-1.53	-1.33	-2.16	2.68	-4.76	1.38	-1.00	5.85	-5.48	-1.00	-0.65	6.58	-0.72	6.20	3.03	-3.07	-4.05	3.67	-3.54
CGPLPA47	-4.13	-2.22	-1.14	-1.85	3.51	-3.36	2.94	-3.24	4.67	-3.15	-1.20	-2.08	2.56	-0.50	4.05	2.74	-1.60	-1.66	0.45	-3.24
CGPLPA48	-0.12	0.38	-0.15	0.49	0.96	-0.49	0.60	-0.30	0.52	-0.01	0.07	1.12	-0.40	-0.24	0.92	1.72	-0.02	-0.57	-0.56	-0.41
CGPLPA52	0.25	-0.28	-0.48	-1.57	0.57	-0.78	1.00	1.70	1.73	-1.46	-1.27	0.17	-0.84	-0.25	0.13	-0.62	1.08	-0.83	-1.24	-0.43
CGPLPA53	-0.70	0.67	1.47	0.31	0.51	-0.79	1.75	-0.30	1.72	0.39	0.55	-0.78	1.22	-0.46	-0.08	1.72	0.16	-0.97	-0.91	-0.21
CGPLPA58	-0.39	0.10	-0.40	-1.17	-0.24	-0.92	-0.03	0.11	0.47	-0.10	-0.59	-1.27	0.05	0.74	-0.56	0.81	0.02	-1.24	0.58	-0.72
CGPLPA59	-2.28	-0.19	-1.16	-1.53	-0.01	-0.80	2.16	1.39	2.23	-0.27	-1.27	-0.47	-0.18	0.84	0.29	0.62	0.84	-3.70	-1.08	-1.44
CGPLPA67	0.04	1.64	1.06	0.39	0.41	1.18	0.60	0.54	0.84	0.25	-0.53	0.04	0.99	-1.22	0.79	1.38	0.01	0.34	-0.18	0.62
CGPLPA69	0.74	1.19	0.39	0.76	-0.83	2.14	-0.95	2.26	-0.58	0.42	0.39	0.67	-0.72	0.59	-0.43	-0.36	0.10	0.19	0.49	0.20

CGPLPA71	1.46	0.77	1.01	1.24	0.82	2.07	0.34	2.59	-0.46	0.06	0.54	1.62	1.17	0.69	-0.95	1.16	0.00	-0.45	-0.06	0.44
CGPLPA74	0.89	1.50	1.13	-0.97	-1.39	-0.95	-0.85	-0.94	-0.22	-0.94	0.64	-1.10	1.02	-1.46	-1.41	-1.08	-1.46	-0.40	0.79	0.60
CGPLPA76	-0.58	0.47	0.89	-0.64	-0.20	-1.54	0.42	-1.87	0.43	-1.25	0.07	-2.22	0.75	-1.71	-0.76	-0.52	-1.62	0.07	-0.61	0.91
CGPLPA85	-0.56	1.11	0.06	-0.38	-2.29	1.06	-0.18	0.48	-0.23	-1.20	-0.87	0.91	0.40	1.79	-0.17	0.69	-0.94	-0.19	-0.48	-0.55
CGPLPA86	-2.21	0.70	0.56	-0.07	2.24	0.03	2.47	2.79	3.66	1.92	-0.28	2.24	0.81	2.12	0.65	3.31	1.19	-3.76	0.00	-0.70
CGPLPA92	-0.15	0.72	-0.54	-1.43	-0.35	0.34	0.15	0.04	-0.25	-0.09	0.52	0.47	0.05	-0.65	-0.70	-1.08	0.24	-1.27	-0.34	-1.54
CGPLPA93	-3.48	-0.04	0.36	-0.09	0.97	-1.12	3.77	2.28	3.85	0.71	-2.01	1.30	4.11	4.26	1.07	2.78	0.73	-3.41	0.00	0.03
CGPLPA94	0.44	1.90	2.59	2.51	1.23	1.27	0.29	0.45	0.11	2.26	0.57	0.63	2.12	1.07	0.55	3.49	-0.65	1.16	1.42	1.25
CGPLPA95	-2.95	-0.66	-0.18	-0.61	3.29	-0.32	2.70	-0.57	4.29	1.72	-0.62	0.46	3.02	-0.48	0.80	5.63	1.17	-1.60	-0.57	-0.91
CGST102	1.84	2.14	0.98	1.49	-0.07	3.48	-0.71	1.87	-1.21	1.19	1.86	0.98	-0.08	-1.32	-0.89	2.89	0.33	1.53	1.30	0.98
CGST11	1.14	1.83	0.93	0.90	-0.98	0.53	-0.50	0.90	-1.18	0.16	1.19	1.41	-0.02	-0.55	-1.33	0.04	-0.19	1.08	0.39	1.05
CGST110	0.79	1.76	0.23	-0.07	-1.19	1.50	-0.80	-0.16	-0.72	0.04	0.82	0.62	-2.29	0.44	-0.79	0.63	-0.54	0.07	1.06	-1.37
CGST114	0.14	1.06	0.48	0.55	-1.87	0.05	0.31	0.70	0.65	-0.42	0.59	-0.15	1.19	-0.65	1.08	1.50	-0.17	-0.35	0.38	1.17
CGST13	-1.67	-0.69	-0.73	0.20	0.10	-0.47	1.94	0.79	2.06	-1.17	-0.85	0.49	0.34	-0.51	0.59	1.31	0.51	0.39	0.04	0.09
CGST131	1.48	2.14	0.74	3.11	-0.16	3.04	-0.61	2.22	-1.41	3.79	0.89	4.77	0.21	0.08	0.50	3.20	0.91	1.06	1.56	1.24
CGST141	0.47	0.32	-0.44	-0.70	-0.73	-0.26	0.79	0.57	0.80	-2.09	-0.80	0.58	-2.45	-0.97	1.02	-0.61	1.21	-1.09	-0.89	-0.11
CGST16	-3.73	-0.92	0.01	0.05	-0.48	-0.73	3.57	1.53	3.96	0.87	-1.17	2.05	4.12	1.54	-4.83	4.10	-0.32	-1.79	-0.05	-0.66
CGST18	0.73	0.79	1.38	1.12	-0.31	0.24	-0.59	1.15	0.38	-1.50	0.91	0.23	0.28	-1.27	0.39	0.12	-0.39	1.89	2.06	1.74
CGST21	-6.54	0.61	1.90	0.32	-4.48	2.20	2.65	8.20	4.84	-5.76	-0.58	8.92	6.60	4.16	2.19	-0.85	-2.32	-5.41	2.48	-1.94
CGST26	1.16	1.32	0.42	0.87	-1.17	2.33	-0.46	2.48	-0.07	1.62	0.90	2.16	-0.82	0.82	-0.35	1.43	-0.08	0.63	0.11	-0.07
CGST28	0.18	1.84	0.47	0.57	-0.76	2.60	0.10	1.54	-0.85	2.36	1.60	0.51	-0.42	-0.05	4.30	10.78	2.09	-1.06	0.24	0.51
CGST30	1.72	2.43	0.38	2.03	1.22	4.51	-0.94	2.42	-2.30	4.53	1.42	4.10	-0.79	2.13	-2.18	1.81	0.98	-0.02	-0.02	0.01
CGST32	-2.96	1.90	8.76	0.90	-4.35	9.48	-2.30	-4.13	0.66	-6.24	0.66	0.19	-0.37	-2.53	-4.43	4.43	1.20	2.92	-1.20	-1.61
CGST33	1.07	4.23	1.72	2.64	-8.33	5.77	-4.09	1.97	1.90	-4.05	2.84	5.42	2.32	1.62	-2.28	5.84	-4.97	-1.95	2.49	0.20
CGST38	-0.13	0.90	1.74	2.62	-3.05	0.95	-1.47	4.71	-0.07	1.19	0.42	4.22	0.82	1.90	0.76	1.31	0.30	-0.09	2.59	1.37
CGST39	-0.85	-0.34	0.01	-0.98	-2.81	-0.69	1.51	1.00	1.87	-2.62	-1.26	1.18	0.11	0.59	1.25	0.15	-0.35	-1.05	1.28	0.10
CGST41	-0.88	-0.15	-0.06	1.96	-5.00	-0.51	-0.78	1.81	0.68	-3.88	0.05	0.98	4.48	2.05	1.15	6.29	-0.85	-1.05	0.73	-1.24
CGST45	-1.06	0.19	-0.60	0.61	-2.37	-0.57	1.31	1.36	0.61	-0.32	-0.44	2.35	3.48	0.36	1.19	1.60	-1.01	-0.84	1.95	-0.08

CGST47	-1.13	-0.78	0.81	0.95	-3.31	-0.75	0.37	1.16	0.85	-1.94	-0.72	2.54	1.25	0.32	2.24	0.60	-1.84	-0.19	1.92	1.09
CGST48	-4.37	-1.18	-2.14	4.10	-4.05	6.33	-4.06	-4.12	1.44	1.86	0.51	-0.01	5.64	13.96	-0.26	9.79	-5.06	-3.17	4.25	-0.95
CGST53	-3.73	0.70	-0.17	2.92	-2.70	2.46	0.41	4.70	0.11	1.98	-0.99	7.46	9.52	9.30	7.22	8.55	1.99	1.58	2.54	-1.46
CGST58	-0.73	0.68	-0.64	-0.46	-4.37	-1.49	-0.71	0.36	-1.33	-2.02	0.30	0.16	1.52	0.95	1.90	1.06	-1.34	1.53	1.68	-1.19
CGST67	0.11	0.79	-2.01	0.70	-3.93	1.22	-1.27	3.59	-1.15	0.77	-0.40	5.10	1.27	2.62	0.11	0.63	-0.75	0.56	2.88	-0.49
CGST77	-2.61	-0.65	-0.55	2.99	-0.31	0.51	2.89	3.27	0.91	1.40	-0.95	7.26	4.12	3.16	4.07	4.28	-0.65	-0.85	1.14	-0.52
CGST80	0.11	1.11	1.09	-0.90	-2.51	-2.54	-3.01	-3.70	-1.54	-6.00	0.23	-2.09	0.73	-1.22	1.54	6.81	2.03	0.81	3.47	0.68
CGST81	2.37	3.31	1.96	1.60	0.52	3.13	-1.37	1.21	-2.07	2.27	2.31	0.80	-0.48	-0.41	-1.97	2.14	-0.70	1.02	0.17	1.24

Table 4.8. Summary of whole genome cfDNA analyses of chromosomal copy number changes (cont.).

Patient	Z Score Chromosome Arm																		
	chr11p	chr11q	chr12p	chr12q	chr13q	chr14q	chr15q	chr16p	chr16q	chr17p	chr17q	chr18p	chr18q	chr19p	chr19q	chr20p	chr20q	chr21q	chr22q
CGCRC291	19.58	27.70	52.78	42.80	196.21	-33.87	-18.31	-6.22	-19.94	-11.38	-16.30	-25.22	-27.27	-0.54	-7.89	26.07	25.47	-8.72	-11.60
CGCRC292	-1.73	-2.00	-1.97	-3.15	1.34	-0.75	-1.04	2.25	1.73	0.92	-0.73	2.06	-2.02	1.85	1.54	0.00	-0.21	-0.42	0.63
CGCRC293	-1.09	-2.01	-1.58	-4.05	-3.48	-3.93	-1.39	-0.70	-2.15	-1.75	-0.32	-3.70	-3.86	-0.87	-1.43	-1.09	-0.58	-1.63	-0.66
CGCRC294	-3.05	-3.12	-2.09	-3.89	0.22	-3.26	-0.99	1.95	1.71	1.44	0.12	3.35	-1.16	2.38	1.89	-1.57	0.09	0.83	2.57
CGCRC296	0.12	-0.30	-2.12	-1.22	1.51	-2.04	-2.97	1.07	-0.30	0.53	-1.71	1.16	0.64	0.45	1.13	1.12	0.67	0.63	0.66
CGCRC299	1.25	1.38	0.10	-2.18	1.24	-1.22	1.86	-2.13	-0.87	-0.84	1.75	1.81	-2.73	-0.40	-1.51	-0.09	0.23	2.31	2.00
CGCRC300	2.10	-0.09	2.01	0.79	-0.31	1.27	1.68	-1.25	-0.57	-0.50	0.41	2.36	-0.06	-2.11	-2.18	1.02	1.95	0.87	1.89
CGCRC301	1.02	-0.60	-1.80	-1.31	0.86	-1.77	0.22	0.58	0.81	0.62	1.41	0.48	-0.40	-0.18	-1.36	-1.51	2.37	0.93	1.90
CGCRC302	-1.51	-1.49	-0.66	-3.47	1.53	-1.15	1.51	-0.70	-0.32	1.03	2.11	2.84	-1.46	0.34	-0.89	-0.42	-0.71	3.66	4.14
CGCRC304	-0.82	-0.72	-1.17	-4.29	1.75	-1.17	0.73	-0.86	-1.00	-0.52	1.19	2.03	-1.36	0.72	-0.88	-0.55	0.58	2.09	3.42
CGCRC305	-1.33	-2.25	-0.46	-0.41	1.68	-0.23	-0.05	-0.26	0.29	0.72	0.07	2.57	-1.17	1.05	0.07	-2.31	0.82	2.00	1.30
CGCRC306	-0.79	-0.35	-0.72	0.48	30.50	-0.84	-2.11	0.36	-0.98	-1.64	-2.72	-0.22	-0.01	0.10	0.12	1.08	-0.76	-0.56	-1.31
CGCRC307	-0.20	-0.56	-0.85	-1.21	1.54	-1.27	0.42	-0.25	0.26	-1.03	-0.67	0.71	0.04	0.45	-0.44	-0.50	-0.26	2.58	0.97
CGCRC308	-1.59	-1.78	-2.03	0.24	1.85	0.47	-1.38	1.20	0.29	1.03	-1.83	2.52	0.66	0.12	0.51	0.73	1.37	1.60	1.64
CGCRC311	0.58	-0.37	-1.45	0.09	1.10	-0.58	0.78	0.24	-0.43	0.13	-1.69	1.69	1.18	-0.56	-1.10	-0.47	0.14	0.88	-0.37
CGCRC315	-3.12	-2.53	-2.07	-3.06	2.15	-2.17	-0.24	1.86	0.90	2.44	-0.04	-0.65	-2.11	2.36	1.31	-0.53	-0.52	2.60	3.05
CGCRC316	3.98	-20.57	-7.80	-38.60	90.29	-26.34	-26.34	2.72	-6.28	-24.89	9.90	-31.14	-18.45	0.92	-3.39	78.90	64.81	-17.78	-10.66
CGCRC317	-2.01	-2.76	-1.99	-3.15	2.28	-3.53	-1.69	1.11	0.25	-0.62	-1.10	-0.18	-1.46	1.15	0.11	-0.88	1.38	0.65	1.86
CGCRC318	-2.37	-4.12	-2.78	-6.00	2.55	-1.46	-0.70	1.84	1.30	2.10	0.28	0.10	-0.90	2.55	1.30	-1.08	-0.30	4.53	2.89
CGCRC319	-2.94	-1.76	-1.77	-4.23	0.80	-1.98	-0.92	1.38	-0.39	0.11	-0.40	2.62	-1.74	2.18	1.71	-1.24	-0.68	1.88	0.97
CGCRC320	-2.86	-1.85	-0.94	-3.21	1.64	-1.30	-0.33	0.98	1.42	-0.03	-0.44	3.16	0.16	0.53	-0.59	-0.25	0.54	3.89	2.49
CGCRC321	0.04	-0.85	-1.04	-0.24	2.01	1.10	-1.31	1.25	-0.48	-0.07	-1.96	0.28	0.13	0.57	0.27	0.03	-0.46	1.76	-1.98
CGCRC333	-86.46	77.65	23.72	46.14	187.13	37.84	-27.25	-26.75	-22.51	-51.87	-21.92	57.32	-47.36	-9.88	-0.41	35.28	96.06	14.98	-7.71

CGCRC336	-102.44	-133.85	-24.76	55.25	168.68	-23.94	-12.40	25.10	50.03	-78.34	-3.93	-123.32	-122.02	0.15	-1.76	-67.95	184.24	-5.40	-69.43
CGCRC338	-23.70	-26.13	22.40	54.88	107.91	-35.45	-20.88	-9.83	-22.24	20.83	15.73	-28.75	-27.68	-3.07	-4.73	76.65	67.28	-29.82	-16.91
CGCRC341	-1.13	-1.84	-1.75	-1.33	2.25	-1.98	-2.30	1.09	-0.50	0.89	-1.15	1.52	-1.00	2.47	1.53	-0.14	-0.04	1.50	0.67
CGCRC342	105.68	-13.58	-23.25	-57.44	180.22	-40.52	-78.09	10.27	-18.11	-82.89	-57.47	-131.18	-128.50	9.25	10.52	21.92	155.64	-27.56	-56.40
CGPLBR100	1.43	-1.61	0.85	0.09	2.41	0.76	-1.09	-0.20	-1.08	-1.08	-1.85	1.67	0.73	-0.03	0.31	-2.16	-2.29	0.09	-2.89
CGPLBR101	0.09	-0.54	-1.53	0.10	1.33	-0.11	-1.27	1.01	0.35	0.06	-2.13	1.48	1.17	0.38	0.86	-0.25	-1.31	-0.06	0.22
CGPLBR102	0.05	0.34	-0.60	2.02	0.00	-0.56	0.17	0.64	1.10	-1.33	-1.87	-0.28	3.30	-0.71	-0.41	1.33	0.11	-0.13	-0.79
CGPLBR103	-0.07	0.97	-0.85	-1.12	0.61	-0.33	-0.29	0.91	1.10	0.37	-2.19	1.22	2.13	-0.45	0.53	0.90	0.28	-1.24	1.30
CGPLBR104	0.77	1.17	-2.35	1.32	3.05	-0.05	-2.55	0.04	0.29	-2.49	-3.54	2.57	1.47	-0.80	-0.76	0.58	-1.38	0.20	-2.27
CGPLBR12	0.33	-2.53	1.69	-1.63	-0.45	-1.24	-1.04	0.08	0.79	-1.45	3.86	-2.18	-2.04	-0.55	-0.23	-0.74	1.48	2.57	-0.28
CGPLBR18	-1.87	-0.72	0.86	0.53	-0.25	-0.01	0.75	0.27	-1.56	0.92	4.10	-1.17	-2.67	0.69	0.32	-2.23	-0.27	0.82	1.31
CGPLBR23	1.46	0.47	-0.23	-1.02	-0.25	1.00	1.11	0.18	0.09	1.74	-0.25	0.25	-0.35	-0.94	-0.34	1.99	1.26	0.82	0.49
CGPLBR24	-1.07	-1.17	-0.85	-1.66	0.85	0.01	-0.43	0.27	-0.28	0.52	-0.18	2.18	-0.23	0.83	0.47	1.15	0.60	1.40	0.92
CGPLBR28	1.57	-1.62	-0.47	1.35	2.37	0.93	-1.61	0.19	-0.48	-0.90	-2.45	-0.03	0.04	0.40	0.89	-1.49	-1.64	-0.13	-3.10
CGPLBR30	76.19	-23.73	18.94	34.07	-57.23	-15.33	-42.43	-6.60	4.97	8.93	59.41	-14.70	-13.90	-1.16	-11.97	8.41	1.50	-20.14	-32.55
CGPLBR31	-0.68	0.03	-0.34	-0.17	0.69	0.64	-0.18	-0.18	-1.30	0.12	0.04	-1.35	-1.80	0.30	0.55	-0.23	0.20	-1.59	0.89
CGPLBR32	-0.21	0.87	0.68	2.11	1.37	0.87	-0.84	-1.02	-1.94	-2.02	-2.92	0.49	0.30	-1.26	-1.07	-1.57	-1.75	-1.16	-2.33
CGPLBR33	-0.07	0.94	-0.86	0.75	1.26	-0.58	-0.85	0.02	-0.18	0.51	-1.20	0.97	0.87	0.19	0.85	-0.32	-0.80	-0.66	-1.44
CGPLBR34	0.42	-0.88	0.11	0.08	0.31	-0.49	-0.37	0.22	-1.11	-0.01	0.02	0.68	-1.03	0.41	-0.16	-1.71	-0.53	0.06	-0.73
CGPLBR35	0.20	-0.28	-0.67	1.10	1.57	0.48	-0.83	0.00	0.45	-0.46	-1.98	2.99	1.09	-0.35	0.47	-1.14	-1.38	-1.18	-0.98
CGPLBR36	-1.20	-3.09	0.41	0.21	-1.30	0.29	0.11	1.97	1.53	2.74	1.30	2.16	0.77	0.93	2.09	0.51	-0.25	0.90	0.41
CGPLBR37	0.11	-0.36	-0.45	0.55	1.52	-0.15	-0.71	-0.24	0.09	0.70	-0.32	0.36	-0.24	0.29	0.67	-0.35	-0.68	0.24	-0.39
CGPLBR38	0.91	-0.05	0.42	-0.77	1.49	0.21	0.90	-1.43	-0.72	-1.29	1.75	-0.74	-2.54	-0.51	-0.53	-1.59	0.11	0.14	0.00
CGPLBR40	0.30	-0.14	-1.62	-0.89	0.49	-0.28	-1.28	1.10	1.69	-0.05	-3.80	1.65	1.95	-0.61	-0.26	0.62	-0.69	-1.23	0.36
CGPLBR41	-0.02	-0.70	-0.71	0.48	-0.10	0.77	-0.61	1.18	0.61	-0.12	-1.64	-1.12	-0.03	0.73	0.65	-0.89	0.29	-0.13	-0.46
CGPLBR45	-0.55	0.38	0.50	-0.77	0.99	0.14	2.01	-0.68	-1.52	0.60	1.73	-1.79	-2.21	-0.33	0.06	-0.30	0.22	-0.69	0.47
CGPLBR46	-0.66	-0.65	0.69	1.78	0.84	-0.51	-1.08	-0.05	-1.43	-1.40	-1.39	2.59	-0.58	-0.83	-0.26	0.93	-0.99	-0.29	-3.04
CGPLBR47	0.95	0.91	1.24	-0.02	0.09	1.63	0.16	-1.33	-1.21	-0.32	0.27	1.09	-1.05	-0.96	-0.96	-0.85	0.50	0.04	0.12

CGPLBR48	-1.74	0.81	6.00	5.88	0.77	0.06	0.07	-3.80	-4.76	-2.83	-0.48	1.89	0.87	-3.11	-4.50	-4.55	-4.46	-1.72	-1.08
CGPLBR49	-5.23	-1.20	5.12	6.33	-0.01	-1.00	-0.35	-3.97	-6.48	-2.07	0.05	4.56	-0.84	-0.42	-2.66	-3.89	-5.77	-0.49	-0.62
CGPLBR50	-0.52	0.76	-1.51	-1.51	0.81	-0.30	-1.08	0.79	0.52	-1.30	-3.43	1.99	2.56	-0.31	-0.43	2.79	0.33	0.15	0.18
CGPLBR51	0.79	2.38	0.96	1.05	-1.25	-0.60	0.27	-0.39	-0.58	-1.44	-0.57	0.35	-1.26	-1.13	-0.53	2.97	0.43	-0.92	0.09
CGPLBR52	0.13	0.20	-1.98	0.18	-0.74	-0.87	-0.14	1.81	0.83	1.79	-0.64	3.54	0.65	1.12	1.99	1.07	-0.24	-0.42	1.47
CGPLBR55	2.03	0.57	-0.66	1.85	-0.60	0.50	-0.90	0.70	-1.47	-0.29	-2.75	-1.89	-0.20	-0.35	-0.06	-0.34	-0.90	-0.13	-1.79
CGPLBR56	-0.20	0.35	-0.22	-0.42	1.55	-0.99	-0.04	-0.06	-0.58	-0.36	-0.31	0.17	-0.69	0.31	0.19	1.79	0.61	1.37	0.68
CGPLBR57	-0.20	-0.08	0.29	1.35	0.30	0.71	-0.05	-0.03	-0.93	0.81	-0.65	2.63	-0.28	-0.08	0.14	-0.31	-0.51	-0.32	-1.12
CGPLBR59	2.32	0.03	-0.39	-0.91	1.24	-0.94	0.77	0.50	0.59	-0.54	-2.00	-0.28	-0.42	-0.32	0.43	0.91	1.37	0.49	-0.43
CGPLBR60	0.91	0.45	-0.65	2.77	1.30	1.30	-0.71	0.22	0.99	-1.64	-2.13	-0.76	0.89	-0.93	0.18	-0.64	0.61	-2.25	-0.15
CGPLBR61	0.54	1.32	-1.38	-0.33	0.30	0.06	-0.25	0.30	0.30	0.09	-0.42	0.16	-0.07	-0.22	0.11	-0.41	-0.04	-0.23	0.72
CGPLBR63	0.87	0.43	1.75	2.44	1.33	1.16	0.07	-0.93	-0.42	-1.85	-2.35	0.75	1.86	-1.29	-1.55	-0.47	-1.64	-0.70	-1.47
CGPLBR65	-0.65	-0.98	1.27	3.48	0.24	0.24	-0.50	-1.06	-0.98	-1.64	-2.04	4.79	1.20	-1.30	-0.70	-0.64	-2.07	-1.20	-1.54
CGPLBR68	0.37	1.63	1.61	-2.19	-0.07	-0.61	1.91	-1.66	-1.44	-0.80	1.45	-1.34	-0.44	-1.41	-2.16	1.79	2.26	1.85	2.02
CGPLBR69	0.89	0.31	-1.50	-0.27	1.52	0.65	0.68	-0.32	-0.53	-0.95	-0.91	0.84	0.38	-0.81	-0.34	0.99	-0.04	1.15	0.05
CGPLBR70	0.78	0.00	-1.12	-0.59	1.14	-0.52	-0.48	0.51	0.72	-0.65	-2.12	1.86	1.42	0.04	0.26	0.29	-0.53	-0.97	-1.02
CGPLBR71	1.69	-0.08	-0.89	1.19	1.47	-1.32	-0.87	0.63	-0.43	-0.56	-1.74	-0.60	0.56	0.21	0.67	-1.38	-1.74	-0.63	-1.80
CGPLBR72	-0.32	-1.09	-1.30	-1.31	0.93	-0.31	-0.65	1.00	0.09	0.79	-0.46	1.26	-0.01	1.55	1.37	-1.03	-0.70	0.30	1.06
CGPLBR73	-0.53	0.10	-1.32	-1.14	0.02	-0.53	0.23	0.47	0.76	0.58	-1.49	1.01	0.54	0.00	0.56	1.28	0.29	0.47	1.08
CGPLBR76	-0.23	0.66	-0.75	-0.31	1.69	-0.71	-0.70	0.12	1.41	-1.50	-3.13	1.18	2.27	-0.79	-0.21	-0.75	-1.02	-0.64	-0.19
CGPLBR81	-0.99	0.00	3.50	5.95	2.11	0.53	-0.43	-3.17	-3.40	-3.68	-3.13	4.89	0.51	-2.97	-3.01	-2.74	-4.12	-2.19	-2.39
CGPLBR82	-0.45	-0.32	0.72	-0.62	2.10	-0.67	0.01	-1.56	-2.13	-0.87	-0.16	1.02	0.88	-0.54	-1.39	-0.70	-0.11	1.89	1.10
CGPLBR83	0.91	0.33	3.71	2.97	-0.70	0.60	1.01	-2.19	-1.83	-2.52	-1.27	2.70	1.64	-2.13	-2.25	0.38	-1.27	0.41	-0.68
CGPLBR84	0.06	0.83	3.64	5.94	-0.06	0.71	-1.38	-1.84	-2.48	-3.96	-3.95	2.06	0.86	-2.05	-2.49	-1.48	-4.77	-2.21	-2.28
CGPLBR87	-2.18	-0.60	4.23	6.41	-0.60	-0.01	-0.79	-2.58	-4.58	-3.73	-2.21	6.75	0.98	-2.21	-3.23	-3.69	-3.94	-1.11	-1.76
CGPLBR88	-3.66	-1.76	3.31	2.05	-1.13	0.28	-1.43	-2.15	-2.59	-3.61	-4.63	9.21	2.68	-1.85	-3.01	-1.99	-3.32	-0.77	-0.83
CGPLBR90	-0.20	-1.25	3.37	4.93	2.25	0.80	-0.43	-2.30	-4.43	-3.11	-2.34	3.06	1.52	-2.14	-2.41	-2.80	-3.91	-2.51	-3.12
CGPLBR91	0.59	0.50	-1.11	-0.04	-0.09	-0.63	-0.96	0.10	0.06	0.30	-2.20	-0.38	0.92	-0.49	-0.11	0.65	0.44	-0.87	-0.03

CGPLBR92	-2.89	-2.35	-1.98	-4.06	0.30	-2.48	-0.11	1.22	0.50	2.11	1.70	2.69	-0.99	2.12	0.73	0.27	2.26	2.20	2.94
CGPLBR93	0.66	-0.53	-0.71	0.34	-0.07	-0.94	-0.70	0.03	0.64	0.57	-0.48	1.59	-1.11	-0.15	-0.31	-0.78	0.59	-0.36	0.14
CGPLH189	-0.01	-0.95	-0.20	-0.33	0.27	1.39	0.97	-1.85	0.35	-0.18	0.07	1.68	1.01	-1.20	-1.22	1.28	-0.18	0.90	0.44
CGPLH190	-0.33	1.59	-2.55	-1.10	1.29	-1.55	-0.83	0.25	0.86	0.14	-2.39	-0.39	0.01	-0.50	0.10	2.13	0.20	-0.05	-0.56
CGPLH192	-0.69	0.46	-0.45	-0.84	-0.84	-0.90	-0.22	0.55	-0.39	0.95	0.13	-0.38	-1.18	0.21	0.44	-0.11	0.86	-1.46	-0.11
CGPLH193	1.15	0.38	-0.22	1.10	-0.12	-1.01	-0.78	0.35	0.53	0.50	-0.74	-1.30	-0.39	0.63	0.52	-0.27	-0.88	-1.08	-0.38
CGPLH194	0.66	1.17	1.53	-1.51	-0.01	-0.35	1.08	-2.16	-0.64	-0.35	1.14	1.34	-0.95	-2.05	-2.68	1.39	1.63	0.36	1.00
CGPLH196	0.23	0.64	-0.54	-0.60	0.63	-0.75	0.19	0.18	-0.51	1.04	0.67	-0.13	-0.83	-0.25	-0.13	1.64	0.00	-0.07	-0.07
CGPLH197	0.14	-0.33	-1.14	0.79	1.73	0.06	-1.31	-0.21	-1.24	0.40	-1.16	0.12	-0.92	0.02	0.46	-1.94	-1.98	-2.61	-1.36
CGPLH198	-0.23	0.47	0.30	0.34	-1.93	-1.47	-0.01	0.56	0.48	0.87	0.71	-0.61	-0.36	0.00	0.15	0.17	0.85	-2.42	-0.76
CGPLH199	2.60	1.01	-1.72	2.68	-0.70	0.33	0.17	1.62	2.18	-1.54	0.00	1.37	-1.13	-0.45	0.64	0.47	-0.69	-0.57	0.32
CGPLH200	0.17	-0.61	-1.31	0.62	-0.74	-1.55	-1.33	1.07	1.25	1.45	-0.33	-0.29	-1.05	1.42	1.54	-0.81	-0.42	-0.96	-1.15
CGPLH201	0.43	0.33	-0.49	0.96	-0.78	0.04	-0.94	0.34	0.09	0.36	-0.74	0.16	0.47	0.75	0.54	-1.35	-0.25	-0.52	-0.77
CGPLH202	-0.66	-0.40	-0.36	0.59	-0.53	-0.22	0.50	0.57	-0.54	0.12	0.00	-1.10	-0.39	0.03	-0.29	-0.51	0.72	-1.33	0.90
CGPLH203	0.52	0.42	1.02	-1.19	0.43	0.01	1.21	-0.12	-0.96	-1.13	0.59	-0.43	-0.90	-0.84	-0.85	0.87	0.22	0.24	1.00
CGPLH205	0.00	0.57	1.67	1.25	-1.85	-0.69	1.07	-1.32	-1.35	-0.02	2.25	0.74	-0.42	-1.18	-1.57	-0.94	-0.11	-0.18	0.29
CGPLH208	0.43	1.07	-1.22	-0.11	-0.34	-1.01	-1.83	0.69	0.23	-0.34	-0.85	-2.31	-0.34	0.43	0.49	0.66	0.06	-0.51	-0.80
CGPLH209	0.72	0.76	-1.52	-0.39	0.24	0.23	-1.01	0.33	0.67	-0.63	-2.22	-0.30	0.69	-0.06	0.27	1.50	0.44	-0.37	0.43
CGPLH210	0.38	0.48	-1.13	-1.34	-0.47	-0.63	-0.26	-0.55	1.31	-1.06	-1.32	0.90	1.80	-1.47	-0.60	1.02	0.69	-0.22	0.17
CGPLH211	0.10	0.01	4.32	0.15	-0.32	-0.41	-0.23	-1.63	-0.85	-0.92	-0.42	0.82	0.52	-1.01	-1.04	0.57	0.23	-0.38	0.73
CGPLH300	0.15	0.36	-1.26	1.03	0.74	-0.35	0.45	-0.49	-1.58	0.39	-0.91	2.19	-0.02	-0.71	0.07	0.10	0.31	-1.95	0.06
CGPLH307	0.20	-1.01	-0.02	1.93	0.23	1.15	-0.13	-0.57	-1.91	-0.70	-1.11	1.60	-0.29	-0.43	-0.75	-1.13	-0.37	-0.13	-1.35
CGPLH308	0.87	0.66	0.21	0.94	1.07	0.35	0.66	0.48	-0.13	-1.32	-0.65	0.03	-0.27	-1.21	-0.89	-0.33	1.12	-0.15	-0.02
CGPLH309	0.66	-0.52	1.14	0.15	-0.52	0.65	0.87	-0.09	-0.64	-0.41	2.34	0.91	-0.30	-1.25	-1.09	-0.26	-0.49	-0.10	-0.16
CGPLH310	1.73	0.47	-2.72	0.36	1.37	-0.98	-0.64	0.19	0.26	0.19	-1.95	0.76	0.91	-0.35	-0.32	-0.30	-0.11	1.45	-0.76
CGPLH311	0.33	-1.61	-0.62	0.38	0.48	0.58	-0.41	0.78	0.09	0.83	-0.48	0.59	-0.93	0.42	0.83	-1.33	-0.26	-0.41	-0.78
CGPLH314	0.34	0.56	-0.68	0.35	-0.45	0.19	0.95	0.28	0.42	0.41	0.70	-0.02	-0.34	-0.80	-1.06	1.76	1.85	0.67	0.82
CGPLH315	0.13	-0.09	-0.82	0.42	0.49	-0.34	-0.36	0.86	-0.42	0.95	-0.27	1.34	-0.78	1.36	0.90	0.76	0.36	0.49	0.27

CGPLH316	1.38	0.79	-1.55	-0.56	0.43	-1.15	0.01	0.48	1.12	-0.30	-0.61	1.68	-0.59	-0.44	-0.02	2.65	0.79	1.05	0.30
CGPLH317	0.40	1.35	-0.86	-0.63	0.32	-0.98	0.19	0.68	0.97	-1.73	-1.87	0.95	-0.07	-1.15	-0.90	0.69	0.83	-1.50	1.13
CGPLH319	0.49	-0.80	-1.20	0.76	1.50	-0.20	-1.00	0.45	0.42	-0.31	-2.32	0.09	0.27	-0.41	0.10	-1.11	-1.31	0.13	-0.76
CGPLH320	0.62	-0.72	-0.41	2.05	0.28	-0.37	0.16	0.41	0.23	-0.38	0.21	-0.04	-0.34	0.19	-0.04	0.28	-0.61	0.24	-0.34
CGPLH322	0.34	0.12	-0.01	-0.53	1.16	-0.61	0.61	-0.10	-0.57	-0.08	0.95	-0.44	-0.49	-0.57	-0.47	1.04	1.84	0.34	1.54
CGPLH324	0.12	0.44	-1.11	1.13	0.14	0.46	-0.02	-0.19	-0.15	0.21	-0.07	-0.12	0.23	-0.49	0.13	-0.19	-0.23	0.48	0.35
CGPLH325	-0.27	-0.74	-0.84	0.85	0.34	-0.61	-0.20	0.36	-1.01	0.31	-1.11	-1.31	-0.98	0.67	0.53	-1.32	-0.73	-1.17	-0.37
CGPLH326	0.09	1.37	-0.64	0.35	0.48	-0.54	0.31	1.15	-1.23	-0.24	0.28	0.68	0.34	-0.49	-0.97	0.10	0.24	0.43	-0.03
CGPLH327	-0.04	-0.22	-0.66	0.72	1.10	0.40	-1.11	2.54	-0.12	0.11	-0.75	-0.79	-0.89	0.38	0.65	-0.72	-0.40	-0.59	-0.63
CGPLH328	-0.89	-1.53	-1.41	1.61	0.60	-1.61	-2.13	1.16	-0.33	1.28	-0.71	-1.41	-0.33	2.08	1.88	-0.74	-1.07	-0.06	-1.54
CGPLH329	0.00	0.85	-0.16	0.99	-0.38	0.05	0.29	0.60	-7.35	0.37	-0.02	-0.41	-0.78	-0.26	-0.49	0.97	-0.04	1.29	0.25
CGPLH330	-0.20	-1.11	-0.74	0.63	0.91	-0.63	-1.10	1.34	-0.39	0.73	0.33	-0.85	-0.89	1.26	0.43	-1.74	-1.30	-0.03	0.39
CGPLH331	-0.68	-1.45	-0.37	1.42	-0.63	0.83	0.17	1.06	-1.42	1.85	1.10	0.55	-1.90	0.94	1.08	-0.81	-0.37	0.01	-0.27
CGPLH333	0.71	0.38	-0.90	0.70	-0.63	0.69	0.31	0.50	0.49	0.86	-1.03	0.73	1.10	-1.10	-0.25	0.18	0.42	-1.15	0.86
CGPLH335	-0.71	-0.44	-0.34	1.62	0.21	0.08	-0.31	0.88	-0.52	0.07	-1.02	-1.39	0.42	-0.01	0.12	-0.22	0.17	0.36	-0.11
CGPLH336	-0.13	0.97	-0.92	0.14	1.35	0.65	-0.26	-0.01	-1.53	-0.48	-0.25	1.30	1.17	-0.54	0.14	-0.48	-0.86	-1.09	2.62
CGPLH337	0.87	1.16	0.54	0.19	1.45	0.90	0.54	-1.20	-0.04	-0.90	0.05	0.21	0.06	-0.74	-0.50	-0.71	0.20	-0.50	0.15
CGPLH338	0.95	1.14	-1.26	0.37	2.56	-1.76	-1.18	-0.04	-1.04	-0.70	-1.72	-0.61	0.87	0.38	0.04	-0.19	-0.22	0.34	-0.72
CGPLH339	0.92	0.06	-0.74	-0.78	0.33	0.04	0.67	0.29	-0.33	0.48	-1.40	2.54	0.09	-0.60	0.07	0.10	-2.01	-0.79	0.50
CGPLH340	1.23	-0.16	-0.27	1.23	0.36	0.60	-0.23	-0.10	-0.11	0.53	-0.71	-0.36	-0.80	-0.13	0.52	0.57	-0.23	0.72	-1.15
CGPLH341	0.02	0.59	-1.84	2.46	2.37	0.35	-1.07	1.60	0.46	-1.32	-2.54	0.53	0.67	-0.22	0.98	-0.19	-2.03	-2.63	-2.37
CGPLH342	-0.11	0.70	-1.61	0.14	1.38	0.24	-1.24	-0.30	0.66	0.32	-1.27	0.72	-0.18	0.21	0.69	0.72	-0.05	0.17	-0.11
CGPLH343	-1.36	0.11	-1.08	0.29	0.08	0.45	0.49	0.36	0.94	2.15	0.42	-0.06	0.18	0.36	1.38	-0.70	0.93	-1.04	0.42
CGPLH344	0.84	0.25	-0.90	-0.36	0.08	0.56	0.63	-0.67	-0.81	-0.17	-1.64	2.65	0.96	-1.56	-0.52	1.08	0.92	-0.67	-0.44
CGPLH345	0.28	0.63	1.82	0.65	-0.24	0.03	0.52	0.02	0.72	1.09	-0.35	0.96	0.78	-0.92	0.28	-0.60	0.74	-1.17	0.64
CGPLH346	0.88	0.42	-0.28	0.94	-0.41	0.63	-0.15	0.37	-0.99	-0.04	-0.85	0.37	-0.35	0.11	0.36	-0.54	-1.87	-1.77	-0.01
CGPLH350	-0.55	-0.61	0.21	-0.20	-2.19	1.66	1.19	0.56	0.85	0.62	-0.38	2.99	0.60	-1.04	-1.21	-1.29	1.75	0.51	2.94
CGPLH351	-2.51	-1.75	-0.85	-0.36	-0.04	-1.18	-0.57	1.48	-0.38	1.75	0.03	2.84	-0.44	1.80	1.75	-1.69	-0.25	-0.25	0.51

CGPLH352	0.81	1.02	-0.34	0.70	-1.18	1.51	0.17	-0.11	-0.26	1.20	0.62	-0.59	-1.29	-0.01	0.32	0.40	0.62	0.09	0.15
CGPLH353	-0.33	0.32	0.40	1.24	0.82	0.57	0.88	-1.69	-0.46	-0.93	0.52	1.32	0.24	-1.08	-0.33	-0.32	-0.11	-0.17	0.49
CGPLH354	0.60	0.84	-1.45	1.67	-0.73	0.16	0.50	0.40	0.22	1.27	-0.19	-0.57	-0.86	0.11	0.48	-0.03	0.72	-1.15	-0.32
CGPLH355	0.17	-1.01	1.83	2.87	0.38	2.56	0.00	-0.90	-2.34	-0.53	1.46	1.44	-2.02	-0.41	-0.74	-1.07	-0.58	-0.30	-0.68
CGPLH356	1.22	1.25	2.71	-1.11	3.04	0.46	3.36	-3.98	-3.19	-1.99	2.37	0.35	-1.44	-2.12	-2.62	0.76	-0.37	0.68	1.75
CGPLH357	0.11	-0.91	-1.50	-0.06	-0.08	-1.42	-1.36	0.82	-0.27	1.23	0.56	0.14	-0.84	1.93	1.82	-1.05	-0.04	-0.09	0.36
CGPLH358	0.20	-1.44	-0.42	-2.46	2.55	0.05	0.05	-0.64	-1.32	0.30	-0.94	0.42	1.20	0.17	-1.04	-0.71	-0.29	1.17	-0.01
CGPLH360	0.50	0.52	0.03	0.70	-0.28	-0.16	0.04	-0.48	-0.65	0.27	-0.77	0.73	-0.33	-0.25	0.01	-0.74	-0.66	-1.62	1.66
CGPLH361	0.55	-0.11	-0.53	-1.37	0.99	-0.66	0.68	-0.73	0.46	0.07	0.25	-0.24	0.17	-0.02	-0.27	0.76	1.39	-0.11	2.47
CGPLH362	0.83	-1.15	-1.64	0.48	0.72	-0.38	-0.44	0.24	-0.18	-0.16	0.12	0.85	-0.03	0.91	0.83	-0.77	-2.00	0.22	-0.05
CGPLH363	0.42	1.12	-2.08	-0.53	0.96	-0.71	-0.97	0.10	0.38	-0.08	-1.54	0.54	0.15	-0.25	0.17	0.36	1.11	-1.06	0.02
CGPLH364	-1.10	-1.55	-2.88	-2.03	0.18	-0.17	-0.91	1.29	0.68	0.27	-0.84	3.76	-0.22	1.19	0.83	-1.63	-0.49	1.19	0.63
CGPLH365	0.12	-1.12	0.56	1.66	1.67	1.20	-0.24	-1.84	-3.26	-1.70	0.43	0.93	-0.78	-0.76	-1.13	-2.39	-2.47	0.28	-0.43
CGPLH366	-0.25	1.24	-0.03	0.15	2.33	0.81	0.41	-1.45	-1.40	-0.63	0.45	-0.41	-0.26	-1.27	-1.02	-0.31	-0.37	0.50	0.62
CGPLH367	0.21	0.38	-1.23	0.49	-0.03	-1.44	-0.15	0.64	1.12	-0.02	-0.76	1.37	0.10	0.39	0.57	1.10	0.36	-0.55	0.69
CGPLH368	0.50	1.34	-0.64	-0.38	-0.21	1.00	-0.47	0.22	0.17	-1.46	-1.39	-0.12	0.76	-0.30	-0.04	0.32	-0.20	0.54	-0.79
CGPLH369	0.55	-0.78	-1.79	-0.75	0.80	-0.80	-0.93	0.55	0.77	0.97	-0.54	1.14	-0.95	1.08	0.90	-0.86	-0.11	2.10	-0.34
CGPLH370	0.54	1.01	-1.75	-2.85	1.17	-1.01	-0.31	-0.14	0.26	0.19	-0.72	-1.01	0.82	-0.76	-0.27	3.15	1.88	1.67	1.36
CGPLH371	0.02	1.31	-0.29	-1.08	0.30	-1.06	-0.08	0.36	-0.19	-0.55	-2.62	0.18	1.03	-0.87	-0.42	2.12	0.25	0.05	0.64
CGPLH380	-1.98	-1.65	-0.92	-0.33	-0.51	0.43	0.98	0.88	-0.66	2.65	1.61	0.36	-2.00	1.35	0.95	-2.13	-0.15	-0.40	1.75
CGPLH381	-1.70	-0.46	-1.57	-0.26	0.20	-1.12	-0.17	0.53	0.49	1.91	-0.80	1.66	-0.88	0.99	1.40	-0.48	0.08	-0.69	1.44
CGPLH382	-0.77	-1.44	-1.52	0.09	1.35	-0.04	-1.20	0.53	-0.62	1.34	0.52	0.33	-1.37	1.33	0.94	-1.38	-0.34	0.03	0.51
CGPLH383	-1.77	-0.92	0.41	-0.39	-1.06	0.25	2.01	0.41	-0.26	3.27	2.56	1.99	-1.98	0.45	0.29	-1.28	1.77	-0.11	2.74
CGPLH384	0.69	1.15	-0.34	1.66	0.60	1.49	0.97	-1.15	-1.11	-0.65	0.58	0.10	-0.71	-0.97	-0.58	-0.40	-0.33	-1.77	1.55
CGPLH385	-0.40	-0.36	-0.99	-0.90	0.35	-1.51	0.63	1.30	0.18	0.89	-0.46	1.08	-0.91	0.55	0.68	0.09	0.92	-1.25	1.24
CGPLH386	1.56	0.83	0.02	0.54	0.98	-0.24	-0.13	-0.16	-1.17	-0.29	-1.65	0.44	0.03	-0.58	-0.35	-1.19	-0.31	-0.73	-0.76
CGPLH387	1.33	0.24	-0.49	1.47	0.79	1.21	0.12	-0.14	0.12	-0.30	-0.17	0.00	1.82	-0.78	-0.77	-0.03	0.06	0.33	0.87
CGPLH388	0.22	-0.28	0.73	-0.26	0.87	-0.20	1.04	-1.18	-1.00	-0.04	0.84	1.34	-1.79	-0.05	-0.28	-0.41	-0.23	0.43	1.90

CGPLH389	0.36	-0.89	-1.70	1.86	1.41	-0.02	-1.74	0.84	-0.63	-0.37	-2.21	1.02	0.55	0.30	0.52	0.05	-0.67	0.03	-1.28
CGPLH390	0.38	0.94	-0.55	0.48	-0.77	-0.94	1.84	0.29	-0.93	1.72	2.11	-0.50	-0.54	-0.33	-0.50	2.41	1.86	0.41	2.44
CGPLH391	1.11	-0.08	-1.73	0.38	0.74	-0.57	-2.08	0.50	-0.57	-0.06	-1.26	-0.49	-0.55	1.08	1.60	-0.72	-1.41	-1.60	-0.71
CGPLH392	-0.44	-0.44	1.78	1.12	1.74	1.03	-0.99	0.43	-1.91	-0.74	-1.21	0.95	-0.46	0.40	0.36	-2.56	-2.29	-1.45	-1.87
CGPLH393	-0.08	0.52	-0.09	1.04	-0.36	0.25	1.43	-1.22	0.28	0.58	-0.23	2.01	-0.64	-0.74	-0.42	-0.97	-0.36	-0.86	1.47
CGPLH394	0.29	-0.05	0.58	2.25	-0.28	0.61	0.12	-0.32	-2.52	0.05	0.77	-2.02	-1.15	0.43	-0.28	-2.16	0.02	-0.86	0.50
CGPLH395	0.57	-0.42	-0.72	-0.58	-0.31	0.46	-0.85	1.28	-0.81	0.56	0.11	-1.78	-1.73	1.51	1.53	-1.02	-0.06	-0.20	-0.19
CGPLH396	0.74	-0.18	-0.12	-0.47	1.71	-0.26	-0.13	-0.73	0.01	-0.35	-2.27	2.14	1.58	-0.87	0.06	-0.38	0.03	-0.51	-0.15
CGPLH398	0.94	0.77	-2.30	-0.49	1.04	-0.86	-0.79	0.89	0.95	0.68	-2.17	1.68	0.68	-0.13	0.20	0.60	0.47	-0.30	-0.28
CGPLH399	-0.49	-0.94	0.25	2.04	1.75	0.92	-1.06	-0.21	-1.73	0.45	-0.95	0.92	-0.91	0.74	0.43	-2.18	-8.14	-0.69	0.33
CGPLH400	0.06	0.44	2.61	-0.54	0.77	0.84	2.25	-2.69	-2.35	-0.33	2.63	0.85	-0.98	-1.50	-2.37	-2.89	0.72	-0.27	2.60
CGPLH401	0.93	1.44	-1.39	-2.09	-1.27	-0.65	0.32	0.38	-0.22	2.28	-0.31	2.41	-0.34	-0.10	-0.10	1.63	1.44	0.07	0.23
CGPLH402	0.11	1.42	-0.47	1.63	0.01	0.14	-0.36	0.68	-1.72	2.55	0.33	-2.23	-2.07	1.37	1.67	-2.45	0.52	-2.66	0.17
CGPLH403	-0.53	-0.95	-0.07	-1.04	-0.53	-1.04	-0.44	0.56	-2.08	2.61	0.25	-1.05	-2.01	1.19	1.90	-2.01	-0.18	-1.26	1.33
CGPLH404	-1.23	0.22	-0.46	1.35	0.32	-0.11	-1.42	1.03	-1.38	1.95	-1.78	-1.39	-1.36	1.23	2.06	-1.69	-1.84	-2.28	-0.24
CGPLH405	0.45	1.52	0.31	1.93	-0.41	0.76	-1.28	-0.60	-2.76	1.16	0.38	-1.83	-1.80	0.70	0.86	-1.67	-0.36	-0.83	-0.78
CGPLH406	0.03	0.17	1.43	1.24	0.47	0.08	-0.85	-0.27	-1.89	1.50	-0.69	-0.68	-1.91	1.18	2.20	-0.38	-1.97	-2.22	0.31
CGPLH407	0.11	1.14	0.16	1.12	0.13	-0.92	-0.87	0.46	-0.44	0.63	-0.46	-1.27	-2.17	0.42	0.44	-3.04	0.15	-2.11	1.59
CGPLH408	0.18	0.16	-0.70	0.90	-0.03	-0.04	0.00	0.90	0.06	0.91	-0.29	0.11	0.41	1.18	1.64	0.65	-0.85	0.14	0.09
CGPLH409	0.11	0.50	-0.36	-0.68	-0.49	0.09	1.02	-0.49	-0.77	1.74	-0.24	0.68	-1.45	0.08	1.09	-0.59	-0.51	-0.78	0.90
CGPLH410	-0.05	0.52	0.58	0.93	-0.16	-0.56	-0.23	0.38	-1.19	1.55	-0.52	1.31	-1.23	0.21	1.05	-0.53	-1.03	-1.46	-0.17
CGPLH411	0.98	0.62	-0.04	-0.02	0.02	-1.23	-0.08	0.05	-0.64	0.45	-1.91	1.70	0.60	0.14	1.04	-0.61	-0.03	-1.31	1.09
CGPLH412	-0.41	0.49	-0.28	0.63	-0.58	-0.55	-0.28	0.78	-1.14	0.69	-0.04	0.38	-1.08	0.86	1.70	-1.14	-0.01	-1.81	0.04
CGPLH413	-0.92	-0.03	-1.32	0.37	-1.05	-1.46	-0.19	1.82	0.20	1.50	-0.76	0.15	-0.74	1.38	2.15	-1.78	0.77	-1.50	0.74
CGPLH414	-0.91	0.27	-0.10	-0.87	0.24	0.31	-0.23	0.09	-0.83	1.07	-1.75	-0.69	-1.03	0.47	1.21	-0.31	-0.90	-2.31	0.57
CGPLH415	-0.65	0.39	-1.33	0.06	-0.96	-0.29	-0.65	1.47	-1.11	1.15	-1.13	1.64	-0.75	0.63	1.63	-1.60	1.08	-2.83	0.87
CGPLH416	-0.73	1.85	2.23	-0.11	-0.32	-1.32	1.33	-2.40	-2.43	1.08	1.50	2.85	-1.79	-1.26	-1.58	-0.02	3.05	0.25	1.88
CGPLH417	0.03	2.22	2.48	1.08	-0.03	-0.16	0.69	-1.81	-3.69	1.20	1.76	0.49	-2.43	-0.27	-0.56	-0.85	-0.91	-0.51	1.21

CGPLH418	-1.79	0.94	-0.11	-1.68	-0.57	0.16	0.01	-0.21	0.07	0.37	-1.06	3.00	-0.61	-0.50	0.42	-1.94	0.76	-1.68	1.97
CGPLH419	0.15	0.28	1.34	2.05	0.93	0.03	0.19	-0.49	-0.90	-0.41	0.33	1.14	0.14	-0.42	-0.42	-1.50	-0.69	0.76	0.19
CGPLH420	0.46	0.36	-0.92	1.45	-0.20	0.66	0.05	0.40	1.44	0.61	-0.60	-1.12	-0.46	-0.43	0.45	-0.64	0.06	-0.69	-0.23
CGPLH422	-0.53	0.24	0.48	1.27	0.24	0.07	1.13	-0.52	-1.96	0.55	1.66	-0.19	-1.78	-0.26	-0.19	-1.00	0.01	-0.22	1.67
CGPLH423	-1.05	-0.56	0.54	0.82	-1.55	0.84	0.53	-0.09	-0.99	1.56	1.74	0.96	-1.20	0.32	0.30	-0.83	-0.06	-1.01	0.85
CGPLH424	-0.67	-1.30	-0.13	1.12	0.06	-0.91	-0.98	0.89	-0.55	1.90	0.22	-0.16	-1.72	1.44	1.66	0.02	-0.55	-0.62	-0.34
CGPLH425	0.14	-0.23	0.15	1.15	1.07	0.21	-0.28	-0.80	-1.51	-0.29	-0.01	1.49	-1.08	-0.15	-0.06	0.69	-0.16	0.89	0.46
CGPLH426	-1.09	-0.77	0.68	2.27	-0.62	0.46	0.51	0.05	-1.65	1.45	0.03	-0.36	-0.97	-0.17	0.32	-2.18	-0.09	-1.48	0.50
CGPLH427	-0.41	0.09	-0.38	1.19	-0.05	0.24	-0.21	0.11	-0.90	0.40	-0.03	-1.25	-1.58	0.57	1.26	-0.64	-1.04	-1.50	-0.14
CGPLH428	-0.75	0.87	-0.19	1.28	-1.44	-0.27	0.24	0.38	-0.01	-0.47	0.44	0.10	-0.49	0.08	1.18	-0.78	-0.03	-1.53	0.08
CGPLH429	1.36	0.31	1.75	1.63	1.29	0.79	0.89	-1.79	-1.53	-1.93	-0.89	2.28	-0.04	-2.31	-1.92	-1.38	0.15	0.20	0.38
CGPLH430	0.72	-0.10	-0.64	1.69	0.95	-0.59	-0.74	0.49	-0.32	0.42	-0.66	0.72	-0.21	0.43	0.37	-1.07	-0.44	0.56	-1.22
CGPLH431	0.18	1.33	-0.04	0.88	0.27	-0.17	0.94	0.44	-0.98	1.64	1.22	-0.65	-2.32	0.48	0.78	-1.02	0.52	-0.80	0.76
CGPLH432	-0.16	0.13	-0.22	1.61	0.53	-0.25	-0.36	-0.52	-0.17	0.10	-0.32	0.75	-0.98	0.60	0.94	-1.02	-1.28	-2.79	-0.56
CGPLH434	0.26	0.78	-0.15	0.91	0.41	0.73	0.38	-0.40	-0.28	0.75	0.63	-0.92	-0.94	0.31	0.18	0.18	0.01	-0.80	0.45
CGPLH435	0.61	0.05	-0.80	-1.36	0.17	-0.91	-0.19	0.14	0.20	0.89	-0.68	2.58	-0.44	0.27	0.24	-0.39	1.33	0.35	0.91
CGPLH436	0.35	-0.22	0.14	2.37	1.09	1.39	-1.20	0.47	-0.89	-1.42	-0.83	0.64	-0.49	0.34	0.58	-0.43	-1.77	-0.83	-0.82
CGPLH437	-1.26	0.57	-0.67	1.46	-1.06	0.17	-0.43	1.88	0.52	1.86	-0.69	-1.58	-1.04	0.42	1.05	0.76	0.23	-2.13	0.39
CGPLH438	-0.06	0.00	-0.16	2.63	0.17	0.35	-0.25	0.46	0.18	0.50	-1.16	-0.80	0.60	0.08	0.78	-1.31	-1.16	-1.25	-1.13
CGPLH439	-0.40	-1.09	-0.74	1.67	0.37	1.12	-0.46	0.80	0.72	-0.28	-0.86	0.12	0.26	-0.14	0.78	-0.86	-0.96	-0.61	0.07
CGPLH440	-0.15	-1.22	-0.72	1.21	-0.13	-0.03	-0.08	-0.26	0.26	1.12	-0.65	1.14	-0.98	0.05	0.43	-0.75	-0.20	-1.14	0.92
CGPLH441	-0.56	0.90	-0.62	0.07	-0.33	-0.18	-0.87	1.01	0.16	0.35	-0.89	-0.67	-0.54	0.33	0.74	0.00	0.16	-1.33	0.94
CGPLH442	-0.24	0.11	-0.38	1.49	0.58	0.28	0.12	-0.40	-1.16	0.14	0.30	-2.10	-2.07	0.62	0.56	-0.82	1.25	0.74	1.01
CGPLH443	0.90	0.37	-0.22	-0.70	0.88	1.91	-0.17	-0.93	-0.80	-1.12	-0.28	3.17	1.37	-1.16	-1.23	-2.85	-0.73	-1.02	-0.24
CGPLH444	-0.14	-0.01	0.88	0.35	0.38	1.47	1.37	-1.10	-0.63	0.78	1.77	2.35	-0.57	-0.57	-0.78	-2.10	0.77	0.04	1.49
CGPLH445	-0.08	-0.58	1.42	1.71	0.43	0.90	0.57	0.29	-0.67	-0.67	-0.34	2.37	0.27	-0.57	-0.18	-0.82	-1.72	-1.15	-0.22
CGPLH446	-0.59	1.21	0.29	0.67	1.15	0.81	1.12	-0.65	-1.03	-0.17	0.87	-0.64	-0.90	-0.58	-0.42	-1.80	-0.29	-0.99	0.01
CGPLH447	-0.50	-0.99	0.03	-0.76	1.12	1.24	0.20	-0.29	-1.02	0.31	-0.38	0.97	-0.06	-0.29	0.24	-2.14	0.09	-0.69	1.24

CGPLH448	-0.16	-0.36	0.04	0.06	1.64	1.05	-0.37	-0.30	-0.29	0.38	-0.77	-0.26	-1.35	0.41	1.35	-0.94	-0.40	-0.62	-1.60
CGPLH449	0.01	0.52	0.83	-0.31	-0.77	1.19	1.54	-1.42	-0.83	0.55	2.17	2.35	-1.06	-0.91	-0.62	-1.33	1.45	1.13	1.98
CGPLH450	-0.48	-1.07	0.22	0.08	0.20	1.53	0.25	-0.03	-0.06	2.00	0.25	0.17	-1.76	0.97	1.31	-0.44	0.16	-0.89	0.78
CGPLH451	0.21	0.78	0.07	-0.39	-0.05	1.17	1.39	-0.51	-0.53	0.72	0.26	2.53	0.06	-1.03	-0.28	-1.12	0.44	-0.48	0.83
CGPLH452	1.34	-1.70	0.95	2.07	2.35	0.85	-0.29	-0.43	-1.66	0.02	-0.78	2.98	-0.09	0.00	-0.48	-3.32	-2.05	0.28	-1.89
CGPLH453	0.14	0.45	-1.03	-0.41	-1.46	-0.34	1.31	0.82	-0.08	1.11	2.27	-0.34	-1.56	0.30	-0.03	-0.52	1.24	-1.17	1.87
CGPLH455	-0.67	0.51	1.28	1.06	1.48	0.82	-0.81	-0.61	-1.88	-0.88	0.39	-0.84	-1.89	0.48	0.11	-1.98	0.05	-0.74	-0.52
CGPLH456	-0.82	-1.19	0.80	1.66	0.61	1.47	0.19	0.38	0.20	0.88	-0.27	-0.01	-1.10	0.74	1.09	-2.45	-2.16	-1.77	-0.22
CGPLH457	-1.25	-0.99	-0.38	1.22	1.31	-0.78	-0.77	0.73	0.61	0.66	-0.77	2.40	-1.02	0.24	0.63	-0.86	-0.64	-1.33	-1.09
CGPLH458	0.03	0.26	1.30	1.81	1.15	1.42	0.14	-1.60	-2.44	0.00	1.36	0.42	-1.43	-0.43	-0.61	-2.48	-1.09	-1.00	-0.19
CGPLH459	-0.02	-0.61	-0.16	1.05	0.26	0.01	-0.04	-0.26	-1.09	0.74	1.91	2.34	-0.85	-0.42	-0.12	-1.11	-1.25	-0.75	-0.22
CGPLH460	-1.12	-1.60	-0.59	-0.14	-0.36	0.15	0.70	0.95	-0.13	3.00	0.73	0.27	-2.19	1.61	1.82	-1.20	-0.36	-0.71	1.02
CGPLH463	0.42	0.31	-0.39	0.55	0.68	-0.01	-0.03	1.32	-0.29	0.17	-0.11	-0.35	-0.63	0.71	0.79	-0.10	0.57	-0.63	-0.15
CGPLH464	0.38	-0.52	0.00	0.31	0.32	-0.13	0.99	0.63	-0.94	0.49	-0.89	2.19	-0.39	-0.22	0.14	-2.56	-1.97	-2.10	-0.26
CGPLH465	0.10	-0.19	0.57	0.41	1.24	0.64	0.65	-0.12	-0.31	0.32	0.05	0.56	0.99	-0.60	-0.15	0.17	-0.06	-1.59	0.21
CGPLH466	-0.90	-1.53	0.44	0.65	-0.66	1.16	1.11	0.77	-1.53	1.69	0.97	-1.09	-1.45	0.64	0.95	-0.73	0.79	0.35	0.27
CGPLH467	0.88	-0.12	0.61	1.55	0.35	1.53	0.11	-0.06	-1.20	-0.52	-1.30	0.15	0.15	-0.79	-0.13	-1.09	-1.19	-0.70	-1.33
CGPLH468	-0.23	-1.33	-0.03	1.46	-0.10	0.37	-0.79	0.24	0.21	0.21	-1.32	1.53	0.17	0.26	0.65	-1.55	-1.21	0.25	-0.89
CGPLH469	0.29	-0.63	1.35	3.32	2.00	2.72	0.56	-0.59	-1.64	-0.42	-1.25	-0.81	0.25	-0.65	-0.60	-2.07	-1.42	-1.67	-2.10
CGPLH470	0.39	0.49	-0.37	-0.75	0.75	-0.67	-0.51	0.89	-0.68	0.16	-1.06	1.32	0.65	-0.10	0.37	0.63	0.65	-0.62	0.53
CGPLH471	1.07	-0.03	-0.54	1.00	0.32	0.06	-0.08	0.69	-0.63	0.99	0.40	0.04	-1.14	0.86	-0.21	-0.43	0.37	0.72	0.28
CGPLH472	-0.76	0.16	-1.30	0.47	1.38	-0.34	-1.98	1.69	-0.55	0.10	-2.37	-1.02	-0.86	1.04	1.58	0.19	-1.62	-0.47	-2.15
CGPLH473	-0.40	-1.14	-0.90	1.80	0.65	1.06	-1.04	0.76	-0.86	0.58	-0.71	0.57	-0.63	1.18	1.16	-2.23	-2.59	-0.23	-1.50
CGPLH474	-0.72	-0.49	-0.63	2.02	0.32	0.87	-1.24	0.61	-0.45	1.08	-1.08	1.89	0.62	0.40	0.20	-0.38	-0.34	1.67	-0.59
CGPLH475	-0.83	-0.07	-0.45	1.80	0.90	-0.61	-1.17	0.90	0.38	-0.53	-1.04	1.94	0.08	0.40	0.79	-1.08	-1.04	-1.21	-0.31
CGPLH476	-0.96	-1.43	-1.01	0.50	0.98	0.02	-0.88	0.77	0.33	0.22	-2.24	0.79	-0.01	0.25	0.90	-0.40	-0.60	-0.59	-0.57
CGPLH477	-0.10	0.85	0.46	2.55	0.18	0.31	0.78	-0.92	-1.54	-0.14	1.34	1.33	-0.83	-0.71	-0.95	-1.13	0.91	0.29	1.38
CGPLH478	0.72	-0.51	-0.21	-1.74	1.44	0.53	0.20	-0.68	-0.20	0.09	-1.20	1.79	0.29	-1.18	-0.85	0.15	1.64	0.05	0.82

CGPLH479	1.00	-0.08	0.41	1.16	0.84	1.54	1.36	-1.21	-1.51	-0.01	1.21	0.05	-1.99	-0.85	-1.37	-0.76	1.11	0.61	1.67
CGPLH480	0.54	0.19	-1.60	1.04	1.72	0.70	-1.29	-0.40	-1.39	-0.54	-1.72	1.17	1.66	-0.80	-0.56	-0.43	-0.72	-0.61	-1.64
CGPLH481	-0.26	-0.71	0.43	0.60	0.86	1.95	0.17	-0.11	-0.67	1.36	0.27	1.74	-0.02	0.19	0.06	-1.65	-0.85	0.13	-1.22
CGPLH482	-0.02	-0.07	-1.48	0.36	0.38	0.72	-0.16	-0.20	0.75	2.05	-0.54	-1.10	-1.57	0.51	0.74	0.69	0.73	-1.18	1.03
CGPLH483	-1.00	0.10	-0.85	1.71	1.08	0.36	-0.96	1.50	-0.31	-0.32	-0.08	-0.24	-1.97	1.20	1.54	-1.87	-0.53	-1.01	-0.68
CGPLH484	-1.40	-0.74	-1.31	-0.10	-0.84	-0.94	0.11	1.15	-0.45	2.06	-0.09	1.05	-0.96	0.87	1.00	-1.04	0.42	-0.03	0.49
CGPLH485	-1.19	-1.61	-0.75	1.40	1.29	0.48	-0.95	0.39	-0.33	0.76	-0.56	1.08	-0.23	1.03	1.12	-1.11	-1.42	-1.04	-0.80
CGPLH486	-0.79	0.02	1.72	0.59	0.30	1.46	1.34	-0.17	-0.90	-0.58	-0.54	1.30	-0.07	-1.12	-1.21	-0.25	-0.92	-1.44	-0.94
CGPLH487	1.33	-0.80	0.75	1.17	1.50	0.57	0.64	-2.48	-1.59	-0.72	-0.18	1.71	0.19	-1.27	-1.49	-0.61	-0.68	1.97	-0.10
CGPLH488	1.17	1.16	0.40	-1.30	0.59	0.48	1.71	-1.57	-1.29	0.75	1.58	-0.17	-0.33	-1.32	-1.21	-0.28	1.11	0.29	1.28
CGPLH490	0.44	1.23	3.26	-0.66	1.10	2.02	2.02	-2.72	-2.55	-1.74	1.65	0.71	0.67	-2.35	-2.48	-1.17	0.16	-0.26	1.63
CGPLH491	1.66	0.92	-0.09	0.55	1.71	0.15	0.21	-0.14	-0.84	-0.60	-0.83	1.28	0.90	-0.90	-0.58	-0.17	0.45	-0.22	-0.20
CGPLH492	-0.29	-1.02	-0.81	0.00	0.17	1.24	-0.16	0.55	0.27	1.25	-1.55	1.93	1.12	-0.54	-0.27	-0.89	-0.75	-0.81	-0.13
CGPLH493	0.36	-1.26	-0.87	0.93	-0.14	-0.73	-0.17	1.86	0.83	0.35	-0.70	0.54	-0.28	0.41	0.61	-0.10	0.25	-0.37	-0.01
CGPLH494	0.33	-0.51	-0.53	0.23	0.92	0.55	0.13	1.98	-0.25	0.50	-1.09	1.37	-0.04	0.38	0.28	1.80	-0.07	-0.27	-0.50
CGPLH495	-0.16	0.75	-0.35	-0.72	1.23	0.87	0.62	-2.02	-0.62	-0.43	-0.01	2.70	0.46	-0.77	-0.66	0.17	0.48	1.01	0.88
CGPLH496	0.93	0.10	-0.35	-0.11	1.51	0.05	-0.47	-0.79	-0.70	-0.21	-0.36	0.48	0.33	-0.14	-0.57	-1.65	-0.89	-0.03	-1.12
CGPLH497	-0.44	0.32	-0.26	0.26	0.52	-0.20	0.36	-0.33	-0.76	-0.13	0.14	-0.87	-0.88	-0.10	0.45	-0.81	-0.39	-0.12	1.00
CGPLH498	-0.36	-0.43	-0.02	-0.92	0.05	1.38	1.19	0.06	1.44	0.66	0.38	2.05	1.28	-1.00	0.08	0.30	0.02	-0.02	1.40
CGPLH499	0.01	-0.37	0.03	0.71	2.04	0.07	-0.25	-0.20	-0.89	0.28	-0.01	0.49	-0.01	-0.10	0.67	-0.97	-0.87	0.06	-0.25
CGPLH500	-0.91	-2.46	-1.23	0.37	1.58	-0.10	-0.51	0.27	0.34	1.23	-0.57	0.73	-0.82	0.95	1.35	-0.89	-0.37	-1.21	0.35
CGPLH501	0.49	1.25	-0.77	-0.22	1.42	0.43	0.86	-0.88	0.51	-0.59	-0.48	0.37	1.34	-1.91	-1.18	1.03	1.17	-0.86	1.26
CGPLH502	-0.88	-0.54	-1.48	-1.96	0.99	-0.95	0.11	1.21	-0.21	1.57	-0.35	-0.45	-0.61	1.24	1.49	-1.22	-0.12	-1.61	1.01
CGPLH503	0.42	0.58	-0.91	-2.01	1.34	-0.93	0.49	-0.37	0.09	-0.38	-1.52	0.81	1.57	-1.53	-0.76	1.77	0.09	0.87	0.85
CGPLH504	-0.71	-0.26	-0.96	-0.14	2.21	-0.47	-0.62	0.22	0.11	0.55	-1.18	1.23	-0.55	0.68	1.17	-0.76	-1.35	-1.57	-0.78
CGPLH505	0.44	0.24	-0.50	1.43	0.98	1.22	0.79	-1.62	0.12	-0.71	0.68	-1.08	-0.81	-0.57	-0.08	0.43	-0.15	0.63	0.06
CGPLH506	0.48	0.18	-0.87	0.14	0.24	0.26	-0.76	0.69	0.37	-0.65	-0.66	6.21	0.05	-0.35	0.14	0.07	-0.47	0.65	-0.83
CGPLH507	0.88	0.97	-0.25	-2.51	0.81	-0.56	1.36	-2.63	-1.38	-1.36	0.36	1.28	-0.75	-1.76	-1.66	-0.06	1.41	0.83	1.76

CGPLH508	0.16	1.09	0.28	-1.65	0.00	-0.57	2.09	-1.39	-0.62	0.34	2.72	-0.80	-0.43	-1.57	-2.06	0.99	2.09	1.12	1.81
CGPLH509	-0.65	1.68	0.34	0.30	1.48	0.00	1.08	-1.05	-0.51	-0.45	1.29	-1.20	-0.41	-1.02	-0.63	1.26	1.17	1.54	1.67
CGPLH510	0.19	2.35	0.35	-1.19	-0.58	-0.52	1.46	-0.91	-1.94	0.45	0.84	0.92	-0.47	-0.33	-0.99	-0.10	0.44	0.65	1.56
CGPLH511	1.41	0.96	-0.78	2.13	0.26	1.40	-0.30	-0.60	0.21	-1.02	-1.72	0.33	0.65	-1.75	-1.28	-0.09	1.46	0.37	0.31
CGPLH512	0.79	0.38	-0.21	0.27	0.66	0.77	0.94	-0.57	-0.73	-0.36	0.50	-0.02	0.36	-0.95	-0.72	0.10	0.05	0.59	0.42
CGPLH513	-0.06	-0.88	-1.53	-0.30	1.43	-0.90	-0.53	0.20	0.75	-0.38	-1.74	1.34	0.60	-0.12	0.11	1.31	0.80	-0.09	0.70
CGPLH514	1.25	0.72	-0.32	0.24	0.43	-0.21	0.35	0.38	-0.73	1.18	0.69	-0.14	-0.32	-0.38	-0.06	0.55	-0.52	-0.83	-0.76
CGPLH515	1.28	1.21	-1.51	0.55	1.76	0.34	-0.05	-1.18	-0.40	-1.14	-1.35	2.78	-0.10	-1.18	-0.66	1.18	0.23	-0.09	0.24
CGPLH516	1.51	-0.45	-0.52	0.56	0.38	1.52	0.93	-0.18	-0.10	0.45	-0.45	-0.05	0.18	-0.47	-0.29	0.24	-0.22	-0.32	-0.56
CGPLH517	0.12	-0.14	-1.20	-0.06	-0.51	0.09	0.64	0.56	1.11	1.11	0.85	0.99	-1.32	-0.03	0.75	-0.99	0.55	-1.13	0.54
CGPLH518	-0.47	-0.02	-1.31	-0.94	0.33	-0.03	0.29	0.12	0.79	0.02	-0.30	1.55	0.52	-0.21	0.27	0.66	0.25	-1.87	0.88
CGPLH519	-0.39	-0.24	-1.85	-0.90	0.01	-0.33	-0.03	-0.53	-0.09	0.30	-1.08	1.21	-0.78	0.09	1.17	0.34	-0.82	-1.22	0.86
CGPLH520	0.47	0.28	-1.18	-0.76	2.37	0.40	0.53	-0.57	-0.63	1.37	-0.15	2.21	-0.06	-0.50	0.25	1.01	0.54	0.71	0.30
CGPLH625	-0.30	-0.39	0.37	-0.22	1.01	1.01	0.64	-1.03	-1.12	-0.26	-0.92	-0.22	0.79	0.11	-0.16	-0.66	-1.82	-0.03	-1.00
CGPLH626	-0.45	-0.69	-0.66	-1.06	-0.11	0.08	0.65	0.97	1.45	0.59	-1.71	1.67	2.70	-0.81	0.38	1.07	0.18	0.61	1.34
CGPLH639	1.32	1.21	-0.37	-0.43	2.29	-0.18	0.02	-0.63	-1.13	-0.58	-0.56	-2.80	-0.14	0.11	-0.33	-0.45	-0.64	0.00	0.33
CGPLH640	0.89	1.31	-1.57	-1.23	-0.19	-0.53	-0.10	0.81	0.07	1.46	-1.89	0.67	0.08	-0.07	1.32	1.41	-1.29	-2.72	-0.18
CGPLH642	0.32	0.85	-0.69	0.23	1.62	0.68	-0.09	-0.60	-0.78	-1.33	-0.34	-1.89	-0.45	-1.01	-0.68	0.03	1.37	0.50	0.08
CGPLH643	0.61	-0.48	-0.26	1.71	0.66	0.19	0.01	0.48	0.21	-0.79	-1.67	0.82	0.55	-0.53	-0.56	0.05	-0.93	-0.21	-0.54
CGPLH644	0.62	1.70	-0.89	0.05	1.27	0.88	-0.45	-0.84	0.38	-1.82	-1.80	-0.23	0.16	-1.83	-0.56	0.84	-0.90	-1.26	-0.46
CGPLH646	0.94	-0.07	-0.04	-0.08	-2.08	0.36	0.87	0.50	1.27	1.39	-0.05	-0.70	1.01	-0.94	0.08	1.43	0.68	-0.45	0.16
CGPLLU144	11.14	-0.91	-1.16	-1.77	0.00	-4.65	-6.46	2.72	-4.24	-4.27	-3.77	7.92	-0.42	-0.07	1.15	2.20	-2.17	-1.28	-2.50
CGPLLU161	-0.90	-0.23	0.14	-0.95	1.18	-1.65	-0.48	-0.32	-1.01	-0.66	-1.69	2.28	0.59	-0.29	-1.16	0.58	0.55	1.55	0.51
CGPLLU162	-0.42	-0.58	-0.37	0.40	-0.29	-1.48	-1.95	0.20	-1.79	-1.37	-2.14	2.61	-0.15	0.03	0.09	0.48	-1.08	0.73	-1.33
CGPLLU163	-4.81	-3.34	-1.11	68.97	8.82	1.59	-23.01	6.25	-6.11	-6.47	-9.87	-0.21	-5.50	-1.09	-1.83	10.36	14.85	-7.16	-10.44
CGPLLU168	-0.54	-0.47	-0.40	1.30	1.28	0.24	-1.25	1.53	-0.49	-0.76	-1.35	-0.66	-1.52	0.98	1.78	-1.31	-1.01	-0.80	-1.03
CGPLLU169	0.45	0.03	-0.37	-0.08	0.37	0.04	-0.54	1.29	-0.66	0.23	-1.29	0.84	0.12	0.46	1.34	-0.44	-1.82	-0.87	-2.26
CGPLLU176	0.17	-0.69	0.17	3.45	0.33	1.79	-0.83	-0.47	-0.15	-0.09	-2.13	1.69	-0.17	-0.31	0.37	-1.10	-1.11	0.01	-1.43

CGPLLU177	-1.12	3.20	2.02	4.61	-1.91	5.12	-2.75	-1.81	-3.71	0.09	-1.46	1.46	-0.50	-2.75	-0.96	0.86	0.10	2.43	-4.22
CGPLLU203	0.84	0.63	0.32	1.11	0.93	-0.91	-2.36	1.16	-0.25	1.72	-1.46	1.63	-0.99	0.50	0.92	-1.61	-1.84	-0.38	-1.90
CGPLLU205	1.34	1.65	-0.56	2.29	1.27	-0.91	-0.76	0.15	-0.73	-0.70	-1.28	-1.24	0.69	0.38	0.91	-0.26	-1.68	0.48	-1.29
CGPLLU207	0.56	-0.77	-1.22	-0.70	1.43	0.52	-1.62	0.57	-0.04	-0.66	-1.66	0.77	0.49	0.52	0.53	-2.35	-1.06	1.04	-1.33
CGPLLU208	1.49	3.21	-1.13	1.89	-1.25	3.44	-3.39	1.29	0.02	-2.59	-1.49	0.56	-1.32	-0.18	0.71	-0.56	1.39	-2.68	-2.85
CGPLOV11	2.85	1.71	-0.11	-3.55	0.67	-4.81	-3.03	-0.27	-5.05	-4.96	-1.00	-2.91	0.25	-0.15	-1.79	2.56	1.63	2.12	1.73
CGPLOV12	-0.69	0.82	-0.95	0.55	1.68	-0.55	-2.16	0.13	3.82	-1.05	-2.26	-0.20	-1.08	0.25	0.40	-1.70	-1.32	-0.34	-1.70
CGPLOV13	0.60	0.00	-0.73	-0.02	0.65	-0.50	-0.78	0.66	-0.19	-0.24	-1.18	-0.61	0.06	0.44	0.59	0.34	1.04	1.67	0.35
CGPLOV15	-3.85	0.36	14.20	-10.50	-2.62	-5.24	-2.96	-2.13	-4.32	-5.59	-5.05	2.11	-4.13	-1.17	-0.44	8.76	6.80	-6.83	-6.84
CGPLOV16	-2.54	-0.20	-1.04	-4.76	2.58	-0.35	-2.36	-0.25	-2.32	-1.97	-0.55	1.42	1.10	0.34	0.08	4.14	-0.83	1.79	1.49
CGPLOV19	-14.01	-19.40	-50.86	-104.56	61.93	-95.47	-10.00	20.99	39.79	-100.59	-12.67	-80.06	-73.16	-0.96	0.04	6.95	170.74	-11.61	-10.54
CGPLOV20	0.97	-0.96	-1.72	2.02	1.75	-0.81	-2.57	1.15	-0.44	-1.85	-3.87	-0.94	2.16	0.81	0.66	-1.04	-3.07	0.28	-2.96
CGPLOV21	-4.03	2.33	-5.93	-2.63	0.19	-2.59	-4.16	1.68	-6.53	-2.21	-2.25	0.68	-0.12	1.88	3.80	9.16	0.84	-5.14	0.22
CGPLOV22	0.40	0.77	-0.17	0.42	2.71	-0.41	-1.07	-0.26	-0.75	-1.15	-0.43	-0.56	-0.97	0.42	0.30	1.48	2.51	0.86	-0.13
CGPLOV23	-1.61	-2.29	-2.31	2.28	-0.03	-0.12	-2.37	1.27	0.34	-0.53	-4.25	-2.02	0.96	0.78	1.57	1.20	2.41	-1.80	-1.63
CGPLOV24	2.54	1.13	0.16	0.78	1.28	0.94	-0.80	0.17	-0.09	-0.80	-1.45	-1.91	1.48	-1.01	-0.45	0.86	-1.18	1.75	-1.79
CGPLOV25	1.63	1.14	-0.30	0.18	2.72	1.41	-0.86	-0.07	-0.60	-1.11	-1.89	5.15	0.61	-1.32	-0.47	0.29	-1.33	0.78	-1.43
CGPLOV26	1.66	-0.19	-0.83	2.72	1.73	0.30	-2.06	0.67	0.02	-1.67	-2.73	-0.71	1.13	0.57	1.00	-0.86	-2.25	-1.56	-2.97
CGPLOV28	-0.11	-0.50	-0.89	0.79	0.88	-0.38	-1.12	0.85	-0.92	1.32	-0.62	1.03	-1.03	0.78	0.61	-1.45	-1.41	-0.48	0.04
CGPLOV31	-0.61	-1.11	-0.31	0.33	0.81	-0.95	-0.73	0.56	-0.19	0.47	-0.82	0.28	-0.75	0.77	0.85	-0.43	0.31	-0.33	0.03
CGPLOV32	-0.04	-0.14	-0.37	0.88	0.99	0.25	-0.63	0.38	-0.22	-0.70	-1.34	-0.22	0.52	0.13	-0.40	-0.25	-1.13	0.53	-0.09
CGPLOV37	-0.90	-1.85	-1.55	-0.51	1.75	-1.56	-1.59	0.95	-0.22	-0.53	-3.97	3.75	1.70	-0.48	-0.16	0.24	-0.41	0.26	0.19
CGPLOV38	2.02	15.28	2.36	-11.82	-3.16	0.64	-1.65	-6.19	-13.51	-10.47	-8.04	-15.59	-14.83	-0.99	0.99	22.29	2.10	5.07	-1.39
CGPLOV40	-1.83	-2.18	-5.31	-4.54	2.68	-1.84	-3.89	1.69	-0.48	-0.67	-5.12	5.03	2.37	0.94	1.07	-0.61	0.02	-0.70	-1.37
CGPLOV41	-1.08	-0.98	-0.19	-0.22	-0.09	1.41	-1.05	-1.13	-2.68	-1.54	-0.80	3.69	0.93	0.59	0.60	-0.01	1.34	1.84	-0.47
CGPLOV42	-2.06	4.27	3.01	-0.94	1.71	0.56	-0.86	0.09	-1.21	-1.30	-1.49	-0.99	-0.84	1.20	1.12	-1.41	-1.68	-1.43	-0.45
CGPLOV43	-0.10	0.05	1.11	0.64	1.24	0.07	0.24	-0.84	-0.86	-0.84	-1.55	0.49	1.66	-0.90	-0.65	-1.62	-1.94	0.32	-1.50
CGPLOV44	-0.01	-0.82	-0.82	1.34	2.69	0.28	-3.55	1.11	-0.92	-1.44	-3.50	0.74	0.03	0.60	1.52	0.11	-2.24	-1.77	-3.05

CGPLOV46	0.87	-1.42	-0.92	2.09	1.20	0.47	-1.51	-0.26	-0.02	-0.15	-2.35	0.55	-0.05	1.27	1.22	0.60	-1.59	-1.05	-0.86
CGPLOV47	1.03	2.12	-1.02	-1.80	-0.01	0.91	0.33	-0.02	-0.43	-0.22	-0.86	0.12	0.84	-0.68	0.17	1.21	0.19	0.07	0.75
CGPLOV48	0.37	0.75	0.89	-0.72	1.24	-0.34	0.82	-1.39	-0.44	-1.85	1.03	0.13	-0.30	-1.09	-1.00	-1.34	-0.39	-1.45	1.91
CGPLOV49	-4.21	-1.92	4.86	0.43	4.30	-5.03	-2.80	-1.45	-5.60	-3.27	-6.36	-4.30	-1.42	-0.36	1.76	5.20	3.07	-5.15	-5.78
CGPLOV50	0.55	0.30	-1.18	0.66	1.44	0.02	-2.65	0.33	1.02	-0.94	-3.60	0.16	1.01	0.33	0.81	-0.66	-1.86	-1.06	-0.77
CGPLPA112	0.89	0.22	-1.02	-0.96	0.32	-0.10	0.56	-0.55	0.15	0.05	0.09	-1.12	-0.20	-0.58	-0.41	0.60	0.73	0.34	0.21
CGPLPA113	1.50	1.06	-2.41	0.01	1.72	1.62	-2.90	-0.90	-0.94	-1.98	-3.82	2.23	4.04	-2.37	-0.90	1.27	-1.18	-0.69	-4.36
CGPLPA114	0.38	0.14	-1.29	-0.33	0.68	-0.32	-0.86	0.65	0.08	-0.03	-1.36	1.16	0.21	0.41	1.02	1.14	0.08	-0.72	-0.74
CGPLPA115	-9.24	-14.11	0.57	0.79	-22.22	-6.31	-8.67	-1.81	-3.64	-8.58	-7.45	14.51	3.87	-1.46	6.27	-5.04	-2.80	-4.79	-1.47
CGPLPA117	-0.81	-3.22	-0.37	1.90	1.20	1.33	-0.91	0.82	-1.29	-1.48	-1.28	2.34	-1.44	0.71	1.12	3.65	-2.13	0.21	-2.93
CGPLPA118	1.12	1.76	-1.33	1.30	1.64	0.39	-0.89	-0.29	-0.50	-0.90	-2.61	-0.44	0.88	-1.39	-0.68	1.40	0.14	0.51	-2.57
CGPLPA122	2.11	0.95	-3.11	-13.76	3.35	-1.55	-3.74	1.17	1.47	-2.43	-5.07	2.98	-1.57	-0.33	1.36	-0.70	-0.73	-0.75	-4.10
CGPLPA124	-0.72	-0.13	-0.90	0.63	2.50	0.68	-0.97	-0.04	0.12	-0.95	-2.40	2.56	0.05	-0.10	0.53	-0.13	-0.17	-0.58	-1.04
CGPLPA125	0.84	1.30	-0.45	3.30	1.51	1.47	-0.20	0.13	-0.37	-0.15	-0.34	-0.04	-0.26	-0.95	-0.73	-1.17	-1.29	-2.51	-0.67
CGPLPA126	-0.69	-0.48	-2.73	-1.81	4.12	-0.09	-1.76	0.55	1.82	-1.85	-3.79	3.38	2.26	-0.45	0.24	0.49	-0.99	1.04	-0.23
CGPLPA127	2.18	1.94	-1.29	1.14	1.62	-0.18	-1.95	-0.60	-0.67	-2.30	-2.93	-0.42	0.14	-1.06	-0.22	-0.32	-0.74	-0.93	-4.02
CGPLPA128	0.55	-0.57	-0.05	0.50	2.45	0.78	0.50	-0.60	0.24	-1.32	-1.40	2.05	0.76	-0.98	-0.99	-1.57	-0.74	1.29	-0.80
CGPLPA129	0.45	-0.97	-3.39	0.59	3.46	-0.35	-2.67	0.38	0.93	-1.43	-4.19	4.71	1.90	-0.46	0.20	-0.19	-0.44	0.56	-1.61
CGPLPA130	-0.60	0.42	-1.56	-0.18	2.15	-1.12	-0.54	-0.52	0.04	-0.73	-1.36	1.80	1.99	-1.00	-0.85	-1.35	-1.73	-0.51	-1.55
CGPLPA131	-1.62	-2.37	0.72	-0.23	0.35	2.31	0.17	0.33	1.01	1.80	-0.36	4.34	0.17	-0.24	0.41	1.23	2.11	1.51	2.45
CGPLPA134	0.71	-0.30	-1.85	-3.83	1.81	-1.34	-0.65	-1.15	0.68	-0.37	-1.31	1.74	2.06	-0.86	-0.77	2.45	1.07	3.61	0.73
CGPLPA135	1.86	3.15	-1.24	1.49	0.99	-1.10	-0.89	-0.80	-0.39	-0.98	-1.00	-0.35	-0.67	-1.31	-0.75	0.34	0.67	-0.64	-0.21
CGPLPA136	0.29	-0.24	-0.42	-1.40	2.44	0.51	0.75	-0.91	0.48	-1.17	-0.46	-0.27	0.29	-1.99	-2.18	0.41	0.51	2.01	1.25
CGPLPA137	2.27	1.27	0.69	0.36	1.96	1.36	0.84	-1.50	-1.17	-1.15	-1.47	1.66	-0.78	-1.72	-1.11	2.08	-0.38	0.05	-1.17
CGPLPA139	1.30	2.53	-1.29	-1.90	-0.41	0.13	0.20	-0.31	-0.30	0.31	-1.10	-1.44	-0.69	-1.24	-0.43	2.68	3.53	-0.13	1.70
CGPLPA14	1.51	0.86	-1.29	1.01	0.04	-0.87	-1.75	1.55	2.60	-1.93	-3.45	-3.06	2.81	-0.62	-0.48	1.92	-0.60	0.08	-3.79
CGPLPA140	-0.83	-1.64	-2.84	-2.57	1.87	-1.75	-1.80	1.22	0.67	0.43	-1.85	3.82	0.05	1.56	0.88	-0.23	-0.16	2.34	1.50
CGPLPA141	-0.47	-1.32	-2.02	-0.93	0.11	-3.05	-1.94	1.43	1.30	-1.00	-2.61	0.41	2.18	0.72	0.32	3.29	0.27	1.91	-1.72

CGPLPA15	1.20	2.10	0.06	0.89	0.34	0.30	-0.20	-0.40	1.37	-2.20	-2.04	0.11	2.03	-1.97	-1.08	1.25	-0.52	0.03	-2.09
CGPLPA155	1.94	1.49	-1.15	-0.12	-0.08	0.43	0.24	-1.12	0.60	-1.83	-2.75	-0.83	1.23	-2.67	-1.43	3.86	1.77	-0.01	-0.19
CGPLPA156	-0.03	-0.13	-1.07	0.15	1.39	0.57	-0.10	-0.28	-0.51	-0.01	-0.71	2.07	0.20	-0.24	0.63	0.04	-0.25	-0.55	0.42
CGPLPA165	1.02	0.59	-1.01	-0.06	-0.26	0.59	0.14	-0.81	0.98	-0.12	-1.74	0.07	0.12	-0.91	0.03	2.21	1.27	0.78	-0.02
CGPLPA168	0.07	1.03	-5.35	-2.96	3.92	-3.23	-4.47	1.40	2.00	-2.67	-6.38	2.52	2.99	-0.54	0.78	1.83	-1.37	-0.66	-4.34
CGPLPA17	-9.09	-8.49	-8.04	-8.15	4.93	-9.32	-3.95	7.02	4.28	1.36	-9.38	5.93	5.44	2.19	2.60	10.73	5.14	4.33	-3.52
CGPLPA184	1.64	2.02	-2.10	-1.19	0.87	-0.25	-0.72	0.31	1.41	-0.90	-2.48	-0.01	1.74	-0.79	-0.51	2.35	2.37	1.42	-0.52
CGPLPA187	1.98	0.89	-0.65	-0.72	1.60	0.10	0.42	-0.63	-0.51	-2.18	-3.07	0.39	0.23	-1.93	-1.67	3.13	1.14	1.01	-0.99
CGPLPA23	0.19	0.99	-4.32	1.94	1.70	-2.89	-5.50	3.18	0.49	-2.53	-6.27	-2.96	1.43	1.98	2.86	2.90	-1.14	-0.80	-6.50
CGPLPA25	1.20	0.42	-1.16	2.56	-0.39	-0.01	-1.39	1.04	0.50	-0.02	-2.40	-0.35	0.73	0.23	0.92	0.35	0.37	-2.14	-2.19
CGPLPA26	0.93	0.96	0.25	1.09	0.25	-0.34	-0.50	-0.41	-0.78	0.17	-0.36	0.08	0.09	-1.00	-0.40	1.27	0.89	1.05	0.95
CGPLPA28	0.35	-0.15	-0.47	0.96	1.10	-0.05	-1.98	1.05	1.55	-1.09	-3.30	0.32	1.78	-0.04	0.75	0.93	-1.30	-0.93	-2.06
CGPLPA33	2.01	0.69	-2.21	4.30	-0.10	-1.83	-3.31	1.98	0.38	-3.61	-4.49	-3.22	2.44	0.06	-0.07	3.17	0.77	-1.21	-5.32
CGPLPA34	0.30	0.63	-0.32	1.22	0.11	-0.47	-0.70	1.15	0.89	-1.10	-2.04	1.06	1.61	-0.14	0.95	0.67	-1.03	-0.29	-1.37
CGPLPA37	0.68	1.45	-2.40	-2.06	0.52	-2.48	-1.74	1.05	1.25	-2.74	-3.95	-1.60	4.06	-0.63	-0.23	4.67	1.17	0.19	-1.30
CGPLPA38	1.40	0.43	-0.37	1.89	-1.05	-1.70	-1.16	1.56	0.84	-1.65	-1.09	-2.72	0.97	-0.08	-0.20	1.93	0.51	-0.78	-2.74
CGPLPA39	0.45	0.22	-3.01	1.02	-0.32	-1.73	-2.80	1.67	0.14	-1.44	-3.70	-0.76	-0.19	1.01	2.29	2.69	0.33	-1.90	-5.03
CGPLPA40	0.65	1.08	-2.79	-0.67	-0.40	-2.67	-2.12	1.80	1.62	-1.70	-4.60	-3.03	2.55	-0.50	0.38	4.21	2.27	0.67	-2.81
CGPLPA42	1.73	1.55	0.60	0.47	0.87	-0.75	0.82	-1.63	-0.21	-0.30	0.65	-4.60	0.55	-1.74	-1.56	0.50	-0.21	0.07	0.52
CGPLPA46	-7.16	-7.43	-6.38	-1.76	3.11	-8.09	-3.60	5.66	2.35	-1.48	-6.35	2.68	5.03	1.65	1.33	8.16	3.91	2.30	-4.79
CGPLPA47	-0.74	-1.90	-4.09	-0.71	1.54	-5.38	-3.68	4.83	2.61	-0.48	-5.62	-3.31	3.66	1.31	1.40	5.68	2.07	1.15	-3.55
CGPLPA48	0.05	0.61	-0.42	0.71	-0.05	-1.27	-0.60	-0.17	0.66	-0.56	-1.44	-0.94	-0.12	-0.17	0.98	1.42	-0.07	-1.85	-0.38
CGPLPA52	0.47	-0.09	-0.46	1.91	0.90	0.09	-0.34	0.04	-0.60	0.72	-1.60	1.98	-0.44	0.18	0.75	-0.32	-0.38	-1.19	-0.38
CGPLPA53	1.38	3.25	-1.65	-0.96	-0.53	-1.69	-1.47	-0.10	0.18	-0.41	-2.05	-1.02	0.07	-0.30	0.75	1.88	1.44	-0.57	-2.46
CGPLPA58	0.64	0.11	-1.17	0.88	-1.18	-0.16	-0.53	1.24	0.56	1.57	-0.65	-1.09	-1.14	1.03	1.27	-0.86	0.14	-3.51	-1.40
CGPLPA59	1.40	-0.28	-2.01	2.23	1.48	0.62	-2.68	2.05	-0.92	-0.19	-3.08	0.69	-0.27	1.36	1.84	0.66	-0.96	-0.37	-3.21
CGPLPA67	1.99	1.96	0.39	1.00	1.62	0.58	0.10	-0.85	-0.37	-0.17	-1.24	-0.31	0.43	-1.45	-0.85	0.64	-0.82	0.32	-0.31
CGPLPA69	-0.35	-0.91	1.30	1.65	1.72	0.18	0.84	-1.33	-2.20	0.78	0.52	0.92	-0.29	-0.35	-0.86	-1.79	-1.08	0.59	0.05

CGPLPA71	-0.53	-0.52	0.86	1.05	0.18	2.03	1.09	-1.25	-1.42	-0.39	0.23	1.97	-0.94	-0.78	-0.23	-2.56	-2.26	-1.89	-0.22
CGPLPA74	0.32	0.94	0.41	-1.33	0.77	-0.15	0.93	-0.68	-1.03	1.71	1.82	-0.24	-2.63	0.03	0.09	-0.75	0.56	-0.49	1.70
CGPLPA76	1.66	1.41	-1.14	-0.34	1.43	-0.72	-0.13	-0.24	3.86	0.64	-0.55	-1.69	0.05	0.06	0.51	1.97	1.05	0.11	-0.77
CGPLPA85	-1.41	-0.30	0.32	0.70	1.07	-0.23	-0.26	0.20	-0.32	0.85	-1.53	1.46	-0.66	0.67	0.48	-1.67	-0.92	0.69	0.35
CGPLPA86	0.33	0.95	-1.41	2.38	2.77	-0.20	-2.88	0.33	-1.49	-1.62	-4.17	1.42	0.47	-0.50	1.16	1.00	-1.58	-1.08	-5.50
CGPLPA92	-0.79	-1.30	0.13	1.48	-0.69	1.09	0.08	0.44	-0.59	0.83	1.15	-0.51	-1.29	0.82	1.45	-2.15	-0.59	-1.43	-0.71
CGPLPA93	0.64	-1.44	-2.16	-0.97	3.56	-1.02	-3.45	1.34	1.10	-1.93	-5.16	3.48	0.91	0.62	1.00	0.40	-5.50	-0.26	-4.45
CGPLPA94	1.87	1.46	0.09	-0.98	1.26	0.29	0.13	-0.72	-2.10	-2.41	-1.66	0.55	0.80	-2.30	-1.81	1.50	0.37	-0.59	-0.62
CGPLPA95	1.17	2.79	-3.30	-1.96	-0.64	-2.17	-2.28	1.26	-0.21	-2.36	-4.83	-1.45	0.17	0.09	1.35	3.93	0.84	-0.91	-4.27
CGST102	-0.90	0.29	0.50	1.13	2.39	1.56	1.60	-1.56	-2.04	-1.43	0.61	2.51	-1.77	-1.45	-1.09	-2.65	-0.48	-2.89	-0.17
CGST11	0.25	-0.17	1.48	0.21	0.14	-0.13	0.82	-1.31	-0.98	0.27	1.41	0.65	-1.05	-0.64	-1.05	-1.38	-0.73	-0.32	1.08
CGST110	0.14	-1.32	0.86	2.37	0.09	1.91	-0.10	0.25	-1.61	0.77	1.22	-0.63	-3.18	0.72	0.14	-2.38	0.13	-2.11	-1.07
CGST114	1.84	1.65	-0.03	-0.54	0.85	0.22	0.76	-1.43	-1.48	-0.35	-0.59	2.54	0.05	-1.50	-0.62	0.30	1.40	-0.71	0.35
CGST13	0.11	-2.36	-0.61	0.26	1.89	1.69	-1.23	0.38	-0.08	-0.27	-1.48	2.07	1.26	-0.27	-0.27	-0.35	-1.44	1.95	-1.10
CGST131	0.95	1.14	3.13	2.70	-0.64	1.39	1.14	-2.33	-2.39	-1.17	-0.64	3.93	-0.93	-2.58	-2.24	-2.13	-1.24	-2.92	0.81
CGST141	0.64	-0.28	-0.55	0.05	-0.43	1.19	0.07	0.56	-0.15	1.40	-0.72	0.06	-0.35	-0.68	0.26	0.33	0.22	0.32	1.43
CGST16	0.32	-1.46	-3.47	-0.62	3.85	-1.33	-2.90	0.79	0.35	-2.21	-3.52	1.76	-2.16	1.48	1.58	-0.52	-0.84	0.52	-2.41
CGST18	0.90	-0.75	0.74	-0.46	-0.09	0.05	1.54	-0.81	0.45	-1.49	-0.07	2.33	1.18	-1.74	-2.16	0.34	0.03	1.25	0.39
CGST21	-5.36	-8.70	-1.83	-0.92	11.09	-4.96	-1.49	-3.12	-6.49	1.14	-3.98	5.59	1.01	2.56	2.11	-8.91	-4.25	5.57	-3.64
CGST26	0.99	-1.34	1.48	2.79	1.22	1.34	0.96	-0.77	-2.27	-0.87	0.49	0.84	-0.86	-0.63	-0.73	-2.78	-3.02	-0.09	-0.87
CGST28	0.42	-0.42	0.36	0.33	0.01	-0.82	-0.44	-2.30	-3.65	-2.26	-0.62	-0.82	-2.39	-1.62	-1.40	5.73	4.11	-1.40	-2.29
CGST30	0.53	-1.87	1.92	5.82	-0.70	1.53	-0.04	-1.13	-2.34	-1.43	1.29	-1.47	-2.42	-0.57	-1.09	-2.11	-2.04	-1.94	-0.80
CGST32	-2.01	-0.17	2.31	8.22	-4.82	4.02	0.23	1.27	-3.39	-2.35	8.07	-6.06	-6.60	-1.25	-0.87	5.92	4.43	-3.01	-0.21
CGST33	-1.95	-1.20	2.32	2.42	0.61	0.10	0.35	-3.42	-4.79	0.03	3.08	3.38	-1.52	-0.90	-1.26	-0.87	1.72	-1.20	0.16
CGST38	-1.56	-3.15	1.96	2.74	4.50	1.77	1.30	-2.11	-1.98	-1.11	0.36	7.44	1.03	-2.22	-2.52	-2.71	-2.09	2.34	-1.40
CGST39	-1.51	-3.57	-1.69	-0.41	2.93	0.17	0.04	0.32	0.66	0.33	-1.09	3.15	0.95	0.32	0.39	-2.64	-2.09	2.09	-0.54
CGST41	-1.39	-2.94	-0.03	1.44	0.54	1.53	-0.91	0.48	-2.80	1.79	3.33	3.87	-1.39	-0.54	-0.14	-4.26	-1.92	-0.39	1.08
CGST45	-1.82	-3.29	-0.22	0.75	3.39	-0.28	-0.94	-0.63	-1.12	-0.22	-0.09	4.09	0.21	-0.06	-0.87	-2.76	-0.93	3.01	-0.17

CGST47	-1.61	-2.77	-0.59	-0.24	3.29	-0.51	0.42	-0.53	1.56	-0.83	0.48	4.02	1.54	-1.06	-1.41	-0.95	0.87	2.99	0.68
CGST48	5.19	-1.06	7.29	10.95	1.85	-6.77	-5.15	0.99	-6.29	-5.41	1.57	17.71	0.53	-2.09	-0.55	-2.32	2.44	-5.12	-4.20
CGST53	-3.70	-6.15	1.47	0.52	10.62	-1.00	-2.57	-2.35	-3.74	-2.12	-3.51	8.07	4.16	-1.11	-2.74	-7.39	-5.96	0.05	-2.83
CGST58	-3.50	-3.48	-0.17	0.83	0.93	-1.33	-1.12	1.08	-0.65	2.19	0.85	2.91	0.08	0.84	0.08	-2.94	-1.01	0.22	1.06
CGST67	-3.80	-3.95	2.49	2.42	0.89	-0.24	-0.05	-0.85	-2.36	0.71	-0.77	6.03	-0.98	0.32	-0.58	-3.98	-1.85	0.80	-0.03
CGST77	-2.96	-1.59	1.07	0.25	1.58	-1.87	-2.29	-0.05	-0.80	-2.00	-4.32	6.75	1.58	-0.08	-1.64	-2.17	-3.23	-0.13	-1.20
CGST80	-2.42	-4.30	0.79	1.77	3.38	0.75	1.45	-0.68	-0.64	0.02	1.22	3.50	-1.36	-0.63	-1.05	-0.05	1.88	0.17	1.34
CGST81	2.24	1.39	1.37	2.06	2.07	2.12	0.59	-1.77	-3.30	-1.50	0.66	-1.68	-1.08	-1.49	-1.58	1.44	-1.64	0.44	-0.37

Table 4.9. DELFI performance for cancer detection.

		Individuals analyzed	95% specificity		98% specificity	
			Individuals detected	Sensitivity	Individuals detected	Sensitivity
Healthy		215	10	-	4	-
Cancer		208	166	80%	152	73%
Type	Breast	54	38	70%	31	57%
	Bile duct	26	23	88%	21	81%
	Colorectal	27	22	81%	19	70%
	Gastric	27	22	81%	22	81%
	Lung	12	12	100%	12	100%
	Ovarian	28	25	89%	25	89%
	Pancreatic	34	24	71%	22	65%
Stage	I	41	30	73%	28	68%
	II	109	85	78%	78	72%
	III	33	30	91%	26	79%
	IV	22	18	82%	17	77%
	0, X	3	3	100%	3	100%

Table 4.10. DELFI tissue of origin prediction.

Cancer Type	Patients Detected*	Top Prediction		Top Two Predictions		Random Assignment	
		Patients	Accuracy (95% CI)	Patients	Accuracy (95% CI)	Patients	Accuracy
Breast	42	32	76% (61%-88%)	38	91% (77%-97%)	9	22%
Bile Duct	23	10	44% (23%-66%)	15	65% (43%-84%)	3	12%
Colorectal	24	17	71% (49%-87%)	19	79% (58%-93%)	3	12%
Gastric	24	16	67% (45%-84%)	19	79% (58%-93%)	3	12%
Lung	30	16	53% (34%-72%)	23	77% (58%-90%)	2	6%
Ovarian	27	13	48% (29%-68%)	16	59% (38%-78%)	4	14%
Pancreatic	24	12	50% (29%-71%)	16	67% (45%-84%)	3	12%
Total	194	116	61% (53%-67%)	146	75% (69%-81%)	26	13%

DISCUSSION

The three studies herein presented indicate the feasibility of novel liquid biopsy approaches in the cancer care continuum of patients with early- and late-stage cancers, adding value to the body of evidence that shows ctDNA analyses as a useful biomarker for early detection, minimal residual disease, and treatment response assessment.

Despite the success of targeted therapies for many cancers, durable responses eventually lead to progressive disease through the evolution of resistant clones. The standard approach for assessing treatment efficacy has been based on imaging measurement of tumor dimensions (70) which may not capture changes in clonal subpopulations and may be confounded by the tumor microenvironment. More recently, ctDNA methods have been used for disease monitoring, but these have largely been based on technologies that evaluate a limited number of genes or specific mutations and do not allow for evaluation of the dynamics of multiple tumor clones (20-22, 25-28).

In our first study, we have developed an approach for evaluating tumor burden through a cell-free tumor load measurement that incorporates both sequence changes across many driver genes as well as whole genome structural changes, allowing detection of tumor-related alterations in all patients analyzed. This effort addresses the value of comprehensive measurements of ctDNA within hours to days after targeted therapy initiation.

Through this approach we demonstrate that dynamic changes in plasma ctDNA after drug exposure may provide insights into clinical efficacy of targeted therapy. We observed a reduction of cell-free tumor load in patients with radiographic response and limited changes in ctDNA in non-responders after initiation of therapy. We also showed that patients with radiographic non-measurable disease and those with stable disease at first imaging evaluation can be more accurately classified using ctDNA analyses after TKI initiation. These examples reflect the utility of ctDNA for addressing current unmet clinical needs for real-time biomarkers of response and evolution of tumor burden. Although individual mutation analyses may miss specific subclones or may be

absent in individual patients, the integrated analysis of sequence and structural changes permitted evaluation of the majority of cases for cfTL changes. The tiered complementary approach has the benefit of incorporating sequence mutations in cfDNA that have both qualitative and quantitative characteristics in the type and level of detected alterations, while chromosomal changes add quantitative assessment of genome-wide alterations that are typically present in every cancer.

Despite the clinical utility of this approach, these analyses have a number of limitations. First, our genome-wide analyses were based on whole genome data at low coverage (<1x) and these could be improved in the future through deeper complementary sequencing. Additionally, the cohort analyzed in this study was small and may not reflect the full repertoire of the disease complexity of advanced NSCLC patients. Larger studies will be needed to validate these observations for patients with lung cancer treated with these and other targeted therapies, as well as for patients with other cancer types. Prospective trials with blood samples collected at regular intervals would allow for standardization of liquid biopsy analyses and for evaluation of responses to treatment compared to CT imaging.

Despite the value of multimodal curative treatment approaches, a significant fraction of patients will eventually perish as a consequence of locoregional relapse, peritoneal recurrence, or distant metastasis (40, 41). Current methods to estimate the risk of disease recurrence after surgery mostly rely on the assessment of pathological staging and microscopic residual disease score systems (44-46). However, there are several limitations with these approaches, especially with tumor regression grading scales, that make their implementation difficult in daily clinical practice, including interobserver variability and lack of standardization. Furthermore, the poor sensitivity of currently available imaging methods and blood protein biomarkers to detect remaining disease after curative surgery has provided an opportunity for ctDNA analyses for minimal residual disease assessment in gastric cancer.

In our second study, we have developed a tissue-independent sequencing approach using ultrasensitive sequencing of matched cfDNA and white blood cells to detect tumor-specific mutations in cfDNA after completion of preoperative chemotherapy as well as after surgery in patients with resectable gastric cancer.

To our knowledge, this is the first study to investigate the value of parallel deep sequencing of cfDNA and WBCs to detect cfDNA alterations associated with clonal hematopoiesis in the circulation and to use this approach to longitudinally identify bona fide tumor-specific alterations. This approach allows direct identification of ctDNA without requiring tumor tissue, which is often available to a limited extent and where sequencing analyses may be hampered by intra-tumoral heterogeneity. We observed that plasma samples from patients with Lauren's intestinal subtype were associated with higher mutant allele fractions when compared with patients with diffuse subtype tumors. Further work will be needed to determine if intracellular mucin, stromal reaction, vascular density, or other pathological features in diffuse carcinomas play a role in determining lower levels of ctDNA alterations in the blood.

A major challenge for the development of MRD assays using noninvasive liquid biopsies is distinguishing tumor-specific mutations from background changes associated with biological variation. The vast majority of cfDNA in healthy individuals arises from hematopoietic cells (95). Normal ageing is associated with the accumulation of somatic mutations in bone marrow-derived hematopoietic cells in the form of CHIP in asymptomatic individuals (35). WBC-derived alterations that arise as a consequence of CHIP may confound liquid biopsy analyses that are based on characterization of cfDNA as these may occur in common cancer driver genes, as observed with hotspot alterations in *TP53* and *KRAS* (96). As we have shown in our cohort of 50 patients, cfDNA analyses without WBC filters would have been unable to appropriately identify patients that benefit from perioperative treatment in terms of event-free and overall survival.

Finally, in our third study, we have determined that genome-wide cfDNA fragmentation profiles are different between cancer patients and healthy individuals. The variability in fragment lengths and coverage in a position dependent manner throughout the genome may explain the apparently contradictory observations of previous analyses of cfDNA at specific loci or of overall fragment sizes. In patients with cancer, heterogeneous fragmentation patterns in cfDNA appear to be a result of mixtures of nucleosomal DNA from both blood and neoplastic cells. Despite these encouraging results, our approach can be improved in the future, including through recovery of smaller cfDNA fragments (<100 bp) (64, 97), evaluation of single-stranded libraries (65, 98, 99), or use of alternative sequencing technologies. Additionally, generation of libraries without the use of PCR could reduce GC bias and potential sequence and structural artifacts.

Although analyses of a larger numbers of individuals will be needed to validate this approach for clinical use, these observations already have important implications for future research and applications of non-invasive approaches for detection of human cancer. First, these studies provide a method for simultaneous analysis of tens to potentially hundreds of tumor-specific abnormalities from minute amounts of cfDNA, overcoming a limitation that has precluded the possibility of more sensitive analyses of cfDNA. DELFI analyses detected a higher fraction of cancer patients than previous cfDNA analysis methods that have focused on sequence or overall fragmentation sizes.

As we have shown, combining DELFI with analyses of other cfDNA alterations may further increase the sensitivity of detection. Second, as fragmentation profiles appear related to nucleosomal DNA patterns, DELFI may be useful for determining the primary source of tumor-derived cfDNA. Our identification of the source of circulating tumor DNA in over half of patients analyzed may be further improved by including clinical characteristics, other biomarkers, including methylation changes (100), and additional diagnostic approaches (15, 54).

In summary, these studies provide a new paradigm for the use of liquid biopsy approaches in the management of patients with cancer. In late-stage disease, longitudinal ctDNA assessment in patients receiving systemic treatment may be helpful for the development of new molecular response criteria and to provide insight into survival outcomes. In patients with localized cancer treated with perioperative chemotherapy, tissue-independent approaches designed to detect tumor-specific cfDNA alterations can be applied to early risk stratification. Finally, cfDNA fragmentation analyses may be used to detect early-stage cancers and identify their tissue of origin. Overall, the results of these analyses highlight the clinical value of ctDNA as a biomarker in the cancer care continuum, providing evidence for treatment response assessment, detection of minimal residual disease, and cancer screening. Future larger studies are warranted to validate our study findinds.

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Peer-reviewed publications:

Leal A*, van Grieken NCT*, Palsgrove DN, Phallen J, Medina JE, Hruban C, Broeckaert MAM, Anagnostou V, Adleff V, Bruhm DC, Canzoniero J, Fiksel J, Warmerdam FARM, Verheul HMW, van Spronsen DJ, Beerepoot LV, Geenen MM, Portielje JEA, , Jansen EPM, van Sandick J, Kranenbarg EM, van Laarhoven HWM, van der Peet DL, van de Velde CJH, Verheij M, Fijneman R, Scharpf RB, Meijer G, Cats A, Velculescu VE. Matched white-blood cell and cell-free DNA analyses for detection of circulating tumor DNA and minimal residual disease in patients with gastric cancer. *Submitted*, 2019. *Equal contribution

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Anagnostou V, Forde P, Naidoo J, Marrone K, White J, Sivakumar A, Smith K, Phallen J, **Leal A**, Adleff V, Rhymee L, Hruban C, Hann C, Levy B, Cottrell T, Georgiades C, Verde F, Illei P, Li QK, Gabrielson E,

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Garicochea B*, **Leal AIC***, Ferreira FSB, Villela VAL, Sartorelli AC, Novis Y, Hoff PM. Angioimmunoblastic T-cell lymphoma: clinical aspects and recent advances in biology and therapy. *Journal of Analytical Oncology*, 2014; 3:191-200. *Equal contribution

Abstracts at Scientific Meetings:

Leal A, Cristiano S, Phallen J, Fiksel J, et al. Genome-wide cell-free DNA fragmentation profiling for early cancer detection. Poster presentation at 2019 ASCO annual meeting, Chicago, IL, June, 2019. Abstract number: 3018 (Merit Award Recipient)

Leal A, van Grieken N, Phallen J, et al. Circulating Tumor DNA dynamics in operable gastric cancer. Poster presentation at 2018 ASCO annual meeting. Chicago, IL, June, 2018. Abstract number: 4069

Phallen J, **Leal A**, Woodward B, Forde P, et al. Early noninvasive prediction of response to targeted therapy in non-small cell lung cancer. Poster presented at 2018 AACR annual meeting. Chicago, IL, May, 2018. Abstract number: 4596

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Leal AIC, Barra WF, Saragiotto DF, Saad ED, Hoff PM. Publication bias in randomized controlled trials (RCTs) of colorectal cancer. Poster presentation at 2010 ASCO annual meeting. Chicago, IL, June, 2010. J Clin Oncol 28:15s, 2010 (suppl; abstr 6116)

US Patent Applications

62/673,516	Cell-free DNA for assessing and/or treating cancer
62/657,618	Non-invasive detection of response to a targeted therapy